

RESULT 717

AAV01603/c  
ID AAV01603 standard; DNA; 15 BP.

XX AC AAV01603;

XX DT 25-MAR-2003 (updated)

XX DT 31-MAR-1998 (first entry)

XX DE Oligonucleotide containing phosphoramidate linkages.

XX KW phosphoramidate linkage; solid phase synthesis; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc\_feature 1..15

XX FT /tag= a

XX FT /note= "these residues have N3'--&gt;P5' phosphoramidate linkages"

XX PN WO9731009-A1.

XX PD 28-AUG-1997.

XX PF 14-JUN-1996; 96WO-US10418.

XX PR 21-FEB-1996; 96US-0603566.

XX PR 21-FEB-1996; 96US-0603566.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Fearon KL, Gryaznov SM, Hirschbein BL, McCurdy SN;

XX PI Nelson JS, Schultz RG;

XX DR WPI; 1997-435080/40.

XX PT Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidate then oxidation, useful as research, diagnostic and therapeutic agents

XX PS Disclosure; Page 28; 60pp; English.

XX CC A new method is provided for the synthesis of oligonucleotides having N3'-->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected amino nucleoside to a solid support; (b) deprotecting the 3'-amino; (c) reacting with a 3'-protected aminonucleoside-5'-phosphoramidate monomer to form an internucleoside N3'-->P5' phosphoramidate link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b)-(d) until the required oligonucleotide is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large scale. The obtained oligos, containing phosphoramidate linkages, have favourable binding properties, nuclease resistance and solubility, and are useful as research, diagnostic and therapeutic agents. The present sequence is an example of an oligonucleotide in which N3'-->P5' phosphoramidate linkages have been introduced by the new method. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098

Db 15 AAAAAAAAAAAAAA 1

RESULT 718

AAV01604

ID AAV01604 standard; DNA; 15 BP.

XX AC AAV01604;

XX DT 25-MAR-2003 (updated)

XX DT 31-MAR-1998 (first entry)

XX DE Oligonucleotide containing phosphoramidate linkages.

XX KW phosphoramidate linkage; solid phase synthesis; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc\_feature 1..15

XX FT /tag= a

XX FT /note= "these residues have N3'--&gt;P5' phosphoramidate linkages"

XX PN WO9731009-A1.

XX PD 28-AUG-1997.

XX PF 14-JUN-1996; 96WO-US10418.

XX PR 21-FEB-1996; 96US-0603566.

XX PR 21-FEB-1996; 96US-0603566.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Fearon KL, Gryaznov SM, Hirschbein BL, McCurdy SN;

XX PI Nelson JS, Schultz RG;

XX DR WPI; 1997-435080/40.

XX PT Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidate then oxidation, useful as research, diagnostic and therapeutic agents

XX PS Disclosure; Page 28; 60pp; English.

XX CC A new method is provided for the synthesis of oligonucleotides having N3'-->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected amino nucleoside to a solid support; (b) deprotecting the 3'-amino; (c) reacting with a 3'-protected aminonucleoside-5'-phosphoramidate monomer to form an internucleoside N3'-->P5' phosphoramidate link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b)-(d) until the required oligonucleotide is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large scale. The obtained oligos, containing phosphoramidate linkages, have favourable binding properties, nuclease resistance and solubility, and are useful as research, diagnostic and therapeutic agents. The present sequence is an example of an oligonucleotide in which N3'-->P5' phosphoramidate linkages have been introduced by the new method. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098

Db 1 AAAAAAAAAAAAAA 15

RESULT 719

AAV07431/c

ID AAV07431 standard; DNA; 15 BP.

XX

AC AAV07431;  
 XX 27-OCT-1998 (first entry)  
 XX Synthetic peptide-labeled oligonucleotide primer.  
 DE oligonucleotide; peptide; conjugate; release tag compound;  
 KW mass spectrometry; detection; identification; diagnosis; primer; ss.  
 XX Synthetic.  
 OS  
 XX WO9826095-A1.  
 PN 18-JUN-1998.  
 XX 10-DEC-1997; 97WO-US22639.  
 XX 16-MAY-1997; 97US-0046719.  
 PR 10-DEC-1996; 96US-0033037.  
 XX (GENE-) GENETRACE SYSTEMS INC.  
 PA Becker CH, Montforte JA, Pollart DJ, Shaler TA;  
 XX WPI; 1998-348547/30.  
 XX  
 XX New release tag compounds for detecting target molecule(s) -  
 PT comprising a reactive group, a release group and a releasable  
 PT non-volatile mass label detectable by mass spectrometry  
 XX  
 PS Example 3; Page 92; 170pp; English.  
 XX  
 CC The sequence is that of an oligonucleotide primer which was produced  
 CC as part of an oligonucleotide peptide conjugate as an example of  
 CC a release tag compound (RTC). These comprise a reactive group, a  
 CC release group and a non-volatile mass label comprising a  
 CC synthetic polymer or biopolymer detectable by mass spectrometry.  
 CC The RTCs can be used as probes for the detection of TMs.  
 CC They can be used for e.g. identification of gene sequences,  
 CC identification of non-coding nucleotide sequences, identification of  
 CC mutations within a gene or protein sequence, detection of metals,  
 CC characterisation of receptors on an organism or a cell,  
 CC interactions of antibody-antigen interactions, enzyme-substrate  
 CC applications and characterisation of ligand interactions. Multiplex  
 CC polymorphism screening, single nucleotide polymorphism (SNP)  
 CC genotyping, clone and gene mapping, and gene expression analysis.  
 CC The RTCs permit the ready detection of releasable mass labels by  
 CC mass spectroscopy. The releasable mass labels permit the multiplexing  
 CC of tens, hundreds and perhaps even thousands of different mass labels  
 CC that can be used to uniquely identify each desired target.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 720  
 AAT86605/c  
 ID AAT86605 standard; DNA; 15 BP.  
 XX  
 AC AAT86605;  
 XX  
 XX 04-JUN-1998 (first entry)  
 DE Oligonucleotide separated by capillary affinity gel electrophoresis.  
 XX

KW Capillary affinity gel electrophoresis; separation; polymer-gel;  
 KW polyacrylamide; ss.  
 XX Synthetic.  
 XX WO9745721-A1.  
 PN 04-DEC-1997.  
 XX 23-MAY-1997; 97WO-EP02647.  
 XX 24-MAY-1996; 96CH-0001320.  
 PR (NOVS ) NOVARTIS AG.  
 PA Muscate A, Matt F, Paulus A;  
 PI WPI; 1998-041763/04.  
 XX Separation of electrically charged target molecules - by capillary  
 PT affinity gel electrophoresis using polymer-gel to which receptors  
 PT for target molecules are bound  
 XX  
 PS Example D3; Page 25; 41pp; English.  
 XX  
 CC A mixture of oligonucleotides (AAT86604-7) were separated by a new  
 CC process using capillary affinity gel electrophoresis. The invention  
 CC relates to selective separation of electrically charged target molecules  
 CC in an analytical mixture. It comprises capillary affinity gel  
 CC electrophoresis using a capillary tube which is at least partly filled  
 CC with a polymer gel. Receptors for target molecules are covalently bound  
 CC to the polymer. An electric field of at least 50 volts/cm is applied.  
 CC The capillary tube is charged with the analytical mixture. In a first  
 CC separation stage, the target molecules in the mixture are bound to the  
 CC receptors and the remaining components are eluted, optionally whilst  
 CC splitting open. In a second stage, the elution conditions are changed,  
 CC the receptor is eliminated and the target molecules are eluted and  
 CC detected, optionally whilst splitting open. The process is useful for  
 CC selective separation and/or determination of charged organic compounds,  
 CC such as oligonucleotides, peptides or carbohydrates. It may be used,  
 CC e.g. for isolation of specific proteins and DNA molecules, purification  
 CC of antibodies, analysis of antisense compounds or screening for enzyme  
 CC inhibitors. The process achieves higher resolution and selectivity  
 CC than prior art processes, especially in the case of complex biological  
 CC analytical mixtures. It has high sensitivity, even with small amounts of  
 CC samples. The derivatised polymers may be synthesised specifically using  
 CC standard methods.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 721  
 AAT86675/c  
 ID AAT86675 standard; DNA; 15 BP.  
 XX  
 AC AAT86675;  
 XX  
 XX 04-JUN-1998 (first entry)  
 DE Oligonucleotide linked to polyacrylamide.  
 XX  
 KW Capillary affinity gel electrophoresis; separation; polymer-gel;  
 KW polyacrylamide; ss.  
 XX

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OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1
XX /tag= a
XX /note= "Thymine at 5' end attached to a polyacrylamide
XX gel via a linking group"
XX WO9745721-A1.
XX 04-DEC-1997.
XX 23-MAY-1997; 97WO-EF02647.
XX 24-MAY-1996; 96CH-0001320.
XX (NOVS ) NOVARTIS AG.
XX Muscate A, Natt F, Paulus A;
XX WPI; 1998-041763/04.
XX Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors
XX for target molecules are bound
XX Example A1; Page 22; 41pp; English.
XX This sequence represents an oligonucleotide receptor molecule covalently
XX bound to a polyacrylamide gel via a linking group. The invention relates
XX to selective separation of electrically charged target molecules in an
XX analytical mixture. It comprises capillary affinity gel electrophoresis
XX using a capillary tube which is at least partly filled with a polymer
XX gel. Receptors for target molecules are covalently bound to the
XX polymer. An electric field of at least 50 volts/cm is applied. The
XX capillary tube is charged with the analytical mixture. In a first
XX separation stage, the target molecules in the mixture are bound to the
XX receptors and the remaining components are eluted, optionally whilst
XX splitting open. In a second stage, the elution conditions are changed,
XX optionally in stages, so that the affinity of the target molecules for
XX the receptor is eliminated and the target molecules are eluted and
XX detected, optionally whilst splitting open. The process is useful for
XX selective separation and/or determination of charged organic compounds,
XX such as oligonucleotides, peptides or carbohydrates. It may be used,
XX e.g. for isolation of specific proteins and DNA molecules, purification
XX of antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity
XX than prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods.
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
RESULT 722
AAAX00787/c
ID AAX00787 standard; DNA; 15 BP.
XX
XX AAX00787;
XX
XX 13-APR-1999 (first entry)
XX N3-P5 phosphoramidate oligonucleotide #3.
XX

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KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
XX misc_difference 1..15
XX /tag= a
XX /note= "contains internucleotide N3-P5 phosphoramidate
XX internucleotide linkages"
XX US5859233-A.
XX 12-JAN-1999.
XX 20-DEC-1996; 96US-0771789.
XX 20-DEC-1996; 96US-0771789.
XX 21-FEB-1996; 96US-0603566.
XX 14-JUN-1996; 96US-0663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX Fearon KL, Gryaznov SM, Hirschbein BL, McCurdy SN;
XX Nelson JS, Schultz RG;
XX WPI; 1999-120007/10.
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers -
XX used in the synthesis of oligo-nucleotide(s)
XX Example 10; Column 33; 34pp; English.
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a
XX 5'-phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
RESULT 723
AAAX00788
ID AAX00788 standard; DNA; 15 BP.
XX
XX AAX00788;
XX
XX 13-APR-1999 (first entry)
XX N3-P5 phosphoramidate oligonucleotide #4.
XX
XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
XX misc_difference 1..15
XX /tag= a
XX /note= "contains internucleotide N3-P5 phosphoramidate
XX internucleotide linkages"
XX US5859233-A.

```

XX 12-JAN-1999.  
PD 20-DEC-1996; 96US-0771789.  
XX  
XX 20-DEC-1996; 96US-0771789.  
PR 21-FEB-1996; 96US-0603566.  
PR 14-JUN-1996; 96US-0663918.  
XX  
XX (LYNX-) LYNX THERAPEUTICS INC.  
PA  
XX Pearson KL, Gryaznov SM, Hirschbein BL, McCurdy SN;  
PI Nelson JS, Schultz RG;  
XX  
XX WPI; 1999-120007/10.  
XX  
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers  
PT used in the synthesis of oligo-nucleotide(s)  
PT  
XX Example 10; Column 33; 34pp; English.  
PS  
XX This sequence represents an example of an oligonucleotide containing  
CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The  
CC sequence is generated synthetically by using an amine-exchange reaction  
CC of phosphoramidites in which a deprotected 3'-amino group of an  
CC oligonucleotide chain is exchanged for the amino portion of a  
CC 5'-phosphoramidite with a protected 3' amino group. The resulting  
CC phosphoramidite internucleotide linkage is oxidized to form a stable  
CC protected phosphoramidate linkage.  
XX  
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
DB 1 AAAAAAAAAAAAAA 15  
RESULT 724  
AAA75048/c  
ID AAA75048 standard; DNA; 15 BP.  
XX  
AC AAA75048;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
DE Primer used to reverse transcribe human RNA.  
XX  
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;  
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;  
KW wound healing; infection; burn; angiogenesis; restenosis;  
KW atherosclerosis; inflammation; neurodegenerative disease;  
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; prion; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200052178-A1.  
PN  
XX  
PD 08-SEP-2000.  
XX  
PF 14-FEB-2000; 2000WO-US03542.  
XX  
XX 01-MAR-1999; 99US-0258892.  
XX  
XX (INST-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA (FRIE/) FRIEDMAN M M.  
XX  
PI Pecker I, Vlodavsky I, Feinstein E;  
XX

DR WPI; 2000-579289/54.  
XX  
PT New polynucleotides encoding a polypeptide having heparanase activity,  
PT useful in wound healing and in gene therapy, particularly in treating  
PT tumour, inflammation, autoimmunity, neurodegenerative diseases  
XX  
XX Disclosure; Page 44; 152pp; English.  
XX  
XX The present primer was used to reverse transcribe human RNA, from  
CC which a cDNA sequence encoding a protein with heparanase catalytic  
CC activity was amplified. The heparanase (hpa) polynucleotide is useful  
CC in gene therapy, particularly in treating tumour, inflammation or  
CC autoimmunity. Particularly, the polynucleotide is useful in modulating  
CC the bioavailability of heparin-binding growth factors, cellular responses  
CC to heparin-binding growth factors (e.g. bFGF) and cytokines  
CC (e.g. interleukin (IL)-8), cell interaction with plasma lipoproteins,  
CC cellular susceptibility to certain viral and some bacterial and protozoa  
CC infections, or disintegration of neurodegenerative plaques. The  
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical  
CC or radiation burns), and in the treatment of angiogenesis, restenosis,  
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-  
CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,  
CC bacterial or protozoa infections.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
DB 15 AAAAAAAAAAAAAA 1  
RESULT 725  
AAA62347/c  
ID AAA62347 standard; DNA; 15 BP.  
XX  
AC AAA62347;  
XX  
DT 06-NOV-2000 (first entry)  
XX  
XX Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.  
DE Conformationally-locked oligonucleotide; antisense inhibitor;  
KW bicyclic sugar nucleoside analogue; gene probe; ds.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 3  
FT /\*tag= b  
FT /\*mod\_base= OTHER  
FT /\*note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 5  
FT /\*tag= c  
FT /\*mod\_base= OTHER  
FT /\*note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 9  
FT /\*tag= d  
FT /\*mod\_base= OTHER  
FT /\*note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 11  
FT /\*tag= e  
FT /\*mod\_base= OTHER  
FT /\*note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 13  
FT /\*tag= f  
FT



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FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      modified_base
FT      15
FT      /*tag=
FT      g
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      XX
FT      PN      US083482-A.
FT      XX
FT      PD      04-JUL-2000.
FT      XX
FT      PF      11-MAY-1999; 99US-0309742.
FT      XX
FT      PR      11-MAY-1999; 99US-0309742.
FT      XX
FT      PA      (ICNC ) ICN PHARM INC.
FT      XX
FT      PI      Wang G;
FT      XX
FT      DR      WPI; 2000-451496/39.
FT      XX
FT      PT      New conformationally restricted 3',5'-bridged nucleosides and
FT      oligonucleotides useful as antisense therapeutics or as gene-specific
FT      diagnostics -
FT      XX
FT      PS      Example 20; Column 15; 10pp; English.
FT      XX
FT      CC      The present sequence is an oligonucleotide containing
FT      3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside.
FT      CC      All nucleotides in the sequence were incorporated by phosphoramidite
FT      CC      chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are
FT      CC      conformationally restricted 3',5'-bridged nucleosides which can be used
FT      CC      as building blocks for oligonucleotides. Oligonucleotides can be
FT      CC      produced that have certain, desired, geometrical shapes and entropy
FT      CC      advantages. They may have superior hybridisation to DNA and RNA, and
FT      CC      excellent biological stability. The conformationally-modified
FT      CC      oligonucleotides may be useful as antisense inhibitors of gene expression
FT      CC      or as gene probes, and may therefore be used in antisense therapeutics or
FT      CC      gene-specific diagnostics.
FT      XX
FT      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
FT
FT      Query Match      1.4%; Score 15; DB 1; Length 15;
FT      Best Local Similarity 100.0%; Pred. No. 3.5e+02;
FT      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT      Qy      1084 AAAAAAAAAAAAAA 1098
FT      Db      15 AAAAAAAAAAAAAA 1
FT
FT      RESULT 726
FT      AAA62348/C
FT      ID      AAA62348 standard; DNA; 15 BP.
FT      AC
FT      AC      AAA62348;
FT      XX
FT      DT      06-NOV-2000 (first entry)
FT      XX
FT      DE      Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
FT      XX      Conformationally-locked oligonucleotide; antisense inhibitor;
FT      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
FT      XX      Synthetic.
FT      XX
FT      FH      Key      Location/Qualifiers
FT      modified_base      7
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      modified_base      9
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      PN      US083482-A.

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FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT      XX
FT      PN      US083482-A.
FT      XX
FT      PD      04-JUL-2000.
FT      XX
FT      PF      11-MAY-1999; 99US-0309742.
FT      XX
FT      PR      11-MAY-1999; 99US-0309742.
FT      XX
FT      PA      (ICNC ) ICN PHARM INC.
FT      XX
FT      PI      Wang G;
FT      XX
FT      DR      WPI; 2000-451496/39.
FT      XX
FT      PT      New conformationally restricted 3',5'-bridged nucleosides and
FT      oligonucleotides useful as antisense therapeutics or as gene-specific
FT      diagnostics -
FT      XX
FT      PS      Example 20; Column 15; 10pp; English.
FT      XX
FT      CC      The present sequence is an oligonucleotide containing
FT      3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside.
FT      CC      All nucleotides in the sequence were incorporated by phosphoramidite
FT      CC      chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are
FT      CC      conformationally restricted 3',5'-bridged nucleosides which can be used
FT      CC      as building blocks for oligonucleotides. Oligonucleotides can be
FT      CC      produced that have certain, desired, geometrical shapes and entropy
FT      CC      advantages. They may have superior hybridisation to DNA and RNA, and
FT      CC      excellent biological stability. The conformationally-modified
FT      CC      oligonucleotides may be useful as antisense inhibitors of gene expression
FT      CC      or as gene probes, and may therefore be used in antisense therapeutics or
FT      CC      gene-specific diagnostics.
FT      XX
FT      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
FT
FT      Query Match      1.4%; Score 15; DB 1; Length 15;
FT      Best Local Similarity 100.0%; Pred. No. 3.5e+02;
FT      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT      Qy      1084 AAAAAAAAAAAAAA 1098
FT      Db      15 AAAAAAAAAAAAAA 1
FT
FT      RESULT 727
FT      AAA62350/C
FT      ID      AAA62350 standard; DNA; 15 BP.
FT      AC
FT      AC      AAA62350;
FT      XX
FT      DT      06-NOV-2000 (first entry)
FT      XX
FT      DE      Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
FT      XX      Conformationally-locked oligonucleotide; antisense inhibitor;
FT      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
FT      XX      Synthetic.
FT      XX
FT      FH      Key      Location/Qualifiers
FT      modified_base      7
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT      modified_base      9
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT      PN      US083482-A.

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XX PD 04-JUL-2000.  
 XX PF 11-MAY-1999; 99US-0309742.  
 XX PR 11-MAY-1999; 99US-0309742.  
 XX PA (ICNC) ICN PHARM INC.  
 XX PI Wang G;  
 XX DR WPI; 2000-451496/39.  
 XX PT New conformationally restricted 3',5'-bridged nucleosides and  
 PT oligonucleotides useful as antisense therapeutics or as gene-specific  
 PT diagnostics -  
 XX PS Example 20; Column 16; 10pp; English.  
 XX CC The present sequence is an oligonucleotide containing  
 CC 3'-C-amino-5'(S)-C,3'-N-ethanochymidine, a bicyclic-sugar nucleoside.  
 CC All nucleotides in the sequence were incorporated by phosphoramidite  
 CC chemistry using a DNA synthesizer. Bicyclic sugar nucleosides are  
 CC conformationally restricted 3',5'-bridged nucleosides which can be used  
 CC as building blocks for oligonucleotides. Oligonucleotides can be  
 CC produced that have certain, desired, geometrical shapes and entropy  
 CC advantages. They may have superior hybridisation to DNA and RNA, and  
 CC excellent biological stability. The conformationally-modified  
 CC oligonucleotides may be useful as antisense inhibitors of gene expression  
 CC or as gene probes, and may therefore be used in antisense therapeutics or  
 CC gene-specific diagnostics.  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 728  
 AAA46502/c  
 ID AAA46502 standard; cDNA; 15 BP.  
 XX AC AAA46502;  
 XX DT 04-SEP-2000 (first entry)  
 XX DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.  
 XX KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;  
 XX KW PCR primer; ss.  
 XX OS Coffea arabica.  
 XX PN WO200028046-A1.  
 XX PD 18-MAY-2000.  
 XX PF 28-OCT-1999; 99WO-EF08314.  
 XX PR 11-NOV-1998; 98EP-0203742.  
 XX (NEST) SOC PROD NESTLE SA.  
 XX PA Marraccini P, Rogers J;  
 XX PI WPI; 2000-399535/34.  
 XX DR New DNA encoding endo-beta-mannanase from coffee, used e.g. in

PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans  
 PT -  
 XX Disclosure; Page 32; 41pp; French.  
 XX PCR primers AAA46501-02 were used to amplify DNA encoding an  
 CC endo-beta-mannanase enzyme, which is involved in the hydrolysis of  
 CC polysaccharides that consist of molecules of mannan, either simple  
 CC or branched, linked together by beta(1-4) bonds. The mannanase  
 CC polynucleotide sequence is used for in vivo modification  
 CC of the coffee endo-beta-mannanase gene. It is also used to produce  
 CC transgenic plant cells (especially coffee cells) which have modified  
 CC properties of mannan polysaccharide, and thus altered flavour or  
 CC structure. The enzyme is used for modification, degradation or synthesis  
 CC of mannan polysaccharides in vitro, particularly to treat coffee beans  
 CC to increase the percentage of dry matter extraction, and thus reduce the  
 CC quantity of sediment.  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 729  
 AAA07788/c  
 ID AAA07788 standard; DNA; 15 BP.  
 XX AC AAA07788;  
 XX DT 23-JUN-2000 (first entry)  
 XX DE Nucleic acid sequence of ODN-a.  
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 XX KW viral infection; inflammatory response; cellular proliferation;  
 XX KW psoriasis; duplex; ss.  
 XX OS Synthetic.  
 XX PN WO200011013-A1.  
 XX PD 02-MAR-2000.  
 XX PF 20-AUG-1999; 99WO-US19029.  
 XX PR 22-AUG-1998; 98US-0097712.  
 XX (UYNE-) UNIV NEBRASKA.  
 XX PA Gold B;  
 XX PI WPI; 2000-246530/21.  
 XX PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics -  
 XX Disclosure; Page 20; 42pp; English.  
 XX The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation,  
 CC antisense technology, diagnostic applications to detect target sequences  
 CC in biological samples such as those containing pathogenic bacteria,

CC fungi and viruses, oncogenes, growth hormones and enzymes, to target  
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,  
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth  
 CC factors and interleukins associated with pathological conditions such as  
 CC inflammatory conditions, cardiovascular disorders, immune reactions,  
 CC cancer, viral infections and bacterial infections (see AAA07786 for  
 CC details of other uses for which the oligomers are suitable for).  
 CC Oligomers comprising the nucleomonomers exhibit increased duplex DNA  
 CC stability when hybridizing to target nucleic acid sequences, are  
 CC physiologically stable, non-toxic and able to penetrate into cells while  
 CC maintaining stringent base pair fidelity for target DNA sequences. The  
 CC oligomers demonstrate significant single- or double-stranded target  
 CC nucleic acid binding activity to form duplexes, triplexes or other forms  
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.

XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 730  
 AAA07789/C  
 ID AAA07789 standard; DNA; 15 BP.  
 XX  
 AC AAA07789;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-b.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US19029.  
 XX  
 PR 22-AUG-1998; 98US-0097712.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 XX  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics -  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation.  
 CC antisense technology, diagnostic applications to detect target sequences  
 CC in biological samples such as those containing pathogenic bacteria,  
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target  
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,  
 CC

CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth  
 CC factors and interleukins associated with pathological conditions such as  
 CC inflammatory conditions, cardiovascular disorders, immune reactions,  
 CC cancer, viral infections and bacterial infections (see AAA07786 for  
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 CC maintaining stringent base pair fidelity for target DNA sequences. The  
 CC oligomers demonstrate significant single- or double-stranded target  
 CC nucleic acid binding activity to form duplexes, triplexes or other forms  
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.

XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 731  
 AAA07790/C  
 ID AAA07790 standard; DNA; 15 BP.  
 XX  
 AC AAA07790;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-c.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US19029.  
 XX  
 PR 22-AUG-1998; 98US-0097712.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 XX  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics -  
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 XX  
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 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
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 CC infected cells. They are used in oligomers for gene regulation.  
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 CC in biological samples such as those containing pathogenic bacteria,  
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target  
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 CC oligomers demonstrate significant single- or double-stranded target  
 CC nucleic acid binding activity to form duplexes, triplexes or other forms  
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;  
 SQ Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 732  
 AAA07791/C  
 ID AAA07791 standard; DNA; 15 BP.  
 XX AC AAA07791;  
 DT 23-JUN-2000 (first entry)  
 XX DE Nucleic acid sequence of ODN-d.  
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 XX KW viral infection; inflammatory response; cellular proliferation;  
 XX KW psoriasis; duplex; ss.  
 XX OS Synthetic.  
 XX PN WO200011013-A1.  
 XX PD 02-MAR-2000.  
 XX PF 20-AUG-1999; 99WO-US19029.  
 XX PR 22-AUG-1998; 98US-0097712.  
 XX PA (UYNE-) UNIV NEBRASKA.  
 XX PI Gold B;  
 XX DR WPI; 2000-246530/21.  
 XX PT Modified nucleomonomers, used in physiologically stable, non-toxic  
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 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation,  
 CC antisense technology, diagnostic applications to detect target sequences  
 CC in biological samples such as those containing pathogenic bacteria,  
 CC fungi and viruses, oncogenes, growth hormones and enzymes, to target  
 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,  
 CC adhesion molecules, receptor molecules, cytokines, oncogenes, growth  
 CC factors and interleukins associated with pathological conditions such as  
 CC cancer, viral infections and bacterial infections (see AAA07786 for  
 CC details of other uses for which the oligomers are suitable for).

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 CC stability when hybridizing to target nucleic acid sequences, are  
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 CC oligomers demonstrate significant single- or double-stranded target  
 CC nucleic acid binding activity to form duplexes, triplexes or other forms  
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;  
 SQ Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 733  
 AAA07792/C  
 ID AAA07792 standard; DNA; 15 BP.  
 XX AC AAA07792;  
 DT 23-JUN-2000 (first entry)  
 XX DE Nucleic acid sequence of ODN-e.  
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 XX KW viral infection; inflammatory response; cellular proliferation;  
 XX KW psoriasis; duplex; ss.  
 XX OS Synthetic.  
 XX PN WO200011013-A1.  
 XX PD 02-MAR-2000.  
 XX PF 20-AUG-1999; 99WO-US19029.  
 XX PR 22-AUG-1998; 98US-0097712.  
 XX PA (UYNE-) UNIV NEBRASKA.  
 XX PI Gold B;  
 XX DR WPI; 2000-246530/21.  
 XX PT Modified nucleomonomers, used in physiologically stable, non-toxic  
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CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
CC forming a third strand along with the duplex sequences.  
XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Db 15 AAAAAAAAAAAAAA 1

RESULT 734  
AAA07793/c  
ID AAA07793 standard; DNA; 15 BP.

XX AC AAA07793;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-f.

XX KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;  
XX KW viral infection; inflammatory response; cellular proliferation;  
XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX PN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US19029.

XX PR 22-AUG-1998; 98US-0097712.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX WPI; 2000-246530/21.

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CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
CC forming a third strand along with the duplex sequences.  
XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Db 15 AAAAAAAAAAAAAA 1

RESULT 735  
AAA07794/c  
ID AAA07794 standard; DNA; 15 BP.

XX AC AAA07794;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-g.

XX KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;  
XX KW viral infection; inflammatory response; cellular proliferation;  
XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX PN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US19029.

XX PR 22-AUG-1998; 98US-0097712.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

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XX oligomers demonstrate significant single- or double-stranded target

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CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
    Query Match      1.4%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 3.5e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1084 AAAAAAAAAAAAAA 1098
    Db 15 AAAAAAAAAAAAAA 1

RESULT 736
AAA07795/C
ID AAA07795 standard; DNA; 15 BP.
XX
AC AAA07795;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-h.
XX
KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US19029.
XX
PR 22-AUG-1998; 98US-0097712.
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PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
WPI; 2000-246530/21.
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CC oligomers demonstrate significant single- or double-stranded target
CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX
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```
CC forming a third strand along with the duplex sequences.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
    Query Match      1.4%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 3.5e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1084 AAAAAAAAAAAAAA 1098
    Db 15 AAAAAAAAAAAAAA 1

RESULT 737
AAA07796/C
ID AAA07796 standard; DNA; 15 BP.
XX
AC AAA07796;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-i.
XX
KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US19029.
XX
PR 22-AUG-1998; 98US-0097712.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
WPI; 2000-246530/21.
XX
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CC nucleic acid binding activity to form duplexes, triplexes or other forms
CC of stable association. Sequences AAA07788-803 represent oligonucleotides
CC forming a third strand along with the duplex sequences.
XX
```

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
| | | | | | | | | | | | | | | | | |  
Db 15 AAAAAAAAAAAAAA 1

RESULT 738  
AAA07797/c  
ID AAA07797 standard; DNA; 15 BP.  
XX  
AC AAA07797;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Nucleic acid sequence of ODN-j.  
XX  
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US19029.  
XX  
PR 22-AUG-1998; 98US-0097712.  
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PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
WPI; 2000-246530/21.  
XX  
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XX  
Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleomonomers of specified formula and  
their pharmaceutically acceptable salts. The nucleomonomers are used as  
monomers in oligomers, which are used in pharmaceutical compositions to  
inhibit expression of nucleic acid molecules including DNA and RNA in  
cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
infected cells. They are used in oligomers for gene regulation,  
antisense technology, diagnostic applications to detect target sequences  
in biological samples such as those containing pathogenic bacteria,  
fungi and viruses, oncogenes, growth hormones and enzymes, to target  
genes or encoded RNAs that encode enzymes, hormones, serum proteins,  
adhesion molecules, receptor molecules, cytokines, oncogenes, growth  
factors and interleukins associated with pathological conditions such as  
inflammatory conditions, cardiovascular disorders, immune reactions,  
cancer, viral infections and bacterial infections (see AAA07786 for  
details of other uses for which the oligomers are suitable for).  
XX Oligomers comprising the nucleomonomers exhibit increased duplex DNA  
stability when hybridizing to target nucleic acid sequences, are  
physiologically stable, non-toxic and able to penetrate into cells while  
maintaining stringent base pair fidelity for target DNA sequences. The  
oligomers demonstrate significant single- or double-stranded target  
nucleic acid binding activity to form duplexes, triplexes or other forms  
of stable association. Sequences AAA07788-803 represent oligonucleotides  
forming a third strand along with the duplex sequences.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;  
SQ

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

QY 1084 AAAAAAAAAAAAAA 1098  
| | | | | | | | | | | | | | | | | |  
Db 15 AAAAAAAAAAAAAA 1

RESULT 739  
AAA07798/c  
ID AAA07798 standard; DNA; 15 BP.  
XX  
AC AAA07798;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Nucleic acid sequence of ODN-k.  
XX  
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US19029.  
XX  
PR 22-AUG-1998; 98US-0097712.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
WPI; 2000-246530/21.  
XX  
Modified nucleomonomers, used in physiologically stable, non-toxic  
oligomers used to inhibit expression of nucleic acids and in gene  
regulation, antisense technology and diagnostics -  
XX  
Disclosure; Page 20; 42pp; English.

XX The invention provides modified nucleomonomers of specified formula and  
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of stable association. Sequences AAA07788-803 represent oligonucleotides  
forming a third strand along with the duplex sequences.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;  
SQ

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 740  
 AAA07799/c  
 ID AAA07799 standard; DNA; 15 BP.  
 XX  
 AC AAA07799;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-1.  
 XX  
 DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US19029.  
 XX  
 PR 22-AUG-1998; 98US-0097712.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 XX  
 WPI; 2000-246530/21.  
 XX  
 DR Modified nucleonome, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics -  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleonome of specified formula and  
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 CC monomers in oligomers, which are used in pharmaceutical compositions to  
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 CC in biological samples such as those containing pathogenic bacteria,  
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 CC genes or encoded RNAs that encode enzymes, hormones, serum proteins,  
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 CC nucleic acid binding activity to form duplexes, triplexes or other forms  
 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 741  
 AAA07800/c  
 ID AAA07800 standard; DNA; 15 BP.  
 XX  
 AC AAA07800;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-m.  
 XX  
 DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US19029.  
 XX  
 PR 22-AUG-1998; 98US-0097712.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 XX  
 WPI; 2000-246530/21.  
 XX  
 DR Modified nucleonome, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
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 CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
 CC forming a third strand along with the duplex sequences.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 15 AAAAAAAAAAAAAA 1

RESULT 742  
AAA07801/c  
ID AAA07801 standard; DNA; 15 BP.

XX AAA07801;

AC AAA07801;

DT 23-JUN-2000 (first entry)

DE Nucleic acid sequence of ODN-n.

KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.

OS Synthetic.

PN W0200011013-A1.

XX 02-MAR-2000.

XX 20-AUG-1999; 99WO-US19029.

XX 22-AUG-1998; 98US-0097712.

XX (UYNE-) UNIV NEBRASKA.

XX Gold B;

XX WPI; 2000-246530/21.

XX Modified nucleomonomers, used in physiologically stable, non-toxic  
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CC nucleic acid binding activity to form duplexes, triplexes or other forms  
CC of stable association. Sequences AAA07788-803 represent oligonucleotides  
CC forming a third strand along with the duplex sequences.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 other;  
SQ Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db 15 AAAAAAAAAAAAAA 1

RESULT 743

AAA07802/c

ID AAA07802 standard; DNA; 15 BP.

XX AAA07802;

AC AAA07802;

DT 23-JUN-2000 (first entry)

DE Nucleic acid sequence of ODN-0.

KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.

OS Synthetic.

PN W0200011013-A1.

XX 02-MAR-2000.

XX 20-AUG-1999; 99WO-US19029.

XX 22-AUG-1998; 98US-0097712.

XX (UYNE-) UNIV NEBRASKA.

XX Gold B;

XX WPI; 2000-246530/21.

XX Modified nucleomonomers, used in physiologically stable, non-toxic  
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PT regulation, antisense technology and diagnostics -  
XX Disclosure; Page 20; 42pp; English.

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XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;  
SQ Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db 15 AAAAAAAAAAAAAA 1

RESULT 744

XX	AAA07803/c
AC	ID AAA07803 standard; DNA; 15 BP.
XX	AC AAA07803;
XX	DT 23-JUN-2000 (first entry)
DE	Nucleic acid sequence of a strand of triplex oligomer 14.
XX	Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	psoriasis; duplex; ss.
OS	Synthetic.
XX	WO200011013-A1.
PN	02-MAR-2000.
XX	20-AUG-1999; 99WO-US19029.
XX	22-AUG-1998; 98US-0097712.
PA	(UYNE-) UNIV NEBRASKA.
PI	Gold B;
DR	WPI; 2000-246530/21.
PT	Modified nucleomonomers, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
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CC	of stable association. Sequences AAA07788-803 represent oligonucleotides
CC	forming a third strand along with the duplex sequences.
XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
	Query Match 1.4%; Score 15; DB 1; Length 15;
	Best Local Similarity 100.0%; Pred. No. 3.5e+02;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1084 AAAAAAAAAAAAAAA 1098
Db	15 AAAAAAAAAAAAAAA 1
	RESULT 745
	AAA07825/c
ID	AAA07825 standard; DNA; 15 BP.
XX	AC AAA07825;
XX	DT 23-JUN-2000 (first entry)
DE	Nucleic acid sequence of ODN-p.
XX	Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	psoriasis; duplex; ss.
OS	Synthetic.
XX	WO200011013-A1.
PN	02-MAR-2000.
XX	20-AUG-1999; 99WO-US19029.
XX	22-AUG-1998; 98US-0097712.
PA	(UYNE-) UNIV NEBRASKA.
PI	Gold B;
DR	WPI; 2000-246530/21.
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XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;
	Query Match 1.4%; Score 15; DB 1; Length 15;
	Best Local Similarity 100.0%; Pred. No. 3.5e+02;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1084 AAAAAAAAAAAAAAA 1098
Db	15 AAAAAAAAAAAAAAA 1
	RESULT 745
	AAA07825/c
ID	AAA07825 standard; DNA; 15 BP.

```
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 15.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
XX PR 22-AUG-1998; 98US-0097712.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
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XX CC oligomers demonstrate significant single- or double-stranded target
XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
XX CC of stable association. Sequences AAA07820-834 represent sequences forming
XX CC triplex oligomers.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 747
XX AAA07831/c
XX ID AAA07831 standard; DNA; 15 BP.
XX AC AAA07831;
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of a strand of triplex oligomer 17.
```

```
XX DE Nucleic acid sequence of a strand of triplex oligomer 16.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US19029.
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XX CC nucleic acid binding activity to form duplexes, triplexes or other forms
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XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 748
XX AAA07834/c
XX ID AAA07834 standard; DNA; 15 BP.
XX AC AAA07834;
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of a strand of triplex oligomer 17.
```

XX Nucleonome; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; triplex; ss.  
XX Synthetic.  
XX WO200011013-A1.  
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XX  
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 other;  
SQ  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
DB 15 AAAAAAAAAAAAAA 1  
RESULT 749  
AAZ61854/C  
ID AAZ61854 standard; RNA; 15 BP.  
XX AAZ61854;  
AC  
XX 28-MAR-2000 (first entry)  
DT  
DE HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.  
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
KW

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
KW autoimmune disease; ss.  
XX Hepatitis C virus.  
XX WO9955847-A2.  
PN 04-NOV-1999.  
XX 26-APR-1999; 99WO-US09027.  
PF 27-APR-1998; 98US-0083217.  
PR 18-SEP-1998; 98US-0100842.  
PR 25-FEB-1999; 99US-0257608.  
PR 23-MAR-1999; 99US-0274553.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;  
PI WPI; 2000-062023/05.  
XX Novel ribozymes for the treatment of diseases and conditions related to  
PT hepatitis C infection -  
XX Claim 1; Page 49; 123pp; English.  
XX The present sequence represents the preferred target sequence of an  
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region.  
CC The HCV sequence was screened for optimal ribozyme target sites using  
CC a computer folding algorithm and regions of the mRNA which did not form  
CC secondary folding structures and contained potential ribozyme cleavage  
CC sites were identified. Ribozymes were synthesized to target these sites  
CC and their activities optimized by either varying the length of the  
CC binding arms or by modification to prevent degradation by nucleases.  
CC The ribozymes of the invention inhibit gene expression and/or viral  
CC replication, and are used to treat diseases associated with Hepatitis C  
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular  
CC carcinoma. The ribozymes may be used in combination with interferon to  
CC treat HCV infection, other infectious diseases, autoimmune diseases, and  
CC cancer.  
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;  
SQ  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
DB 15 AAAAAAAAAAAAAA 1  
RESULT 750  
AAZ64910/C  
ID AAZ64910 standard; RNA; 15 BP.  
XX AAZ64910;  
AC  
XX 28-MAR-2000 (first entry)  
DT  
DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.  
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
KW autoimmune disease; ss.  
XX Hepatitis C virus.  
XX WO9955847-A2.  
PN 04-NOV-1999.  
PD

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XX PF 26-APR-1999; 99WO-US09027.
XX PR 27-APR-1998; 98US-0083217.
XX PR 18-SEP-1998; 98US-0100842.
XX PR 25-FEB-1999; 99US-0257608.
XX PR 23-MAR-1999; 99US-0274553.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, McSwiggen JA, Roberts E, Pavco PA, Macejak D;
XX DR WPI; 2000-062023/05.
XX PT Novel ribozymes for the treatment of diseases and conditions related to
XX PT hepatitis C infection -
XX PS Claim 1; Page 102; 123pp; English.
XX CC The present sequence represents the preferred target sequence of an
XX CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
XX CC the Hepatitis C virus (HCV) RNA sequence at the base position given
XX CC in the descriptor line.
XX CC The HCV sequence was screened for optimal ribozyme target sites using
XX CC a computer folding algorithm and regions of the mRNA which did not form
XX CC secondary folding structures and contained potential ribozyme cleavage
XX CC sites were identified. Ribozymes were synthesised to target these sites
XX CC and their activities optimised by either varying the length of the
XX CC binding arms or by modification to prevent degradation by nucleases.
XX CC The ribozymes of the invention inhibit gene expression and/or viral
XX CC replication, and are used to treat diseases associated with Hepatitis C
XX CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
XX CC carcinoma. The ribozymes may be used in combination with interferon to
XX CC treat HCV infection, other infectious diseases, autoimmune diseases, and
XX CC cancer.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1

RESULT 751
AAH20308/c
ID AAH20308 standard; DNA; 15 BP.
XX AC AAH20308;
XX DT 31-JUL-2001 (first entry)
XX DE Oligo dT15 EDTA labelled probe.
XX KW Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently
XX attached at C-5"
XX modified_base 5
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently
XX attached at C-5"
XX modified_base 8
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently
XX attached at C-5"

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FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "Optionally thymidine has EDTA covalently
XX attached at C-5"
XX PN US2001002314-A1.
XX PD 31-MAY-2001.
XX PF 04-AUG-1998; 98US-0128732.
XX PR 30-OCT-1987; 87US-0115922.
XX PR 16-NOV-1990; 90US-0614205.
XX PR 12-NOV-1993; 93US-0152250.
XX PA (FLEH-) FLEHR HOBRACH TEST ALBRITTON & HERBERT.
XX PI Dervan PB, Moser HE;
XX DR WPI; 2001-342909/36.
XX PT New hybridization probe for specific triplex formation with large
XX PT double helices, useful e.g. for site-specific diagnostic cleavage,
XX PT contains attached functional residue -
XX PS Example 1; Fig 3B; 20pp; English.
XX CC This invention relates to hybridisation probes which target a specific
XX CC sequence within a large double-helical nucleic acid. The probe is
XX CC complementary to the target sequence and contains at least one nucleotide
XX CC with an attached molecule that is able to cleave double-helical DNA
XX CC e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The
XX CC probes where the attached molecule is a label or compound that alters
XX CC gene expression, are used for specific detection and/or cleavage of
XX CC double-helical DNA, e.g. for diagnosis, for treatment of disease
XX CC (particularly caused by viruses, genetic defects or oncogenes), for
XX CC chromosomal analysis, and for the isolation and mapping of genes. The
XX CC present sequence represents probe of the invention used in an example
XX CC illustrating how the probe binds to and cleaves double stranded DNA.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1

RESULT 752
AAH20511/c
ID AAH20511 standard; DNA; 15 BP.
XX AC AAH20511;
XX DT 31-JUL-2001 (first entry)
XX DE Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX KW Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX KW phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX KW clinical diagnostic; cancer treatment; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1..14
XX /mod_base= OTHER
XX /note= "Phosphorothioate deoxynucleotides"

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PN DE10051726-A1.
XX 10-MAY-2001.
XX 18-OCT-2000; 2000DE-1051726.
XX 30-OCT-1999; 99DE-1052376.
XX (MERE ) MERCK PATENT GMBH.
XX Seliger H, Sobkowski M, Hinz M;
XX WPI; 2001-336414/36.
XX Intermediate for oligonucleotide synthesis comprises partially
PT hydrolysed cross-linked vinyl acetate copolymer loaded with nucleotide
PT derivative -
XX
XX Example 2; Page 5; 8pp; German.
XX
XX This invention describes a novel chemical product comprising a partially
XX hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
XX with nucleotide derivative(s). The product is an intermediate for the
XX large (gram) scale solid phase synthesis of modified oligonucleotides
XX useful e.g. as clinical diagnostics and therapeutics, e.g. for the
XX treatment of AIDS and cancers. The presence of the partially hydrolysed
XX copolymer facilitates the synthesis of larger amounts of oligonucleotides
XX compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
XX described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
XX Oligonucleotides are obtained in very good quality and high yields. Also,
XX the nucleosides do not display the reduced activity seen in some prior
XX art procedures, less carrier material, reagents and solvent are required.
XX Further, the carrier material is biodegradable and thus does not present
XX disposal problems. It also swells uniformly in a range of solvents, which
XX obviates expansion or contraction during use or solvent exchange.
XX AAH20510-AAH20513 represent oligonucleotides containing modified
XX deoxynucleotides which are used to illustrate the method of the
XX invention.
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 753
AAF53331/c
XX ID AAF53331 standard; DNA; 15 BP.
XX AC AAF53331;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4291.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX PN
XX 21-JUN-2000; 2000WO-AU00693.
XX

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PD 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU00693.
XX 21-JUN-1999; 99US-0140345.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX Example 8; Page 88; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic diseases, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;
XX
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 320 CTGCAGAGAGAGCTGT 334
DB 15 CTGCAGAGAGAGCTGT 1
XX
RESULT 754
AAF53332/c
XX ID AAF53332 standard; DNA; 15 BP.
XX AC AAF53332;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4292.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX PN
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU00693.
XX

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PR 21-JUN-1999; 99US-0140345.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX Example 8; Page 88; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 319 ACTGCAGAGAGCTG 333
XX |||||
XX 15 ACTGCAGAGAGCTG 1
XX
RESULT 755
AAFL16603
ID AAF16603 standard; DNA; 15 BP.
AC AAF16603;
XX
XX 13-MAR-2001 (first entry)
XX
XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
XX
XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
XX stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
XX DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
XX
XX WO2000071164-A1.
XX
XX 30-NOV-2000.
XX
XX 24-MAY-2000; 2000WO-AU00498.
XX
XX 24-MAY-1999; 99AU-0000510.
XX (TACH/) TACHAS G.
XX
XX Tachas G;
XX
XX WPI; 2001-025093/03.
XX
XX Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion -
XX
XX Example 3; Page 148; 164pp; English.
XX
XX The present invention provides oligonucleotides, and methods for their
XX use, which are useful in modulating the action of proteins involved in
XX gastric acid production. The target protein is preferably the histamine
XX H2 receptor or one of the proteins which form part of the gastric proton
XX pump. The sequences and methods of the invention are useful in the
XX treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
XX duodenal ulcers and other gastric acid disturbances, most of which are
XX caused by Helicobacter pylori.
XX
XX Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1083 TAAAAAATAAAAAA 1097
XX |||||
XX 1 TAAAAAATAAAAAA 15
XX
RESULT 756
AAFL30882/C
ID AAF30882 standard; DNA; 15 BP.
XX
XX AAF30882;
XX
XX 09-JUL-2001 (first entry)
XX
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
XX ODN-MGB-LF; oligonucleotide; minor groove binder;
XX latent fluorophore; hybridisation; detection; fluorescence; probe;
XX ss.
XX
XX Synthetic.
XX
XX WO200131063-A1.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US29786.
XX
XX 26-OCT-1999; 99US-0428236.
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX Dempcy RO, Afonina IA, Vermeulen NMJ;
XX
XX WPI; 2001-328656/34.
XX
XX Conjugate of oligonucleotide, minor groove binder and latent
XX fluorophore, useful for detecting specific nucleic acids, e.g. for
XX single-nucleotide mismatch discrimination -
XX
XX Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component
XX of an ODN-MGB (minor groove binder)-LF (latent fluorophore)
XX conjugate of the invention. MGBs bind in a non-intercalating
XX manner to the minor groove of non-single-stranded DNA, RNA or their
XX hybrids, while a LF binds similarly but in an intercalating manner,
XX or lies in the minor groove, or is oriented in some other way to
XX the DNA molecule by MGB, such that it becomes fluorescent (or its
XX fluorescent properties change detectably). The conjugates are used
XX as hybridisation probes and amplification primers for fluorescent
XX detection of specifically hybridising sequences, for analysis or
XX diagnosis, especially (real-time) PCR, for single-nucleotide
XX mismatch discrimination, target or signal amplification,

```

CC array-based assays and sequencing, including detection of  
 CC double-stranded DNA by triplex formation. Many different targets  
 CC can be detected at a single reaction vessel. The present ODN-MGB-LF  
 CC conjugate was used to demonstrate hybridisation-triggered  
 CC fluorescence. Upon hybridisation to the complementary target  
 CC sequence there was an increase in fluorescence yield, measured as  
 CC the ratio of the fluorescence emitted by the hybrid to the fluorescence  
 CC ODN-MGB-LF conjugate and its target sequence to the fluorescence  
 CC emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 757  
 AAH49243/C  
 ID AAH49243 standard; DNA; 15 BP.  
 XX  
 AC AAH49243;  
 XX  
 DT 26-NOV-2001 (first entry)  
 XX  
 DE PNA-forming oligonucleotide #7.  
 XX  
 KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
 KW antiviral; hepatotropic; vasotrophic; antisense inhibition; ribozyme;  
 KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
 KW peptide nucleic acid; ss.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 9 /\*tag= a  
 /mod\_base= OTHER  
 /note= "t-but"  
 modified\_base 15 /\*tag= b  
 /mod\_base= OTHER  
 /note= "t-hex"  
 EP1113021-A2.  
 PD 04-JUL-2001.  
 XX  
 PF 08-MAR-1995; 2001EP-0104012.  
 XX  
 PR 14-MAR-1994; 94DE-4408528.  
 PR 08-MAR-1995; 95EP-0103332.  
 XX  
 PA (AVET) AVENTIS PHARMA DEUT GMBH.  
 XX  
 PI Uhlmann E, Breipohl G;  
 XX  
 DR WPI; 2001-591267/67.  
 XX  
 PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
 PT for treating e.g. cancer, also as diagnostic probes and primers  
 XX  
 PS Example 26; Page 40; 54pp; German.  
 XX  
 CC This invention describes novel polyamide-oligonucleotide derivatives (I)  
 CC and their physiologically acceptable salts of formula  
 CC F((DNA)-Li) q(PNA-Li) r(PNA-Li) s(PNA) t) xF, where q, r, s, t = 0 or 1,  
 CC with the sum of two or more adjacent letters at least 2; x = 1-20; DNA  
 CC = nucleic acid (such as DNA or RNA or their known derivatives); Li =

CC covalent linkage between DNA and PNA, i.e. a bond or a residue containing  
 CC at least one atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide  
 CC structure containing at least one nucleobase different from thymine; and  
 CC F, F' = end groups and/or are connected through a covalent bond. The  
 CC products of the invention have anticancer, antiproliferative, antiviral,  
 CC hepatotropic and vasotrophic activity and can be used for the inhibition  
 CC of gene expression by antisense, ribozyme, sense, or triple-helix  
 CC methods, or by binding to proteins (aptamers). (I) are used for treating  
 CC diseases caused by viruses (human immune deficiency, herpes simplex,  
 CC influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated  
 CC by integrins or cell-cell adhesion reactions, for treating cancer, or  
 CC for inhibiting restenosis, particularly as antisense reagents. They are  
 CC also useful in heterogeneous or homogeneous assays, as primers or probes,  
 CC particularly where the target is amplified before being detected by  
 CC hybridization, for diagnosis of genetic, malignant or pathogen-related  
 CC diseases. (I) retain the increased affinity for complementary strands and  
 CC better stability in serum, associated with conventional peptide nucleic  
 CC acids (PNA), but lack the disadvantages, i.e. have improved cellular  
 CC uptake, do not aggregate in aqueous solution, and have reduced affinity  
 CC for purification materials, reduced cytotoxicity, better sequence  
 CC specificity. They are more active than either DNA or PNA oligomers. When  
 CC used as probes, (I) show different responses to base-pair mismatches in  
 CC the DNA and PNA segments, allowing better discrimination between  
 CC pathogenic and non-pathogenic conditions such as the transition from  
 CC proto-oncogene to oncogene, also, when used as primers, with the PNA  
 CC segment at the 5'-end, they produce amplicons resistant to  
 CC 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA  
 CC primers. The DNA component allows additional reactions not possible with  
 CC PNA alone, e.g. 3'-tailing and (I) may be incorporated into a gene.  
 CC AAH49208-AAH49264 represent oligonucleotides used to illustrate the  
 CC method of the invention.

XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 758  
 ABX00240/C  
 ID ABX00240 standard; RNA; 15 BP.  
 XX  
 AC ABX00240;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-0274553.  
 XX  
 PR 23-MAR-1999; 99US-0274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.



PA (PAVC/) PAVCO P A.  
 XX (MACE/) MACEJACK D.  
 PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;  
 XX WPI; 2002-617759/66.  
 XX  
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit  
 PT viral replication and are useful to treat hepatitis C virus infections  
 PT and cirrhosis, liver failure or hepatocellular carcinoma -  
 XX  
 PS Claim 1; Page 21; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or  
 CC hairpin (HP) motif where the binding arms comprise sequences  
 CC complementary to one of the substrate sequences defined in the  
 CC specification. The HCV ribozymes are useful for modulating the  
 CC expression and/or replication of HCV. They can be used to treat  
 CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV  
 CC ribozymes are also useful for treating a condition associated with  
 CC HCV infection in conjunction with one or more other drug therapies,  
 CC particularly type I interferon, especially interferon alpha, beta or  
 CC gamma or consensus interferon. The present sequence represents a  
 CC substrate for a HCV hammerhead (HH) ribozyme.  
 CC Note: Some of the sequence data for this patent did not form part of  
 CC the printed specification. The complete sequence data for this patent  
 CC was obtained in electronic format directly from the USPTO web site  
 CC at seqdata.uspto.gov/psipdIDEntry.html.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 759  
 ABX03406/C  
 ID ABX03406 standard; RNA; 15 BP.  
 XX  
 AC ABX03406;  
 XX  
 DT 24-DEC-2002 (first entry)  
 DE  
 DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX US2002082225-A1.  
 XX  
 XX 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-0274553.  
 XX  
 PR 23-MAR-1999; 99US-0274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;  
 XX WPI; 2002-617759/66.  
 XX  
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit  
 PT viral replication and are useful to treat hepatitis C virus infections  
 PT and cirrhosis, liver failure or hepatocellular carcinoma -  
 XX  
 PS Claim 1; Page 64; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or  
 CC hairpin (HP) motif where the binding arms comprise sequences  
 CC complementary to one of the substrate sequences defined in the  
 CC specification. The HCV ribozymes are useful for modulating the  
 CC expression and/or replication of HCV. They can be used to treat  
 CC cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV  
 CC ribozymes are also useful for treating a condition associated with  
 CC HCV infection in conjunction with one or more other drug therapies,  
 CC particularly type I interferon, especially interferon alpha, beta or  
 CC gamma or consensus interferon. The present sequence represents a  
 CC substrate for a HCV hammerhead (HH) ribozyme.  
 CC Note: Some of the sequence data for this patent did not form part of  
 CC the printed specification. The complete sequence data for this patent  
 CC was obtained in electronic format directly from the USPTO web site  
 CC at seqdata.uspto.gov/psipdIDEntry.html.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 760  
 ABQ82140  
 ID ABQ82140 standard; DNA; 15 BP.  
 XX  
 AC ABQ82140;  
 XX  
 DT 11-DEC-2002 (first entry)  
 DE  
 DE Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.  
 XX  
 KW Chimeric nucleic acid construct; recombinational cloning; silencing;  
 KW recombination site; double stranded RNA; plant; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200259294-A1.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-AU00073.  
 XX  
 PR 26-JAN-2001; 2001US-264067P.  
 PR 29-NOV-2001; 2001US-333743P.  
 XX  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Wesley S, Waterhouse P, Helliwell C;  
 XX  
 XX WPI; 2002-682669/73.  
 XX  
 PT New vectors comprising operably linked DNA fragments having an origin  
 PT of replication, a selectable marker and a chimeric DNA construct,

PT useful for silencing target nucleic acids and for producing large  
PT amounts of double-stranded RNA -  
XX  
PS Claim 14; Page 74; 104pp; English.  
XX  
CC The present invention describes a vector (I) comprising operably linked  
CC DNA fragments having: (a) origin of replication allowing replication in a  
CC recipient cell, preferably in bacteria such as *Escherichia coli*;  
CC (b) selectable marker region capable of being expressed in the recipient  
CC cell; and (c) a chimeric DNA construct comprising: (i) promoter or  
CC promoter region capable of being recognized by RNA polymerases of a  
CC eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second,  
CC third and fourth recombination sites; (iii) 3' transcription terminating  
CC and polyadenylation region functional in the eukaryotic cell. The first  
CC and fourth recombination sites, or the second and third recombination  
CC sites are capable of reacting with a same recombination site, and  
CC preferably are identical. The first and second recombination sites, or  
CC the third and fourth recombination sites, do not recombine with each  
CC other or with a same recombination site. The vector is useful for  
CC producing large amounts of double-stranded RNA which can be used for  
CC silencing target nucleic acid sequences. The vectors can also be used to  
CC convert a DNA fragment into an inverted repeat structure. Plants  
CC transformed with a vector from the present invention can be used in a  
CC conventional breeding scheme to produce more plants with the same  
CC characteristics or to introduce a chimeric gene for reduction of the  
CC phenotypic expression of nucleic acids. The present sequence represents  
CC an acceptor vector nucleotide sequence from the present invention.

Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
DB 1 AAAAAAAAAAAAAA 15

RESULT 761  
AAL49453  
ID AAL49453 standard; DNA; 15 BP.  
AC AAL49453;  
DT 14-NOV-2002 (first entry)  
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 1.  
KW Mutation detection; primer; mutant; tag; tumour suppressor gene;  
KW protein production; cancer; ds.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..15  
FT /\*tag= a  
FT /product= "tag peptide"  
FT /partial  
FT /note= "no start or stop"  
XX  
PN WO200266675-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 15-FEB-2002; 2002WO-EP01651.  
XX  
PR 16-FEB-2001; 2001DE-1007317.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Kahmann S, Mueller O;  
XX  
XX

DR WPI; 2002-674959/72.  
DR P-PSDB; AAO19054.  
XX  
PT Detecting mutations in nucleic acid, useful for diagnosis and  
PT characterization of tumors, by amplification, in vitro transcription  
PT and translation, then protein detection -  
XX  
XX Claim 11; Fig 5; 62pp; German.

PS The present invention relates to a method of detecting mutations in a  
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded  
CC amplicon, in vitro transcription and translation of this amplicon, and  
CC detection of the translated protein. The primers used for amplification  
CC are designed to produce an amplicon that is translatable and allows  
CC differentiation between translation products of wild-type and mutated  
CC nucleic acids. The method is used to detect mutations in tumour  
CC suppressor genes, for (early) diagnosis, monitoring and characterisation  
CC of tumours (especially of bladder and intestines) and in the germ line  
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector  
CC is used to detect or verify the reading frame of a nucleic acid cloned in  
CC it, and to determine the suitability of detectable peptides for analysis  
CC and/or purification of a recombinant protein, expressed from a sequence  
CC cloned in the vector. The present sequence encodes a tag peptide and was  
CC used in the invention.

Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
DB 1 AAAAAAAAAAAAAA 15

RESULT 762  
AAL49455  
ID AAL49455 standard; DNA; 15 BP.  
AC AAL49455;  
DT 14-NOV-2002 (first entry)  
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 3.  
KW Mutation detection; primer; mutant; tag; tumour suppressor gene;  
KW protein production; cancer; ds.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..15  
FT /\*tag= a  
FT /product= "tag peptide"  
FT /partial  
FT /note= "no start or stop"  
XX  
PN WO200266675-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 15-FEB-2002; 2002WO-EP01651.  
XX  
PR 16-FEB-2001; 2001DE-1007317.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Kahmann S, Mueller O;  
XX  
XX WPI; 2002-674959/72.  
XX P-PSDB; AAO19056.  
XX

PT Detecting mutations in nucleic acid, useful for diagnosis and  
PT characterization of tumors, by amplification, in vitro transcription  
PT and translation, then protein detection  
XX  
PS Claim 11; Fig 5; 62pp; German.  
XX  
CC The present invention relates to a method of detecting mutations in a  
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded  
CC amplicon, in vitro transcription and translation of this amplicon, and  
CC detection of the translated protein. The primers used for amplification  
CC are designed to produce an amplicon that is translatable and allows  
CC differentiation between translation products of wild-type and mutated  
CC nucleic acids. The method is used to detect mutations in tumour  
CC suppressor genes, for (early) diagnosis, monitoring and characterisation  
CC of tumours (especially of bladder and intestines) and in the germ line  
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector  
CC is used to detect or verify the reading frame of a nucleic acid cloned in  
CC it, and to determine the suitability of detectable peptides for analysis  
CC and/or purification of a recombinant protein, expressed from a sequence  
CC cloned in the vector. The present sequence encodes a tag peptide and was  
CC used in the invention.  
XX  
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
Db 1 AAAAAAAAAAAAAA 15

RESULT 763  
ABK98141/c  
ID ABK98141 standard; DNA; 15 BP.  
AC ABK98141;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Triple helix forming associated oligonucleotide #26.  
DE  
DE Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW Gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
XX Synthetic.  
XX  
XX US6403302-B1.  
XX  
XX 11-JUN-2002.  
XX  
XX 16-DEC-1993; 93US-0168920.  
XX  
XX 17-SEP-1992; 92US-0946976.  
XX  
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
XX Dervan PB, Beal PA;  
XX  
XX WPI; 2002-536030/57.  
XX  
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
XX oligonucleotide which binds in parallel and antiparallel orientation,  
XX respectively, for targetting sequences on alternate strands of DHNA to  
XX control gene expression -  
XX  
XX Example 1; Fig 3B; 108pp; English.  
XX  
XX The present invention relates to methods and oligonucleotides for  
XX forming a triple-helix comprising a double helical nucleic acid

CC comprising first and second substantially complementary strands, and  
CC an oligonucleotide bound to a purine-rich target sequence within the  
CC double helical nucleic acid, where the oligonucleotide binds in a  
CC parallel and antiparallel orientation, respectively, to target  
CC sequences on alternate strands of the double helical nucleic acid.  
CC The method has therapeutic applications, where gene expression is  
CC controlled by selective triple-helix formation within expression  
CC regulatory sequences of a target gene. The oligonucleotides can be  
CC used to form triple-helices, and are useful to detect the presence or  
CC absence of specific sequences within genomic DNA for diagnostic and  
CC therapeutic purposes. The oligonucleotides can be selected to  
CC specifically bind to pathogenic double-stranded DNA including specific  
CC sequences required by pathogenic bacteria or viruses for replication or  
CC virulence, reducing their pathogenicity. Alternatively, the  
CC oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or  
CC viral origin. Such therapeutic oligonucleotides are capable of forming  
CC triple-helices with such sequences in cancerous cells containing the  
CC activated oncogene, so preferentially killing or repressing the cancer  
CC causing cell. The present sequence represents an oligonucleotide  
CC used in the methods of the present invention.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1098  
Db 15 AAAAAAAAAAAAAA 1

RESULT 764  
ABK98184/c  
ID ABK98184 standard; DNA; 15 BP.  
AC ABK98184;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Triple helix forming associated oligonucleotide #48.  
DE  
DE Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW Gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
XX Synthetic.  
XX  
XX US6403302-B1.  
XX  
XX 11-JUN-2002.  
XX  
XX 16-DEC-1993; 93US-0168920.  
XX  
XX 17-SEP-1992; 92US-0946976.  
XX  
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
XX Dervan PB, Beal PA;  
XX  
XX WPI; 2002-536030/57.  
XX  
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
XX oligonucleotide which binds in parallel and antiparallel orientation,  
XX respectively, for targetting sequences on alternate strands of DHNA to  
XX control gene expression -  
XX  
XX Example 7; Fig 24A; 108pp; English.  
XX

CC The present invention relates to methods and oligonucleotides for  
CC forming a triple-helix comprising a double helical nucleic acid  
CC comprising first and second substantially complementary strands, and  
CC an oligonucleotide bound to a purine-rich target sequence within the  
CC double helical nucleic acid, where the oligonucleotide binds in a  
CC parallel and antiparallel orientation, respectively, to target  
CC sequences on alternate strands of the double helical nucleic acid.  
CC The method has therapeutic applications, where gene expression is  
CC controlled by selective triple-helix formation within expression is  
CC regulatory sequences of a target gene. The oligonucleotides can be  
CC used to form triple-helices, and are useful to detect the presence or  
CC absence of specific sequences within genomic DNA for diagnostic and  
CC therapeutic purposes. The oligonucleotides can be selected to  
CC specifically bind to pathogenic double-stranded DNA including specific  
CC sequences required by pathogenic bacteria or viruses for replication or  
CC virulence, reducing their pathogenicity. Alternatively, the  
CC oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or  
CC viral origin. Such therapeutic oligonucleotides are capable of forming  
CC triple-helices with such sequences in cancerous cells containing the  
CC activated oncogene, so preferentially killing or repressing the cancer  
CC causing cell. The present sequence represents an oligonucleotide  
CC used in the methods of the present invention.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
DB 15 AAAAAAAAAAAAAA 1

RESULT 765  
ABL57054/c  
ID ABL57054 standard; DNA; 15 BP.

XX AC ABL57054;  
XX 22-JUL-2002 (first entry)  
XX Hydrazide phosphoramidite oligonucleotide O9.  
XX Macromolecule; hydrazide; immobilisation; ss.  
XX Synthetic.

Key	Location/Qualifiers
modified_base 1	/tag= a
	/mod base= "OTHER"
	/note= "6-((2Cyanethoxy)(diisopropylamino)
	phosphanyloxy)-N'-tritylhexanohydrazide"
modified_base 1..15	/tag= b
	/mod base= "OTHER"
	/note= "phosphoramidite linkage"

WO200214558-A2.  
21-FEB-2002.  
10-AUG-2001; 2001WO-US41663.  
11-AUG-2000; 2000WO-US22205.

(NANO-) NANOGEN INC.  
Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
PI Havens JR, Onofrey TJ, Greef CH, Wang D;

XX WPI; 2002-401666/43.  
XX Compound for binding macromolecule to substrate surface or conjugation  
XX targets, contains phosphorus containing reactive group, hydrazide  
XX protecting group and benzene ring, and has predefined formula -  
XX Example 2; Page 40; 120pp; English.

XX The present sequence is of a trityl deprotected hydrazide  
XX phosphoramidite 15-mer, designated oligo O9, which was produced in  
XX an example from the invention. The invention describes an improved  
XX process for immobilisation of macromolecules including DNA, RNA,  
XX peptide nucleic acids, pyranosyl-RNA and peptides, especially  
XX macromolecules containing multiple reactive sites, to a substrate  
XX surface or other conjugation target. It also describes the  
XX preparation of oligos containing one or more hydrazides, which can  
XX be used for conjugation to surface binding moieties, or for other  
XX conjugation reactions. The process is useful e.g. in nucleic acid  
XX hybridisation based assays, DNA chip technology and biosensor  
XX applications.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
DB 15 AAAAAAAAAAAAAA 1

RESULT 766  
ABL57056/c  
ID ABL57056 standard; DNA; 15 BP.

XX AC ABL57056;  
XX 22-JUL-2002 (first entry)  
XX Hydrazide phosphoramidite oligonucleotide O31.  
XX Macromolecule; hydrazide; immobilisation; ss.  
XX Synthetic.

Key	Location/Qualifiers
modified_base 1	/tag= a
	/mod base= "OTHER"
	/note= "6-((2Cyanethoxy)(diisopropylamino)
	phosphanyloxy)-N'-tritylhexanohydrazide"
modified_base 1..15	/tag= b
	/note= "phosphoramidite linkage"
modified_base 15	/tag= c
	/mod base= "OTHER"
	/note= "3' Cy3 dye"

WO200214558-A2.  
21-FEB-2002.  
10-AUG-2001; 2001WO-US41663.  
11-AUG-2000; 2000WO-US22205.

(NANO-) NANOGEN INC.  
Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
PI Havens JR, Onofrey TJ, Greef CH, Wang D;

```
XX DR WPI; 2002-401666/43.
XX
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula -
XX
XX PS Example 2; Page 40; 120pp; English.
XX
XX CC The present sequence is of a trityl deprotected hydrazide
XX CC phosphoramidite 15-mer, designated oligo O31, which was produced in
XX CC an example from the invention. The invention describes an improved
XX CC process for immobilisation of macromolecules including DNA, RNA,
XX CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
XX CC macromolecules containing multiple reactive sites, to a substrate
XX CC surface or other conjugation target. It also describes the
XX CC preparation of oligos containing one or more hydrazides, which can
XX CC be used for conjugation to surface binding moieties, or for other
XX CC conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications.
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 767
ABL57059/C
XX ID ABL57059 standard; DNA; 15 BP.
XX AC ABL57059;
XX
XX DT 22-JUL-2002 (first entry)
XX
XX DE Hydrazide precursor phosphoramidite oligonucleotide O33.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /mod_base= "OTHER"
XX /note= "4-((2-cyanoethyl)-(diisopropylamino)
XX phospharyloxymethyl)-benzoic acid methyl
XX ester"
XX modified_base 1..15
XX /*tag= b
XX /note= "phosphoramidite linkage"
XX modified_base 15
XX /*tag= c
XX /mod_base= "OTHER"
XX /note= "3, Cy3 dye"
XX
XX PN WO200214558-A2.
XX
XX PD 21-FEB-2002.
XX
XX PF 10-AUG-2001; 2001WO-US41663.
XX
XX PR 11-AUG-2000; 2000WO-US22205.
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
```

```
PI XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-401666/43.
XX
XX CC Compound for binding macromolecule to substrate surface or conjugation
XX CC targets, contains phosphorous containing reactive group, hydrazide
XX CC protecting group and benzene ring, and has predefined formula -
XX
XX PS Example 3; Page 43; 120pp; English.
XX
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo O33, which was produced in
XX CC an example from the invention. The invention describes an improved
XX CC process for immobilisation of macromolecules including DNA, RNA,
XX CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
XX CC macromolecules containing multiple reactive sites, to a substrate
XX CC surface or other conjugation target. It also describes the
XX CC preparation of oligos containing one or more hydrazides, which can
XX CC be used for conjugation to surface binding moieties, or for other
XX CC conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications.
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1
XX
RESULT 768
ABL57060/C
XX ID ABL57060 standard; DNA; 15 BP.
XX AC ABL57060;
XX
XX DT 22-JUL-2002 (first entry)
XX
XX DE Hydrazide precursor phosphoramidite oligonucleotide O34.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /mod_base= "OTHER"
XX /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
XX phosphanyloxy)methyl)isophthalate"
XX modified_base 1..15
XX /*tag= b
XX /note= "phosphoramidite linkage"
XX modified_base 15
XX /*tag= c
XX /mod_base= "OTHER"
XX /note= "3, Cy3 dye"
XX
XX PN WO200214558-A2.
XX
XX PD 21-FEB-2002.
XX
XX PF 10-AUG-2001; 2001WO-US41663.
XX
XX PR 11-AUG-2000; 2000WO-US22205.
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
```

PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 XX WPI; 2002-401666/43.  
 XX  
 XX Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula -  
 XX  
 PS Example 3; Page 43; 120pp; English.  
 XX  
 CC The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 15-mer, designated oligo O34, which was produced in  
 CC an example from the invention. The invention describes an improved  
 CC process for immobilisation of macromolecules including DNA, RNA,  
 CC peptide nucleic acids, pyranosyl-RNA and peptides, especially  
 CC macromolecules containing multiple reactive sites, to a substrate  
 CC surface or other conjugation target. It also describes the  
 CC preparation of oligos containing one or more hydrazides, which can  
 CC be used for conjugation to surface binding moieties, or for other  
 CC conjugation reactions. The process is useful e.g. in nucleic acid  
 CC hybridisation based assays, DNA chip technology and biosensor  
 CC applications.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 769  
 ID ABL57061/C  
 XX ABL57061 standard; DNA; 15 BP.  
 AC ABL57061;  
 XX  
 XX 22-JUL-2002 (first entry)  
 DE Hydrazide precursor phosphoramidite oligonucleotide O37.  
 XX  
 KW Macromolecule; hydrazide; immobilisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /mod\_base= "OTHER"  
 FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)  
 FT phenylcarbonylamido)-2-((2'',-cyanoethyloxy)  
 FT (diisopropyl)amino)-phosphanyloxy)-propane"  
 FT modified\_base 1..15  
 FT /\*tag= b  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base 15  
 FT /\*tag= c  
 FT /mod\_base= "OTHER"  
 FT /note= "3' Cy3 dye"  
 XX  
 PN WO200214558-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US41663.  
 XX  
 PR 11-AUG-2000; 2000WO-US22205.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX

PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 XX WPI; 2002-401666/43.  
 XX  
 XX Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula -  
 XX  
 PS Example 3; Page 43; 120pp; English.  
 XX  
 CC The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 15-mer, designated oligo O37, which was produced in  
 CC an example from the invention. The invention describes an improved  
 CC process for immobilisation of macromolecules including DNA, RNA,  
 CC peptide nucleic acids, pyranosyl-RNA and peptides, especially  
 CC macromolecules containing multiple reactive sites, to a substrate  
 CC surface or other conjugation target. It also describes the  
 CC preparation of oligos containing one or more hydrazides, which can  
 CC be used for conjugation to surface binding moieties, or for other  
 CC conjugation reactions. The process is useful e.g. in nucleic acid  
 CC hybridisation based assays, DNA chip technology and biosensor  
 CC applications.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 770  
 ID ABL57063/C  
 XX ABL57063 standard; DNA; 15 BP.  
 AC ABL57063;  
 XX  
 XX 22-JUL-2002 (first entry)  
 DE Hydrazide precursor phosphoramidite oligonucleotide O39.  
 XX  
 KW Macromolecule; hydrazide; immobilisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /mod\_base= "OTHER"  
 FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)  
 FT benzyloxy)-5-((2'-cyanoethyl)(diisopropylamino)  
 FT phosphanyloxy)-benzene"  
 FT modified\_base 1..15  
 FT /\*tag= b  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base 15  
 FT /\*tag= c  
 FT /mod\_base= "OTHER"  
 FT /note= "3' Cy3 dye"  
 XX  
 PN WO200214558-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US41663.  
 XX  
 PR 11-AUG-2000; 2000WO-US22205.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX

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XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
PS Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O39, which was produced in
CC an example from the invention. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX applications.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1
RESULT 771
ABL57064/C
ID ABL57064 standard; DNA; 15 BP.
XX
AC ABL57064;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= "OTHER"
FT /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)methyl)isophthalate, synthetic
FT branching amide"
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 15
FT /tag= c
FT /mod_base= "OTHER"
FT /note= "3, Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US41663.
XX
PR 11-AUG-2000; 2000WO-US22205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;

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PA (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-401666/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula -
XX
PS Example 4; Page 44; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O35, which was produced in
CC an example from the invention and which includes a synthetic
CC branching amide compound. The invention describes an improved
CC process for immobilisation of macromolecules including DNA, RNA,
CC peptide nucleic acids, pyranosyl-RNA and peptides, especially
CC macromolecules containing multiple reactive sites, to a substrate
CC surface or other conjugation target. It also describes the
CC preparation of oligos containing one or more hydrazides, which can
CC be used for conjugation to surface binding moieties, or for other
CC conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX applications.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
Db 15 AAAAAAAAAAAAAA 1
RESULT 772
ABL57066/C
ID ABL57066 standard; DNA; 15 BP.
XX
AC ABL57066;
XX
DT 22-JUL-2002 (first entry)
XX
DE Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= "OTHER"
FT /note= "Amino-C6 modification"
FT modified_base 15
FT /tag= b
FT /mod_base= "OTHER"
FT /note= "3, Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US41663.
XX
PR 11-AUG-2000; 2000WO-US22205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;

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PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 DR WPI; 2002-401666/43.  
 XX  
 PT Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula -  
 XX  
 PS Example 12; Page 57; 120pp; English.  
 XX  
 CC The present sequence is of an amino-C6-modified and Cy3 dye  
 CC labeled T15 oligonucleotide that was used in a comparison of  
 CC hydrazine and amine attachment moieties on active ester surfaces  
 CC in an example from the invention. The invention describes an  
 CC improved process for immobilisation of macromolecules including DNA,  
 CC RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially  
 CC macromolecules containing multiple reactive sites, to a substrate  
 CC surface or other conjugation target. It also describes the  
 CC preparation of oligos containing one or more hydrazides, which can  
 CC be used for conjugation to surface binding moieties, or for other  
 CC conjugation reactions. The process is useful e.g. in nucleic acid  
 CC hybridisation based assays, DNA chip technology and biosensor  
 CC applications.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 773  
 ID ABL40743 standard; DNA; 15 BP.  
 XX  
 AC ABL40743;  
 XX  
 DT 03-JUL-2002 (first entry)  
 XX  
 DE Chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.  
 XX  
 KW Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;  
 KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.  
 XX  
 OS Gallus gallus.  
 XX  
 FN US2002034810-A1.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 16-AUG-2001; 2001US-0930218.  
 XX  
 PR 20-SEP-2000; 2000US-0666390.  
 XX  
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
 XX  
 PI Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;  
 XX  
 DR WPI; 2002-338926/37.  
 XX  
 CC Nucleic acid encoding avian and reptile heparanase polypeptide is  
 CC useful to treat various heparin-related disorders and the signal  
 CC peptide is useful in production of membrane-targeted or secreted  
 CC recombinant proteins -  
 XX  
 PS Disclosure; Page 13; 39pp; English.  
 XX  
 CC The invention relates to an isolated avian and reptile nucleic acid,  
 CC encoding a polypeptide with heparanase catalytic activity. The signal

CC peptide of the nucleic acid can be used to express membrane-associated or  
 CC secreted proteins in heterologous expression systems. The encoded  
 CC polypeptides can be used to prevent tumour angiogenesis, metastasis and  
 CC invasion, and to intervene with pathologies associated with impaired  
 CC heparin-binding growth factors, cellular responses to heparin-binding  
 CC growth factors and cytokines, cell interaction with plasma lipoproteins,  
 CC cellular susceptibility to viral, protozoan and bacterial infections or  
 CC disintegration of neurodegenerative plaques. The present sequence  
 CC represents a chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 15 AAAAAAAAAAAAAA 1  
 RESULT 774  
 ID ABA97403/c  
 XX  
 AC ABA97403;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Nucleotide sequence of oligomer # 10 used to compare mismatches.  
 XX  
 KW Protein nucleic acid molecule; PNA; ds.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200168673-A1.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 13-MAR-2001; 2001WO-US08111.  
 XX  
 PR 14-MAR-2000; 2000US-189190P.  
 PR 30-NOV-2000; 2000US-250334P.  
 XX  
 PA (ACTI-) ACTIVE MOTIF.  
 XX  
 XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;  
 PI Chakhmakhcheu O, Buryakova A, Choob M, Hondorp K;  
 XX  
 DR WPI; 2002-041177/05.  
 XX  
 CC Oligonucleotides analogues useful in detection, separation and  
 CC purification of nucleic acid molecules, comprise monomers, dimers and  
 CC oligomers -  
 XX  
 PS Example 20; Page 123; 197pp; English.  
 XX  
 CC This invention relates to oligonucleotide analogues comprising a protein  
 CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
 CC separation of nucleic acid molecules and as probes, primers, linkers,  
 CC adaptors and antisense agents on solid supports. Modifications enhance  
 CC their use as capture and detection probes e.g. by the incorporation of  
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
 CC fluorescein and reporter molecules such as alkaline phosphatase.  
 CC They are also used for enhancing or inhibiting the activity of an enzyme  
 CC or cellular activity. The compounds are stable to nucleases and  
 CC proteases, have high affinity, binding specificity and solubility. The  
 CC polyanide backbone of PNAs is resistant to both nucleases and proteases.  
 CC PNAs bind nucleic acid molecules with greater affinity than DNA or RNA  
 CC concentration. The compounds are relatively simple to synthesize and  
 CC are used in a wide variety of applications. This sequence  
 CC represents a DNA oligomer which is used to represent the effect of  
 CC single base mismatches on oligonucleotides.



```

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 775
AAD29506/c
ID AAD29506 standard; DNA; 15 BP.
XX AC AAD29506;
XX DT 17-MAY-2002 (first entry)
XX DE Primer used for the expression of adipocytes in human preadipose cells.
XX KW Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
XX KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
XX KW ss.
XX OS Unidentified.
XX PN WO200206450-A1.
XX PD 24-JAN-2002.
XX PF 13-JUL-2001; 2001WO-EP08165.
XX PR 18-JUL-2000; 2000EP-0115489.
XX PA (NEST ) SOC PROD NESTLE SA.
XX PI Darimont C, Mace K, Pfeifer A;
XX DR WPI; 2002-188539/24.
XX KW New human pre-adipose cell line capable of differentiating to adipose
PT cells, useful in developing drug, food ingredients, and supplements
PT against obesity, diabetes and cardiovascular diseases -
XX PS Example 5; Page 10; 30pp; English.
XX CC The present invention relates to new human pre-adipose cell lines capable
CC to differentiate to white adipose cells, exhibiting essentially the same
CC cellular properties of normal white adipose cells. The human pre-adipose
CC cell lines are useful for the identification of substances controlling
CC the regulation of lipid uptake and release by human white adipocytes,
CC and substances controlling the differentiation of preadipocytes into
CC mature adipocytes. They are useful for screening compounds capable to
CC regulate the secretion of any metabolites or hormones from human white
CC adipocytes. Sequences of the invention are useful for developing drugs,
CC food ingredients and supplements against obesity, diabetes and cardio-
CC vascular diseases. The present DNA sequence is a reverse transcription
CC (RT)-PCR primer which is used for the expression of adipocytes in
CC differentiated immortalised human preadipose cells. This primer is
CC used in the exemplification of the invention.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 15 AAAAAAAAAAAAAA 1

RESULT 776
AAD22531
ID AAD22531 standard; RNA; 15 BP.
XX AC AAD22531;
XX DT 12-FEB-2002 (first entry)
XX DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
XX KW RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
XX KW virucide; oncogene; cancer; transcription; translation; leukaemia virus;
XX KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
XX KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
XX OS Retrovirus.
XX PN US6291438-B1.
XX PD 18-SEP-2001.
XX PF 06-OCT-1998; 98US-0167375.
XX PR 24-FEB-1993; 93US-0022055.
XX PR 23-FEB-1994; 94US-0200650.
XX PR 22-FEB-1996; 96US-0604871.
XX PA (WANG/) WANG J H.
XX PI Wang JH;
XX DR WPI; 2002-009339/01.
XX KW Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
PT reverse transcriptase comprises at the 2'-O position of the
PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly
PT substituted phenyl compound -
XX PS Example 3; Column 24; 56pp; English.
XX CC The invention relates to derivatised antisense oligoribonucleotides with
CC enhanced membrane permeability and stability. The derivatised antisense
CC oligoribonucleotide complementary to a sequence of nucleotides found
CC in a virus or a cell is useful for inhibiting e.g. viral reverse
CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
CC the 2'-O position with a hydrophobic carrier reagent containing a poly
CC substituted phenyl compound. The derivatised oligoribonucleotides are
CC used to decrease the expression of oncogenes and thereby decrease the
CC phenotypic and pathological properties. The oligoribonucleotides are also
CC used for increasing the effectiveness of antisense oligonucleotide
CC targeted to a gene associated with a disease or a condition in an
CC animal. To alter gene transcription and/or translation for any gene or
CC gene segment responsible for expression, to inhibit viral reverse
CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis
CC virus, oncogenes and human immunodeficiency virus. The present sequence
CC is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
CC which is used in the treatment of moloney murine leukaemia virus (MuLV)
CC in mammals.
XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 1 AAAAAAAAAAAAAA 15

RESULT 777

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ABZ37501/c
XX ABZ37501 standard; DNA; 15 BP.
XX AC ABZ37501;
XX DT 18-FEB-2003 (first entry)
XX DE Oligonucleotide SEQ ID NO:622.
XX KW Library; cleavage; display; diverse family; ss.
XX OS Synthetic.
XX PN WO200283872-A2.
XX PD 24-OCT-2002.
XX PF 17-APR-2002; 2002WO-US12405.
XX PR 17-APR-2001; 2001US-0837306.
XX PR 24-OCT-2001; 2001US-0000516.
XX PR 25-OCT-2001; 2001US-0045674.
XX (LADN/) LADNER R C.
XX (COHE/) COHEN E H.
XX (NAST/) NASTRI H G.
XX (ROOK/) ROOKEY K L.
XX (HOET/) HOET R.
XX (HOOG/) HOOGENBOOM H R J M.
XX
XX Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
XX Hooogenboom HRJM;
XX
XX WPI; 2003-093015/08.
XX
XX Cleaving single-stranded nucleic acid sequences at a desired location
XX by contacting the nucleic acid with an single strand oligonucleotide
XX complementary to a nucleic acid region where cleavage is desired -
XX
XX Disclosure; Page 481; 485pp; English.
XX
XX The present invention describes a method for cleaving single-stranded
XX nucleic acid sequences at a desired location. Also described: (1) methods
XX for displaying or expressing a member of a diverse family of peptides,
XX polypeptides or proteins on the surface of a genetic package and
XX collectively displaying at least a part of the diversity of the family,
XX where the displayed or expressed peptide, polypeptide or protein is
XX encoded at least in part by a nucleic acid that has been cleaved at a
XX desired location; (2) a method for preparing single-stranded nucleic
XX acids; (3) a method for preparing a library comprising a collection of
XX genetic packages that display a member of a diverse family of peptides,
XX polypeptides or proteins and that collectively display at least a portion
XX of the family; (4) a vector comprising a DNA sequence encoding an
XX antibody variable region linked to a version of pIII anchor which does
XX not mediate infection of phage particles, and wild-type gene III; (5) a
XX method for producing a population or a library of immunoglobulin genes;
XX and (6) a library of immunoglobulins that comprise members having at
XX least one variable domain in which at least one of CDR1 and CDR2 contain
XX synthetic diversity and CDR3 diversity is captured from B cells. The
XX method is useful for cleaving single-stranded nucleic acid sequences at a
XX desired location, which can be subsequently used to produce libraries or
XX genetic packages that display and/or express a diverse family of
XX peptides, polypeptides or proteins. ABZ37510 to ABZ37510 and ABZ55464 to
XX ABP55499 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX i084 AAAAAAAAAAAAAA 1098
XX |||||||

```

```

Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 778
ABV75865/c
ID ABV75865 standard; DNA; 15 BP.
XX AC ABV75865;
XX DT 05-FEB-2003 (first entry)
XX DE Oligonucleotide T15-Q-CDPI3.
XX KW Deprotection; phosphoramidite; ss.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX modified_base 1..15
XX /*tag= a
XX /mod_base= OTHER
XX /note= "phosphoramidite linkage"
XX modified_base 15
XX /*tag= b
XX /mod_base= OTHER
XX /note= "3' Q-CDPI3"
XX
XX WO200272864-A2.
XX
XX 19-SEP-2002.
XX
XX 04-MAR-2002; 2002WO-US06739.
XX
XX 08-MAR-2001; 2001US-274309P.
XX (PEKE ) PE CORP NY.
XX Nelson J;
XX WPI; 2003-046740/04.
XX
XX New oligonucleotide deprotection reagent useful for deprotecting
XX oligonucleotide comprises an active methylene compound and an amine
XX reagent -
XX
XX Example 2; Page 25; 46pp; English.
XX
XX The present invention provides a method for deprotection of an
XX oligonucleotide. This involves reacting a protected
XX oligonucleotide, which is preferably covalently attached to a
XX solid support through a linkage, with a deprotection reagent
XX comprising an active methylene compound and an amine reagent.
XX The process and reagent minimise side-reactions leading to
XX certain impurities that contaminate synthetic oligonucleotides.
XX The present sequence is a T15 phosphoramidite oligonucleotide
XX having a quencher moiety (Q) and minor groove binder (CDPI3) at
XX the 3' end, which was synthesised in an example of the invention.
XX This protected oligonucleotide was treated either with 15%
XX ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in
XX 15% ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis
XX showed that deprotection without DEM yielded a complex mixture
XX of products containing only 26.5% of the desired product. When
XX DEM was used, 76.8% of the desired product was obtained.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX i084 AAAAAAAAAAAAAA 1098
XX |||||||

```

Db 15 AAAAAAAAAAAAAA 1

RESULT 779  
ABV74141/c

ID ABV74141 standard; DNA; 15 BP.

XX  
AC ABV74141;

XX  
DT 23-JAN-2003 (first entry)

XX  
DE Oligonucleotide used in cDNA library array.

XX  
KW G-protein coupled receptor; odourant; receptor; olfaction; array;  
KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer;  
KW ss.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "5, polylinker"

XX  
PN WO200277200-A2.

XX  
PD 03-OCT-2002.

XX  
PF 26-MAR-2002; 2002WO-US09559.

XX  
PR 27-MAR-2001; 2001US-279168P.

XX  
PR 31-JAN-2002; 2002US-353392P.

XX  
PA (INSC-) INSCENT INC.

XX  
PI Woods D, Dimitratos S;

XX  
DR WPI; 2003-029930/02.

XX  
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked  
PT receptors, useful for isolating odourant binding proteins or pesticide  
PT alternatives, by analyzing sequences from a male- and female-specific  
PT nucleic acid library -

XX  
PS Disclosure; Fig 5; 83pp; English.

XX  
CC The present sequence is that of a poly-T oligonucleotide used in a  
CC method designed to rapidly array and normalize a complex cDNA library  
CC obtained from a target species. Clones are arrayed into multi-well  
CC plates. Each well contains 16 oligonucleotides with a 5' polylinker,  
CC a poly-T run capable of binding cDNAs by their poly-A tail and a  
CC unique 3' sequence, which allows an anchored oligonucleotide in each  
CC well to selectively hybridise only to those cDNA clones with a  
CC complementary 5' end. The unique 3' key sequences are designed to  
CC give a comprehensive level of degeneracy since they are diverse and  
CC numerous enough to ensure that every possible cDNA sequence can be  
CC bound by an individual, specific oligonucleotide in a single well.  
CC The cDNA library is heated to denature the clones into single  
CC stranded DNA, and an aliquot is added to every well. The anchored  
CC oligonucleotide serves as the 3' primer in PCR, and the common 5'  
CC region present in every cDNA clone serves as the 5' priming site.  
CC Denaturing and washing leave anchored cDNA in each well. The library  
CC is now arrayed and normalised. The method was used to identify and  
CC isolate clones encoding G-protein coupled receptors, especially  
CC odourant receptors, and active effectors involved in the olfactory  
CC pathway of invertebrates and vertebrates, e.g. odourant binding  
CC proteins, or other olfactory or neuronal proteins. The identified  
CC receptors and proteins are useful for identifying compounds that  
CC reduce a target animal's sensitivity to odours, for manufacturing  
CC compounds or devices that mask odours, or trapping invertebrates with  
CC odourants. Semi-chemicals (e.g. aromatics or pheromone mimetics) can  
CC be developed with desirable effects on specific species, for the

CC development of pest monitoring systems or non-toxic, species-specific  
CC pesticide alternatives, for controlling insect feeding and breeding  
CC behaviour, detecting the presence of small air-borne molecules, etc.

XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAA 1098  
|||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 780  
ABV74142

ID ABV74142 standard; DNA; 15 BP.

XX  
AC ABV74142;

XX  
DT 23-JAN-2003 (first entry)

XX  
DE 5' End of cDNA library clone.

XX  
KW G-protein coupled receptor; odourant; receptor; olfaction; array;  
KW microarray; anosmia; attractant; aromatic; pesticide; ss.

XX  
OS Synthetic.

XX  
PN WO200277200-A2.

XX  
PD 03-OCT-2002.

XX  
PF 26-MAR-2002; 2002WO-US09559.

XX  
PR 27-MAR-2001; 2001US-279168P.

XX  
PR 31-JAN-2002; 2002US-353392P.

XX  
PA (INSC-) INSCENT INC.

XX  
PI Woods D, Dimitratos S;

XX  
DR WPI; 2003-029930/02.

XX  
PT Identifying nucleic acid encoding novel sex-linked-tissue-linked  
PT receptors, useful for isolating odourant binding proteins or pesticide  
PT alternatives, by analyzing sequences from a male- and female-specific  
PT nucleic acid library -

XX  
PS Disclosure; Fig 5; 83pp; English.

XX  
CC The present sequence is that of the 5' end of a cDNA clone  
CC isolated from a cDNA library e.g. a mosquito antenna library. A  
CC clone was isolated using a method designed to rapidly array and  
CC normalize a complex cDNA library obtained from a target species.  
CC Clones are arrayed into multi-well plates. Each well contains 16  
CC oligonucleotides (see ABV74137) with a 5' polylinker, a poly-T run  
CC capable of binding cDNAs by their poly-A tail and a unique 3'  
CC sequence, which allows an anchored oligonucleotide in each well to  
CC selectively hybridise only to those cDNA clones with a complementary  
CC 5' end. The unique 3' key sequences are designed to give a  
CC comprehensive level of degeneracy since they are diverse and  
CC numerous enough to ensure that every possible cDNA sequence can be  
CC bound by an individual, specific oligonucleotide in a single well.  
CC The cDNA library is heated to denature the clones into single  
CC stranded DNA, and an aliquot is added to every well. The anchored  
CC oligonucleotide serves as the 3' primer in PCR, and the common 5'  
CC region present in every cDNA clone serves as the 5' priming site.  
CC Denaturing and washing leave anchored cDNA in each well. The library  
CC is now arrayed and normalised. The method was used to identify and  
CC isolate clones encoding G-protein coupled receptors, especially  
CC odourant receptors, and active effectors involved in the olfactory

CC pathway of invertebrates and vertebrates, e.g. odourant binding  
CC proteins, or other olfactory or neuronal proteins. The identified  
CC receptors and proteins are useful for identifying compounds that  
CC reduce a target animal's sensitivity to odours, for manufacturing  
CC compounds or devices that mask odours, or trapping invertebrates with  
CC odourants. Semiochemicals (e.g. aromatics or pheromone mimetics) can  
CC be developed with desirable effects on specific species, for the  
CC development of pest monitoring systems or non-toxic, species-specific  
CC pesticide alternatives, for controlling insect feeding and breeding  
CC behaviour, detecting the presence of small air-borne molecules, etc.  
XX  
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Db 1 AAAAAAAAAAAAAA 15

RESULT 781  
AAAX18368/c  
ID AAX18368 standard; DNA; 16 BP.

AC AAX18368;

DT 11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 9.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

JP11032765-A.

09-FEB-1999.

18-JUL-1997; 97JP-0208312.

18-JUL-1997; 97JP-0208312.

(TAKI ) TAKARA SHUZO CO LTD.

WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in  
RT-PCR

Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates  
to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

N = adenine, guanine, cytosine or thymine; gamma = thymine;

k = natural number of 3 or over indicating the repetition of gamma, in

which thymine expressed by gamma is composed of 1/3 or less of adenine,

guanine and/or cytosine. The new nucleotides are useful as primers for

RT-PCR and determination of base sequences. The new sequences allow for

reproductive and highly efficient analysis of gene sequences.

Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1097

Db 15 TAAAAAAAAAAAAA 1

RESULT 782

AAAX18369/c

ID AAX18369 standard; DNA; 16 BP.

AC AAX18369;

DT 11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 10.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

JP11032765-A.

09-FEB-1999.

18-JUL-1997; 97JP-0208312.

18-JUL-1997; 97JP-0208312.

(TAKI ) TAKARA SHUZO CO LTD.

WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in  
RT-PCR

Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates  
to sequences of at least two nucleotides of formula:

(X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

X = a labelled compound and/or a nucleotide with voluntary sequence;

m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

N = adenine, guanine, cytosine or thymine; gamma = thymine;

k = natural number of 3 or over indicating the repetition of gamma, in

which thymine expressed by gamma is composed of 1/3 or less of adenine,

guanine and/or cytosine. The new nucleotides are useful as primers for

RT-PCR and determination of base sequences. The new sequences allow for

reproductive and highly efficient analysis of gene sequences.

Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1097

Db 15 TAAAAAAAAAAAAA 1

RESULT 783

ABL57075

ID ABL57075 standard; DNA; 16 BP.

AC ABL57075;

DT 22-JUL-2002 (first entry)

Molecular beacon target sequence.

Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;  
ss.

OS Synthetic.

```

XX FH Key Location/Qualifiers
XX FT misc_binding 1..16
XX FT /tag= a
XX FT /bound_moiety= "Molecular beacon"
XX FT /note= "forms double-stranded region with bases
XX FT 5-21 of sequence in ABL57069"
XX PN WC200218951-A2.
XX PD 07-MAR-2002.
XX PF 29-AUG-2001; 2001WO-US41941.
XX PR 29-AUG-2000; 2000US-228728P.
XX PR 30-MAR-2001; 2001US-280350P.
XX PA (UVRQ ) UNIV ROCKEFELLER.
XX PI Dubertret B, Calame M, Libchaber A;
XX PR WPI; 2002-401727/43.
XX PR Sensitive detecting proximity changes in a system that utilizes an
XX PR interacting fluorophore and quencher, for high sensitivity
XX PR PT applications, involves utilizing a metal surface as quencher
XX PS Example 3; Page 30; 62pp; English.
XX CC The present sequence is that of a perfectly matched target
XX CC sequence for a molecular beacon comprising an oligonucleotide probe
XX CC (see ABL57069) covalently attached at the 3' end to fluorescent
XX CC dye and at the 5' end to a nanoparticle. In the native state, the
XX CC probe forms a hairpin conformation with hybridised termini. The
XX CC proximity of the fluorophore and quencher (gold nanoparticle) in
XX CC the molecular beacon results in little or no detectable
XX CC fluorescence. Upon hybridisation of the central complementary
XX CC stretch of the probe to a target sequence, such as the present
XX CC sequence, the hairpin undergoes a conformational change resulting
XX CC in an increase in fluorescence, the extent of which is proportional
XX CC to the amount of target sequence present. Single mismatches can
XX CC be detected. The invention relates generally to the use of metal
XX CC surface quenchers such as particles or films for high sensitivity
XX CC applications in, for example, detection and diagnostic systems.
XX SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 2 AAAAAAAAAAAAAA 16

RESULT 784
AAK69799/c
ID AAK69799 standard; RNA; 17 BP.
XX AC AAK69799;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WC200218951-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR ) CHIRON CORP.
XX PR WPI; 1997-259017/23.
XX PR Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX PR mRNA stability - useful for treating e.g. tumour angiogenesis,
XX PR psoriasis, rheumatoid arthritis, etc., in a human patient
XX PS Claim 4; Page 79; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX CC be treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AAK67275 to AAK75752 represent specific examples
XX CC of nucleic acid molecules from the present invention.
XX SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 17 AAAAAAAAAAAAAA 3

RESULT 785
AAK69802/c
ID AAK69802 standard; RNA; 17 BP.
XX AC AAK69802;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WC200218951-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR ) CHIRON CORP.

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XX PN WC9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR ) CHIRON CORP.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX PR WPI; 1997-259017/23.
XX PR Nucleic acid molecule modulating VEGF receptor(s) gene expression or
XX PR mRNA stability - useful for treating e.g. tumour angiogenesis,
XX PR psoriasis, rheumatoid arthritis, etc., in a human patient
XX PS Claim 4; Page 79; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
XX CC be treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AAK67275 to AAK75752 represent specific examples
XX CC of nucleic acid molecules from the present invention.
XX SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 U; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 17 AAAAAAAAAAAAAA 3

RESULT 785
AAK69802/c
ID AAK69802 standard; RNA; 17 BP.
XX AC AAK69802;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WC9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR ) CHIRON CORP.

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PA (RIBO-) RIBOZYME PHARM INC.  
 XX Escobedo J, McSwigen J, Pavco P, Stinchcomb D;  
 XX WPI; 1997-259017/23.  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or  
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,  
 PT psoriasis, rheumatoid arthritis, etc., in a human patient  
 XX  
 PS Claim 4; Page 79; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KOR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can  
 CC be treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 U; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 786  
 AAV37934/C  
 ID AAV37934 standard; cDNA; 17 BP.  
 AC AAV37934;  
 XX  
 XX 05-OCT-1998 (first entry)  
 DT  
 DE Primer of the specification.  
 XX  
 XX Leukocyte; Iga nephropathy; diagnosis; treatment; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9824815-A1.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 05-DEC-1997; 97WO-JP04469.  
 XX  
 PR 05-DEC-1996; 96JP-0325752.  
 XX  
 XX (KAZU-) KAZUSA DNA RES INST FOUND.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 XX  
 XX Ishiwata T, Kuga T, Nagase T, Nakagawa S, Nishi T;  
 PI Nishimura A, Nomura N, Sakurada M, Sawada S, Takei M;  
 XX  
 XX WPI; 1998-333259/29.  
 XX  
 XX Protein from leukocytes and DNA encoding it - useful as reagents for  
 PT diagnosing and treating Iga nephropathy  
 PT  
 PS Example 2; Page 33; 41pp; Japanese.  
 XX  
 CC PCR primers AAV37933-39 are used in the course of the invention. The  
 CC specification describes a novel protein isolated from leukocytes of  
 CC patients with Iga nephropathy. Oligonucleotides based on the DNA  
 CC sequence encoding this protein are useful as reagents for diagnosing

CC and treating Iga nephropathy.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2  
 RESULT 787  
 AAV19118/C  
 ID AAV19118 standard; DNA; 17 BP.  
 XX  
 AC AAV19118;  
 XX  
 DT 28-AUG-1998 (first entry)  
 DT  
 DE Anchored oligo(T) primer.  
 XX  
 XX Secreted apoptosis-related protein; SARP; msARPI; mouse;  
 KW prostate cancer; breast cancer; diagnosis; gene therapy; PCR;  
 KW primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9813493-A2.  
 XX  
 PD 02-APR-1998.  
 XX  
 XX 24-SEP-1997; 97WO-US17154.  
 XX  
 PR 11-OCT-1996; 96US-0028363.  
 PR  
 PR 24-SEP-1996; 96US-0026603.  
 XX  
 XX (LXRB-) LXR BIOTECHNOLOGY INC.  
 PA  
 XX  
 XX Melkonyan H, Umansky S;  
 PI  
 XX  
 DR WPI; 1998-230704/20.  
 XX  
 XX New secreted apoptosis-related proteins - useful for modulating  
 PT apoptosis, particularly for treatment of prostatic or breast cancer,  
 PT also for diagnosis and monitoring of disease  
 PT  
 PS Example 1; Page 30; 101pp; English.  
 XX  
 XX This oligo(T) synthetic oligonucleotide was used for first strand  
 CC cDNA synthesis from total RNA isolated from either logarithmically  
 CC growing or quiescent 10T1/2 mouse fibroblast cells. It was also  
 CC used with an arbitrary d(N10) primer in PCR. The PCR products  
 CC were used in a differential display to identify the msARPI gene  
 CC (see AAV19112) that codes for novel murine secreted apoptosis-related  
 CC protein msARPI (see AAW37814). The invention relates to SARP  
 CC polynucleotides (see also AAV19113-15) and polypeptides (see also  
 CC AAW37815-17), antibodies specific for SARP, and use of such  
 CC polynucleotides and antibodies in diagnostic and therapeutic  
 CC methods, and methods for treating diseases related to the  
 CC regulation of SARP expression in tissue and body fluid samples,  
 CC including cancers.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 15 AAAAAAAAAAAAAA 1

```

RESULT 788
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP02732.
XX
PR 27-APR-1999; 99JP-0120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels; useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative
CC to a control. Pollinosis-associated gene 581 is useful in the diagnosis
CC of allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
| | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 789
AAC64163/c
ID AAC64163 standard; DNA; 17 BP.

```

```

XX
AC AAC64163;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP02732.
XX
PR 27-APR-1999; 99JP-0120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels; useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative
CC to a control. Pollinosis-associated gene 581 is useful in the diagnosis
CC of allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
| | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 790
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)

```

PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.

Human; pollinosis-associated gene 513; IGE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065049-A1.

02-NOV-2000.

26-APR-2000; 2000WO-JP02733.

27-APR-1999; 99JP-0120491.

(GENO-) GENOX RES INC.

Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S; Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K; WPI; 2000-687342/67.

Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IGE levels, useful in diagnosis of allergic diseases and screening drug candidates -

Example 6; Page 38; 46pp; Japanese.

The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 513 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 513 nucleic acids; and methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 513 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.

Pollinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 513 cDNA.

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Db |||||||  
16 AAAAAAAAAAAAAA 2

RESULT 791  
AAC64173/c  
ID AAC64173 standard; DNA; 17 BP.  
AC AAC64173;  
XX  
XX  
XX 21-FEB-2001 (first entry)  
DE PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.  
Human; pollinosis-associated gene 513; IGE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
Synthetic.  
WO200065049-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP02733.

XX 27-APR-1999; 99JP-0120491.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S; Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K; WPI; 2000-687342/67.

XX Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IGE levels, useful in diagnosis of allergic diseases and screening drug candidates -

XX Example 6; Page 39; 46pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 513 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 513 nucleic acids; and methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 513 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.

Pollinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 513 cDNA.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

QY Query Match 1.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Db |||||||  
16 AAAAAAAAAAAAAA 2

RESULT 792  
AAC64182/c  
ID AAC64182 standard; DNA; 17 BP.  
XX AAC64182;  
XX  
XX 21-FEB-2001 (first entry)  
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.  
Human; pollinosis-associated gene 419; FAF-1 homologue; Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
Synthetic.  
WO200065045-A1.  
XX  
XX 02-NOV-2000.  
XX 26-APR-2000; 2000WO-JP02729.  
XX 27-APR-1999; 99JP-0120490.  
XX (GENO-) GENOX RES INC.



```

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687338/67.
XX
XX Pollinosis-associated gene 419 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels, useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
XX Example 6; Page 49; 77pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated
CC from T-cells from individuals allergic to cedar pollen using the
CC differential display method. Pollinosis-associated gene 419 has
CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
CC The invention also relates to the protein encoded by pollinosis gene
CC 419; expression constructs and host cells comprising pollinosis-
CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
CC and probes; antibodies against the protein encoded by the gene; methods
CC of detection of pollinosis-associated gene 419 nucleic acids; and a
CC method of diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents
CC a PCR primer used in the isolation of human pollinosis-associated gene
CC 419 cDNA.
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2
RESULT 793
AAC64183/c
ID AAC64183 standard; DNA; 17 BP.
XX
XX AAC64183;
AC
XX 21-FEB-2001 (first entry)
DT
XX PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
DE
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200065045-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP02729.
XX
XX 27-APR-1999; 99JP-0120490.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687338/67.

```

```

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687338/67.
XX
XX Pollinosis-associated gene 419 undergoing significantly low expression
PT in subjects with high cedar pollen-specific IgE levels, useful in
PT diagnosis of allergic diseases and screening drug candidates -
XX
XX Example 6; Page 50; 77pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated
CC from T-cells from individuals allergic to cedar pollen using the
CC differential display method. Pollinosis-associated gene 419 has
CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
CC The invention also relates to the protein encoded by pollinosis gene
CC 419; expression constructs and host cells comprising pollinosis-
CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
CC and probes; antibodies against the protein encoded by the gene; methods
CC of detection of pollinosis-associated gene 419 nucleic acids; and a
CC method of diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents
CC a PCR primer used in the isolation of human pollinosis-associated gene
CC 419 cDNA.
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2
RESULT 794
AAC64203/c
ID AAC64203 standard; DNA; 17 BP.
XX
XX AAC64203;
AC
XX 21-FEB-2001 (first entry)
DT
XX PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
DE
XX Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection;
KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200065046-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP02730.
XX
XX 27-APR-1999; 99JP-0120489.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687339/67.

```



CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 627 nucleic acids; and a method of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence  
 CC of a test compound relative to a control. Pollinosis-associated gene 627  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence  
 CC represents a PCR primer used in the isolation of human pollinosis-  
 CC associated gene 627 cDNA.

CC Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 DB 16 AAAAAAAAAAAAAA 2

RESULT 797  
 AAC64215/c  
 ID AAC64215 standard; DNA; 17 BP.  
 AC AAC64215;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.  
 XX

KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection;  
 KW diagnosis; drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.

XX WO200065051-AL.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP02735.  
 XX  
 PR 27-APR-1999; 99JP-0120493.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687344/67.

XX Pollinosis-associated gene 627 undergoing significantly low expression  
 in subjects with high cedar pollen-specific IgE levels, useful in  
 PT diagnosis of allergic diseases and screening drug candidates -  
 XX  
 PS Example 6; Page 42; 51pp; Japanese.

CC The invention relates to the human pollinosis-associated gene 627 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 627 nucleic acids; and a method of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence

CC of a test compound relative to a control. Pollinosis-associated gene 627  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence  
 CC represents a PCR primer used in the isolation of human pollinosis-  
 CC associated gene 627 cDNA.

CC Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 DB 16 AAAAAAAAAAAAAA 2

RESULT 798  
 AAC64231/c  
 ID AAC64231 standard; DNA; 17 BP.

XX AAC64231;  
 XX  
 DT 21-FEB-2001 (first entry)

XX PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.

KW Human; pollinosis-associated gene 795; vimentin homologue;  
 KW IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

XX WO200065050-AL.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP02734.

XX 27-APR-1999; 99JP-0120494.

XX (GENO-) GENOX RES INC.  
 XX (EISA) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
 XX Yokoi A;

XX WPI; 2000-687343/67.

XX Pollinosis-associated gene 795 undergoing significantly low expression  
 in subjects with high cedar pollen-specific IgE levels, useful in  
 PT diagnosis of allergic diseases and screening drug candidates -

XX Page 45; Example 6; 73pp; Japanese.

CC The invention relates to the human pollinosis-associated gene 795 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. Pollinosis-associated gene 795 has  
 CC homology with the human vimentin gene. The invention also relates also  
 CC relates to the protein encoded by pollinosis gene 795; to expression  
 CC constructs and host cells comprising pollinosis-associated gene 795  
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
 CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 795 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 795 nucleic acids. The invention additionally encompasses methods of  
 CC screening drug candidates for the treatment of allergic disease by  
 CC measuring the expression of pollinosis-associated gene 795 in pollen  
 CC antigen-stimulated T-cells in the presence of a test compound relative to  
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of

CC allergic diseases and in the screening of drug candidates for the  
 CC treatment of such diseases. The present sequence represents a PCR primer  
 CC used in the isolation of human pollinosis-associated gene 795 cDNA.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 799  
 AAC64232/c  
 ID AAC64232 standard; DNA; 17 BP.  
 XX  
 AC AAC64232;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.  
 XX  
 KW Human; pollinosis-associated gene 795; vimentin homologue;  
 KW IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
 OS Synthetic.  
 XX  
 PN WO20006050-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP02734.  
 XX  
 PR 27-APR-1999; 99JP-0120494.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
 PI Yokoi A;  
 XX  
 WPI; 2000-687343/67.  
 XX  
 PT Pollinosis-associated gene 795 undergoing significantly low expression  
 PT in subjects with high cedar pollen-specific IgE levels; useful in  
 PT diagnosis of allergic diseases and screening drug candidates -  
 XX  
 PS Page 46; Example 6; 73pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 795 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. Pollinosis-associated gene 795 has  
 CC homology with the human vimentin gene. The invention also relates also  
 CC relates to the protein encoded by pollinosis gene 795; to expression  
 CC constructs and host cells comprising pollinosis-associated gene 795  
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
 CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 795 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 795 nucleic acids. The invention additionally encompasses methods of  
 CC screening drug candidates for the treatment of allergic disease by  
 CC measuring the expression of pollinosis-associated gene 795 in pollen  
 CC antigen-stimulated T-cells in the presence of a test compound relative to  
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
 CC allergic diseases and in the screening of drug candidates for the  
 CC treatment of such diseases. The present sequence represents a PCR primer

CC used in the isolation of human pollinosis-associated gene 795 cDNA.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 800  
 AAX82721/c  
 ID AAX82721 standard; DNA; 17 BP.  
 XX  
 AC AAX82721;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE Human IgA nephropathy-associated cDNA primer #62.  
 XX  
 KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
 KW human; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO9963085-A1.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-JP02855.  
 XX  
 PR 02-JUN-1998; 98JP-0152603.  
 XX  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 PI Sawada S, Takei M, Shibata K, Furuya A;  
 XX  
 WPI; 2000-097328/08.  
 XX  
 PT DNA sequences preferentially expressed in IgA nephropathy patients,  
 PT proteins encoded by them, and antibodies to those proteins -  
 XX  
 PS Claim 3; Page 170; 180pp; Japanese.  
 XX  
 CC This invention describes novel DNA sequences preferentially expressed in  
 CC IgA nephropathy patients, and DNA sequences stringently hybridizing to  
 CC them. Independent claims cover diagnostic reagents for IgA nephropathy  
 CC incorporating the antisense sequences; the treatment of IgA nephropathy  
 CC using the antisense sequences for mRNA inhibition; proteins associated  
 CC with IgA nephropathy, containing sequences encoded by the DNA sequences;  
 CC antibodies recognizing these proteins; the production of the proteins  
 CC by culture of host cells transformed with DNA encoding them; diagnostic  
 CC reagents for IgA nephropathy containing the antibodies; and compositions  
 CC for the treatment of IgA nephropathy which contain the antibodies. The  
 CC products of the invention can be used for the diagnosis and treatment of  
 CC IgA nephropathy. This sequence represents a primer used in the isolation  
 CC and identification of the human IgA nephropathy-associated proteins  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

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RESULT 801
AA30180/c
ID AAX82722 standard; DNA; 17 BP.
XX
AC AAX82722;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IGA nephropathy-associated cDNA primer #63.
XX
KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP02855.
XX
PR 02-JUN-1998; 98JP-0152603.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Ihiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
KW DNA sequences preferentially expressed in IGA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins
XX
PS Claim 3; Page 170; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IGA nephropathy
CC incorporating the antisense sequences; the treatment of IGA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins
CC by culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IGA nephropathy containing the antibodies; and compositions
CC for the treatment of IGA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IGA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IGA nephropathy-associated proteins
CC described in the method of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1-4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 802
AA30180/c
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15C used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP05506.
XX
PR 06-OCT-1998; 98JP-0284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
KW

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KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX Synthetic.
XX WO200020575-A1.
XX PD 13-APR-2000.
XX PF 06-OCT-1999; 99WO-JP05506.
XX PR 06-OCT-1998; 98JP-0284610.
XX PA (GENO-) GENOX RES INC.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Lu N, Ogawa K;
XX WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1-4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
Db 16 AAAAAAAAAAAAAA 2

RESULT 803
AA30181/c
ID AAA30181 standard; DNA; 17 BP.
XX
AC AAA30181;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15G used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP05506.
XX
PR 06-OCT-1998; 98JP-0284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX

```

DR WPI; 2000-317712/27.

XX Gene highly expressed in patients with high cedar pollen-specific IgE

PT levels, useful for diagnosing pollenosis, and screening candidate

PT compounds for pollenosis treatment -

XX Example 6; Page 38; 44pp; Japanese.

XX This sequence represents a PCR primer used in the identification of a

CC human pollenosis associated gene. The gene is highly expressed in

CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The

CC invention relates to the nucleotide sequence encoding the pollenosis

CC associated protein, diagnosing pollenosis and screening candidate

CC compounds for treating pollenosis. The gene can be used in diagnosing

CC pollenosis, particularly cedar pollenosis, and screening candidate

CC compounds for pollenosis treatment.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

SQ Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 16 AAAAAAAAAAAAAA 2

RESULT 804

AAA25448/c

ID AAA25448 standard; DNA; 17 BP.

XX AAA25448;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.

XX Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;

XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

XX gene expression modification; cancer; phosphorothioate; endonuclease;

XX anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

OS WO9954459-A2.

PN 28-OCT-1999.

PD 19-APR-1999; 99WO-US08547.

PF 20-APR-1998; 98US-0082404.

PR 23-JUN-1998; 98US-0103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target

PT sequences, used to treat cancer -

XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphorodithioate

CC link, having endonuclease activity. (A), and more generally any

CC catalytic nucleic acid (A') that modulates expression of the oestrogen

CC receptor gene, are used to treat cancer (particularly of breast or

CC endometrium), in vivo or by transforming cells ex vivo and implanting

CC treated cells, or for other conditions associated with levels of

CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

CC can also be used to correlate inhibition of gene expression with

CC alterations in phenotype, particularly for identification of therapeutic

CC targets, and as research reagents (for RNA, in the same way that

CC restriction endonucleases are used with DNA). The combination of

CC modifications in (A) improves resistance to nucleases, binding affinity

CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor

CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their

CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen

CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent

CC their corresponding target sequences. AAA26219 to AAA26271 represent

CC other ribozyme sequences and antisense oligonucleotides used in the

CC exemplification of the present invention.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

SQ Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 17 AAAAAAAAAAAAAA 3

RESULT 805

AAZ36740/c

ID AAZ36740 standard; DNA; 17 BP.

XX AAZ36740;

DT 13-MAR-2000 (first entry)

DE Anchored oligo(dT) primer GT15G used for modified differential display.

XX Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;

XX differentially expressed nucleic acid; disease state; cancer;

XX autoimmune disease; infectious disease; aging; developmental disorder;

XX proliferative disorder; neurological disorder; toxicity; primer;

XX treatment resistance; differential expression; drug discovery;

XX growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

XX Synthetic.

OS WO9955913-A2.

PN 04-NOV-1999.

PD 27-APR-1999; 99WO-US09119.

PF 27-APR-1998; 98US-0083331.

PR 27-AUG-1998; 98US-0098070.

PR 04-FEB-1999; 99US-0118624.

XX (KIMM-) KIMMEL CANCER CENT SIDNEY.

XX McClelland M, Welsh J, Trenkle T;

PI WPI; 2000-086388/07.

XX Measuring expression of low abundance reduced complexity target nucleic

PT acid molecules -

XX Example 3; Page 91; 187pp; English.

XX AAZ36739-41 represent oligo(dT) primers used for modified differential

CC display, in the method of the invention. The specification describes a

CC method for measuring the level of two or more nucleic acid molecules in

CC a target. The method comprises contacting a probe with an arbitrarily or

CC statistically sampled target and detecting the amount of specific

CC binding of the target to the probe. The methods can be used to identify

CC differentially expressed nucleic acid molecules associated with disease

CC states, such as cancer, autoimmune disease, infectious disease, aging,  
CC developmental disorder, proliferative disorder or neurological disorder.  
CC Alternatively the methods can be used to assess the efficacy or toxicity  
CC of or a resistance to a treatment. Also the methods can be used to  
CC determine differential expression of nucleic acid molecules in response  
CC to a stimulus, e.g. a chemical, drug or growth factor (especially  
CC epidermal growth factor), radiation, stress or a pathogen. The methods  
CC can also be used to determine co-regulated genes that can be potential  
CC targets for drug discovery.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

SQ Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||

RESULT 806

AAZ35714/c

ID AAZ35714 standard; DNA; 17 BP.

XX AAZ35714;

DT 31-JAN-2000 (first entry)

DE Murine gene anchor PCR primer SEQ ID NO:3.

XX Rare expressed gene; analysis; expression; nucleic acid sample;  
KW PCR primer; ss.

XX Synthetic.

OS Mus sp.

XX EP959141-A2.

XX 24-NOV-1999.

XX 18-MAY-1999; 99EP-0109795.

XX 20-MAY-1998; 98JP-0153651.

XX (HITA) HITACHI LTD.

XX Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;

XX WPI; 2000-001284/01.

XX Preparation of nucleic acid sample, useful for analysis of rare  
PT expressed genes -

PS Disclosure; Page 11; 22pp; English.

XX The present invention describes a process for the preparation of a  
CC nucleic acid sample comprising: (a) providing a nucleic acid sample  
CC having a plurality of species of sequences, and providing one or a  
CC plurality of kinds of probes having a known sequence substantially  
CC complementary to a portion of sequence of the nucleic acid sample; (b)  
CC mixing and hybridizing the nucleic acid sample with probes; (c)  
CC subsequently recovering nucleic acid molecules; or (i) providing a  
CC nucleic acid sample having a plurality of species of sequences, and  
CC providing one or a plurality of kinds of probes having a known sequence  
CC substantially complementary to a portion of sequence of the nucleic acid  
CC sample; (ii) mixing and hybridizing the nucleic acid sample with the  
CC probes; (iii) treating the product of (ii) with nuclease activity of an  
CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic  
CC acid molecules not digested by the nuclease activity in (iii); or (I)  
CC providing a nucleic acid sample having a plurality of species of  
CC sequences and oligonucleotide primer having predetermined sequences for  
CC synthesizing DNA strands; (II) providing one or a plurality of kinds of

CC probes having a known sequence substantially complementary to a portion  
CC of a sequence of the nucleic acid sample having such a structure to  
CC prevent a polymerase reaction from its 3' end and a nuclease reaction  
CC from its 5' end; (iii) mixing and hybridizing the nucleic acid sample  
CC with the primers and probes; (iv) executing polymerase chain reaction  
CC for the samples prepared in (iii); and (v) subsequently recovering  
CC nucleic acid molecules synthesized in (iv). The method is useful for the  
CC preparation of a nucleic acid sample for the analysis of rare expressed  
CC genes. The present sequence represents a PCR primer used in the  
CC exemplification of the present invention.

SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||

RESULT 807

AAC82875/c

ID AAC82875 standard; DNA; 17 BP.

XX AAC82875;

XX 20-MAR-2001 (first entry)

XX Human pollinosis-associated gene 441 primer #2.

XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
KW pollen scattering; antigen; primer; ss.

XX Homo sapiens.

XX WO200073435-A1.

XX 07-DEC-2000.

XX 18-MAY-2000; 2000WO-JP03190.

XX 27-MAY-1999; 99JP-0148783.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX WPI; 2001-061526/07.

XX Pollinosis-associated gene 441 which undergoes lower expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus -

XX Example 6; Page 35; 42pp; Japanese.

XX This invention describes a novel nucleic acid molecule comprising a  
CC sequence (I) which undergoes significantly low expression in subjects  
CC after pollen scattering, and is useful in diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

Db |||||

Db 16 AAAAAAAAAAAAAA 2

RESULT 808  
AAC82876/c  
ID AAC82876 standard; DNA; 17 BP.  
XX  
XX AC AAC82876;  
XX  
XX DT 20-MAR-2001 (first entry)  
XX  
XX DE Human pollinosis-associated gene 441 primer #3.  
XX  
XX KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
XX  
XX KW pollen scattering; antigen; primer; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200073435-A1.  
XX  
XX PD 07-DEC-2000.  
XX  
XX PF 18-MAY-2000; 2000WO-JP03190.  
XX  
XX PR 27-MAY-1999; 99JP-0148783.  
XX  
XX PA (GENO-) GENOX RES INC.  
XX  
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX  
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
XX DR WPI; 2001-061526/07.  
XX  
XX PT Pollinosis-associated gene 441 which undergoes lower expression in  
XX  
XX PT subjects after pollen scattering, useful in diagnosis of allergic  
XX  
XX PT diseases and screening candidate compounds to regulate response of T  
XX  
XX PT cells to antigen stimulus -  
XX  
XX PS Example 6; Page 36; 42pp; Japanese.  
XX  
XX CC This invention describes a novel nucleic acid molecule comprising a  
XX  
XX CC sequence (1) which undergoes significantly low expression in subjects  
XX  
XX CC after pollen scattering, and is useful in diagnosis of allergic diseases  
XX  
XX CC and screening candidate compounds for remedies capable of regulating the  
XX  
XX CC response of T cells to the stimulus by an antigen.  
XX  
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
  
Query Match 1.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAA 1098  
Db |||||  
16 AAAAAAAAAAAAAA 2  
  
RESULT 809  
AAC91720/c  
ID AAC91720 standard; DNA; 17 BP.  
XX  
XX AC AAC91720;  
XX  
XX DT 27-MAR-2001 (first entry)  
XX  
XX DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.  
XX  
XX DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.  
XX  
XX KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;  
XX  
XX KW reduced expression; detection; diagnosis; drug screening;  
XX  
XX KW allergic disease; PCR primer; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN WO200073440-A1.  
XX  
XX PD 07-DEC-2000.

PN WO200073440-A1.  
XX  
XX PD 07-DEC-2000.  
XX  
XX PF 18-MAY-2000; 2000WO-JP03192.  
XX  
XX PR 27-MAY-1999; 99JP-0148785.  
XX  
XX PA (GENO-) GENOX RES INC.  
XX  
XX PA (EISA) EISAI CO LTD.  
XX  
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX  
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
XX  
XX PI Yokoi A;  
XX  
XX DR WPI; 2001-032159/04.  
XX  
XX PT Pollinosis-associated gene 787 undergoing significantly low expression  
XX  
XX PT in subjects after pollen scattering, useful in diagnosis of allergic  
XX  
XX PT diseases and screening candidate compounds to regulate response of T  
XX  
XX PT cells to antigen stimulus -  
XX  
XX PS Example 6; Page 40; 54pp; Japanese.  
XX  
XX CC The invention relates to the human pollinosis-associated gene 787 which  
XX  
XX CC exhibits significantly reduced expression in the T-cells of individuals  
XX  
XX CC after the pollen-scattering season, relative to expression levels in  
XX  
XX CC T-cells before the pollen-scattering season. The gene was isolated from  
XX  
XX CC T-cells from individuals allergic to pollen using the differential  
XX  
XX CC display method. The invention also relates to pollinosis-associated gene  
XX  
XX CC 787 primers and probes; methods of detection of pollinosis-associated  
XX  
XX CC gene 787 nucleic acids; and a method of diagnosis of allergic diseases  
XX  
XX CC via the detection of pollinosis-associated gene 787 nucleic acids. The  
XX  
XX CC invention additionally encompasses a method of screening drug candidates  
XX  
XX CC for the treatment of allergic disease by measuring the expression of  
XX  
XX CC pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in  
XX  
XX CC the presence of a test compound relative to a control. Pollinosis-  
XX  
XX CC associated gene 787 is useful in the diagnosis of allergic diseases and  
XX  
XX CC in the screening of drug candidates for the treatment of such diseases.  
XX  
XX CC The present sequence represents a PCR primer used in the isolation of  
XX  
XX CC human pollinosis-associated gene 787 cDNA.  
XX  
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
  
Query Match 1.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAA 1098  
Db |||||  
16 AAAAAAAAAAAAAA 2  
  
RESULT 810  
AAC91721/c  
ID AAC91721 standard; DNA; 17 BP.  
XX  
XX AC AAC91721;  
XX  
XX DT 27-MAR-2001 (first entry)  
XX  
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.  
XX  
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.  
XX  
XX KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;  
XX  
XX KW reduced expression; detection; diagnosis; drug screening;  
XX  
XX KW allergic disease; PCR primer; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN WO200073440-A1.  
XX  
XX PD 07-DEC-2000.





XX Example 6; Page 44; 61pp; Japanese.

PS The present invention describes the human pollinosis-associated gene 465

CC which has a nucleic acid sequence of 3442 base pairs (bp), given in

CC (AAC92291), that undergoes significantly low expression in subjects

CC after pollen scattering, and is useful in the diagnosis of allergic

CC diseases and screening candidate compounds for remedies capable of

CC regulating the response of T cells to the stimulus by an antigen. The

CC gene is useful in the diagnosis of allergic diseases and screening

CC candidate compounds for remedies capable of regulating the response of T

CC cells to the stimulus by an antigen. The present sequence represents a

CC PCR primer which is used in an example from the present invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

SQ

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 16 AAAAAAAAAAAAAA 2

RESULT 813

AAH47127/c

ID AAH47127 standard; DNA; 17 BP.

XX

AC AAH47127;

XX

DT 30-NOV-2001 (first entry)

XX

DE Nucleotide sequence of primer GT15C.

XX

KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis;

KW human; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200165259-A1.

XX

PD 07-SEP-2001.

XX

PF 23-FEB-2001; 2001WO-JP01372.

XX

PR 02-MAR-2000; 2000JP-0061832.

XX

PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

XX

PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;

XX

DR WPI; 2001-557789/62.

XX

PT Diagnosis of allergies including atopic dermatitis

PS Example 6; Page 66; 83pp; Japanese.

XX

CC The invention provides a method of diagnosis of allergies that involves:

CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151

CC in T-cells; and comparing them with the level of expression in healthy

CC T-cells. The method is useful for diagnosing allergies, particularly

CC atopic dermatitis. The present sequence represents a PCR primer used

CC for analysis of the expression of the above genes.

XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 16 AAAAAAAAAAAAAA 2

RESULT 815

AAH49949/c

ID AAL49949 standard; DNA; 17 BP.

XX

AC AAL49949;

XX

DT 10-DEC-2002 (first entry)

XX

DE Human B1153 expression in allergic disease related PCR primer GT15C.

XX

KW Human; allergy; B1153; differential expression; anti-allergic; asthma;

KW antitachymatic; antiinflammatory; atopic skin inflammation; PCR;

XX

OS Unidentified.

XX

PN WO200250269-A1.

DB 16 AAAAAAAAAAAAAA 2

RESULT 814

AAH47128/c

ID AAH47128 standard; DNA; 17 BP.

XX

AC AAH47128;

XX

DT 30-NOV-2001 (first entry)

XX

DE Nucleotide sequence of primer GT15G.

XX

KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis;

KW human; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200165259-A1.

XX

PD 07-SEP-2001.

XX

PF 23-FEB-2001; 2001WO-JP01372.

XX

PR 02-MAR-2000; 2000JP-0061832.

XX

PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

XX

PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;

XX

DR WPI; 2001-557789/62.

XX

PT Diagnosis of allergies including atopic dermatitis

PS Example 6; Page 66; 83pp; Japanese.

XX

CC The invention provides a method of diagnosis of allergies that involves:

CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151

CC in T-cells; and comparing them with the level of expression in healthy

CC T-cells. The method is useful for diagnosing allergies, particularly

CC atopic dermatitis. The present sequence represents a PCR primer used

CC for analysis of the expression of the above genes.

XX

SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098

DB 16 AAAAAAAAAAAAAA 2

RESULT 815

AAH49949/c

ID AAL49949 standard; DNA; 17 BP.

XX

AC AAL49949;

XX

DT 10-DEC-2002 (first entry)

XX

DE Human B1153 expression in allergic disease related PCR primer GT15C.

XX

KW Human; allergy; B1153; differential expression; anti-allergic; asthma;

KW antitachymatic; antiinflammatory; atopic skin inflammation; PCR;

XX

OS Unidentified.

XX

PN WO200250269-A1.

XX 27-JUN-2002.  
 XX 21-DEC-2001; 2001WO-JP11286.  
 XX 21-DEC-2000; 2000JP-0389476.  
 XX (GENO-) GENOX RES INC.  
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;  
 XX WPI; 2002-713252/77.  
 XX Examination of allergic diseases comprises detecting gene B1153  
 XX over-expressed in T cells of allergy patients for diagnosis treatment  
 XX and investigation of atopic skin inflammation and asthma -  
 XX  
 XX Example 6; Page 82; 102pp; Japanese.  
 XX The present invention relates to a method of examining allergic diseases  
 XX which comprises comparing the expression level of gene B1153 in allergy  
 XX patients with the expression level in healthy subjects. The method is  
 XX useful for the treatment, prevention, diagnosis and study of allergic  
 XX diseases including atopic skin inflammation and asthma. The present  
 XX sequence is a PCR primer described in the exemplification of the  
 XX invention.  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
 XX  
 XX Query Match 1.4%; Score 15; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1084 AAAAAAAAAAAAAA 1098  
 XX |||||||||  
 XX Db 16 AAAAAAAAAAAAAA 2  
 XX  
 XX RESULT 816  
 XX AAL49950/c  
 XX ID AAL49950 standard; DNA; 17 BP.  
 XX AC AAL49950;  
 XX 10-DEC-2002 (first entry)  
 XX Human B1153 expression in allergic disease related PCR primer GT15G.  
 XX Human; allergy; B1153; differential expression; antiallergic; asthma;  
 XX antiasthmatic; antiinflammatory; atopic skin inflammation; PCR;  
 XX primer; ss.  
 XX Unidentified.  
 XX WO200250269-AL.  
 XX 27-JUN-2002.  
 XX 21-DEC-2001; 2001WO-JP11286.  
 XX 21-DEC-2000; 2000JP-0389476.  
 XX (GENO-) GENOX RES INC.  
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;  
 XX WPI; 2002-713252/77.  
 XX Examination of allergic diseases comprises detecting gene B1153  
 XX over-expressed in T cells of allergy patients for diagnosis treatment  
 XX and investigation of atopic skin inflammation and asthma -

XX Example 6; Page 82; 102pp; Japanese.  
 XX The present invention relates to a method of examining allergic diseases  
 XX which comprises comparing the expression level of gene B1153 in allergy  
 XX patients with the expression level in healthy subjects. The method is  
 XX useful for the treatment, prevention, diagnosis and study of allergic  
 XX diseases including atopic skin inflammation and asthma. The present  
 XX sequence is a PCR primer described in the exemplification of the  
 XX invention.  
 XX  
 XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
 XX  
 XX Query Match 1.4%; Score 15; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 4e+02;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1084 AAAAAAAAAAAAAA 1098  
 XX |||||||||  
 XX Db 16 AAAAAAAAAAAAAA 2  
 XX  
 XX RESULT 817  
 XX AAL47235/c  
 XX ID AAL47235 standard; DNA; 17 BP.  
 XX AC AAL47235;  
 XX 22-AUG-2002 (first entry)  
 XX Allergic disease examination method related anchor primer SEQ ID NO: 3.  
 XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;  
 XX atopic dermatitis; human; PCR; primer; ss.  
 XX Unidentified.  
 XX WO200233122-AL.  
 XX 25-APR-2002.  
 XX 11-OCT-2001; 2001WO-JP08937.  
 XX 13-OCT-2000; 2000JP-0314093.  
 XX (GENO-) GENOX RES INC.  
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX (EISA) EISAI CO LTD.  
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
 XX Takahashi E;  
 XX WPI; 2002-372313/40.  
 XX Method for examining allergic diseases by differential display of  
 XX intersectin 2 gene showing different expression particularly  
 XX significant increase in eosinophils in patients -  
 XX  
 XX Example 1; Page 53; 90pp; Japanese.  
 XX The present invention relates to a method for examining allergic diseases  
 XX with intersectin 2 gene or a gene with equivalent function of intersectin  
 XX 2 as an indicator gene, which comprises determining the expression level  
 XX of the gene in the eosinophils in a patient, and comparing the expression  
 XX level with that in the eosinophils of a healthy individual. The method is  
 XX for examining allergic diseases, particularly atopic dermatitis, which is  
 XX also applicable in screening candidate compounds for remedies. The  
 XX present sequence is an anchor primer described in the exemplification  
 XX of the invention.  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
 XX  
 XX Query Match 1.4%; Score 15; DB 1; Length 17;

```

Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 818
ABL47236/c
ID AAL47236 standard; DNA; 17 BP.
AC AAL47236;
XX
DT 22-AUG-2002 (first entry)
DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX
KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW atopic dermatitis; human; PCR; primer; ss.
XX
OS Unidentified.
XX
PN W0200233122-AL.
XX
PD 25-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP08937.
XX
PR 13-OCT-2000; 2000JP-0314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (BISA) BISA CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX
DR WPI; 2002-372313/40.
XX
PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly
PT significant increase in eosinophils in patients -
XX
PS Example 1; Page 53; 90pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin
CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification
CC of the invention.
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 819
ABL59039/c
ID ABL59039 standard; DNA; 17 BP.
AC ABL59039;
XX
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a

```

```

DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15C.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-0291316.
XX
PR 25-SEP-2000; 2000JP-0291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control -
XX
PS Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The
CC method comprises measuring the expression level of the gene given
CC in ABL59037, and comparing it with the expression level of the gene
CC in the eosinophils of a healthy person. The method is used for the
CC examination of allergosis. The present sequence represents a PCR
CC primer, which is used in the course of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098
DB 16 AAAAAAAAAAAAAA 2

RESULT 820
ABL59040/c
ID ABL59040 standard; DNA; 17 BP.
XX
AC ABL59040;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15G.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-0291316.
XX
PR 25-SEP-2000; 2000JP-0291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a

```

PT specific gene, and comparing it to the levels in the eosinophils of a  
 PT healthy control -  
 PS Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergic diseases. The  
 CC method comprises measuring the expression level of the gene given  
 CC in ABL59037, and comparing it with the expression level of the gene  
 CC in the eosinophils of a healthy person. The method is used for the  
 CC examination of allergic diseases. The present sequence represents a PCR  
 CC primer, which is used in the course of the invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 821  
 ABN99830/C  
 ID ABN99830 standard; DNA; 17 BP.

AC ABN99830;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 19.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
 KW primer; ss.

OS Homo sapiens.

PN WO200233069-A1.

XX 25-APR-2002.

PF 28-SEP-2001; 2001WO-JP08574.

PR 13-OCT-2000; 2000JP-0314093.

PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;

DR WPI; 2002-372311/40.

XX Method for examining allergic diseases by differential display of  
 PT seventeen genes showing different expression particularly significant  
 PT increase in eosinophils in patients with mild atopic dermatitis, also  
 PT applicable in screening compounds -

PS Example 1; Page 109; 165pp; Japanese.

XX The present invention relates to a method for examining allergic diseases  
 CC which involves determining the expression level of a gene, having one of  
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
 CC eosinophils in a patient and comparing the expression level with that in  
 CC the eosinophils of a healthy individual. The method can be used to  
 CC examine allergic diseases, particularly atopic dermatitis, and its early  
 CC diagnosis, which is also applicable in screening candidate compounds for  
 CC remedies. The present sequence is a PCR primer described in the  
 CC exemplification of the invention.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 822

ABN99831/C

ID ABN99831 standard; DNA; 17 BP.

XX AC ABN99831;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 20.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
 KW primer; ss.

OS Homo sapiens.

PN WO200233069-A1.

PD 25-APR-2002.

PF 28-SEP-2001; 2001WO-JP08574.

PR 13-OCT-2000; 2000JP-0314093.

PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;

DR WPI; 2002-372311/40.

XX Method for examining allergic diseases by differential display of  
 PT seventeen genes showing different expression particularly significant  
 PT increase in eosinophils in patients with mild atopic dermatitis, also  
 PT applicable in screening compounds -

PS Example 1; Page 110; 165pp; Japanese.

XX The present invention relates to a method for examining allergic diseases  
 CC which involves determining the expression level of a gene, having one of  
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
 CC eosinophils in a patient and comparing the expression level with that in  
 CC the eosinophils of a healthy individual. The method can be used to  
 CC examine allergic diseases, particularly atopic dermatitis, and its early  
 CC diagnosis, which is also applicable in screening candidate compounds for  
 CC remedies. The present sequence is a PCR primer described in the  
 CC exemplification of the invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 823

ABK49635/C

ID ABK49635 standard; DNA; 17 BP.

XX AC ABK49635;

DT 15-JUL-2002 (first entry)

XX DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.  
 XX DE Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
 KW differential display; eosinophil; antiallergic; atopic dermatitis;  
 KW GT15C.  
 XX OS Homo sapiens.  
 XX XX WO200224903-A1.  
 XX PD 28-MAR-2002.  
 XX PF 21-SEP-2001; 2001WO-JP08246.  
 XX PR 25-SEP-2000; 2000JP-0291318.  
 XX PA (GENO-) GENOX RES INC.  
 XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX PA (EISA) EISAI CO LTD.  
 XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;  
 PI Takahashi E;  
 XX WI; 2002-315738/35.  
 XX XX Examining allergic diseases by differential display of gene showing  
 PT different expression particularly increased expression in remission  
 PT stage in eosinophils of patients, also applicable in screening  
 PT candidate compounds for remedies -  
 XX Example 1; Page 56; 72pp; Japanese.  
 XX CC The invention relates to a method for examining allergic diseases  
 CC comprising determining the expression level of a gene containing,  
 CC the human cDNA appearing as ABK49633 which has homology with  
 CC acetyltransferases in the eosinophils of a patient and comparing the  
 CC expression level with that in the eosinophils of a healthy individual  
 CC (i.e. differential display). Also included are methods of screening  
 CC for candidate compounds which affect the expression level of the gene or  
 CC the activity of the protein encoded by the gene (including related  
 CC proteins and mutants), the use of probes based on the gene sequence  
 CC in the examination of allergic diseases, the use of reporter  
 CC constructs in the screening of candidate compounds, a vector containing a  
 CC the transcription-controlling region of the gene, cells transformed  
 CC with the vector, an antibody against the protein, and a model animal for  
 CC allergic diseases which is a transgenic non-human vertebrate with  
 CC lowering of expression intensity of the gene in eosinophils.  
 CC The method is examining allergic diseases particularly atopic  
 CC dermatitis which is also applicable in screening candidate  
 CC compounds for remedies. Such method can be performed in high throughput,  
 CC at low cost. The present sequence is a differential display PCR primer  
 CC for the cDNA encoding the human acetyltransferase-like protein 20-90-05.  
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2  
 RESULT 824  
 ABK49636/C  
 ID ABK49636 standard; DNA; 17 BP.  
 XX AC ABK49636;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human atopic dermatitis cDNA related PCR primer GT15C.

DE XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.  
 KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
 KW differential display; eosinophil; antiallergic; atopic dermatitis;  
 KW GT15G.  
 XX OS Homo sapiens.  
 XX XX WO200224903-A1.  
 XX PD 28-MAR-2002.  
 XX PF 21-SEP-2001; 2001WO-JP08246.  
 XX PR 25-SEP-2000; 2000JP-0291318.  
 XX PA (GENO-) GENOX RES INC.  
 XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX PA (EISA) EISAI CO LTD.  
 XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;  
 PI Takahashi E;  
 XX WI; 2002-315738/35.  
 XX XX Examining allergic diseases by differential display of gene showing  
 PT different expression particularly increased expression in remission  
 PT stage in eosinophils of patients, also applicable in screening  
 PT candidate compounds for remedies -  
 XX Example 1; Page 57; 72pp; Japanese.  
 XX CC The invention relates to a method for examining allergic diseases  
 CC comprising determining the expression level of a gene containing,  
 CC the human cDNA appearing as ABK49633 which has homology with  
 CC acetyltransferases in the eosinophils of a patient and comparing the  
 CC expression level with that in the eosinophils of a healthy individual  
 CC (i.e. differential display). Also included are methods of screening  
 CC for candidate compounds which affect the expression level of the gene or  
 CC the activity of the protein encoded by the gene (including related  
 CC proteins and mutants), the use of probes based on the gene sequence  
 CC in the examination of allergic diseases, the use of reporter  
 CC constructs in the screening of candidate compounds, a vector containing a  
 CC the transcription-controlling region of the gene, cells transformed  
 CC with the vector, an antibody against the protein, and a model animal for  
 CC allergic diseases which is a transgenic non-human vertebrate with  
 CC lowering of expression intensity of the gene in eosinophils.  
 CC The method is examining allergic diseases particularly atopic  
 CC dermatitis which is also applicable in screening candidate  
 CC compounds for remedies. Such method can be performed in high throughput,  
 CC at low cost. The present sequence is a differential display PCR primer  
 CC for the cDNA encoding the human acetyltransferase-like protein 20-90-05.  
 XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 16 AAAAAAAAAAAAAA 2  
 RESULT 825  
 ABK49757/C  
 ID ABK49757 standard; DNA; 17 BP.  
 XX AC ABK49757;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human atopic dermatitis cDNA related PCR primer GT15C.

```

XX      26-SEP-2000; 2000JP-0293021.
PR      (GENO-) GENOX RES INAT.
XX      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA      Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
FA      WPI; 2002-330097/36.
XX      Examining allergic diseases by differential display of genes showing
PT      different expression particularly increase in remission stage in
PT      eosinophils in patients -
XX      Example 1; Page 55; 74pp; Japanese.
PS      This invention relates to gene sequences that are differentially
CC      expressed in eosinophils from patients with atopic dermatitis in the
CC      increment stage as compared with those in the remission stage. These
CC      sequences are used in a novel method for examining allergic diseases
CC      comprising determining the expression levels of these genes and
CC      comparing the expression level with that in the eosinophils of a
CC      healthy individual. The method of the invention may have anti-allergic
CC      or dermatological activities. The method can be used to diagnose
CC      allergic diseases particularly atopic dermatitis, and may also
CC      be used to screen candidate compounds for remedies. The method of the
CC      invention can be performed in high throughput, at low cost. The
CC      present sequence represents the G15g PCR primer used to amplify
CC      the differentially amplified atopic dermatitis related cDNA sequences
CC      of the invention.
XX      Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 other;
SQ      Query Match          1.4%; Score 15; DB 1; Length 17;
        Best Local Similarity 100.0%; Pred. No. 4e+02;
        Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
QY      1084 AAAAAAAAAAAAAA 1098
DB      |||||
        16 AAAAAAAAAAAAAA 2
RESULT 827
ABX79793/c
ID ABX79793 standard; cDNA; 17 BP.
AC ABX79793;
XX
XX
XX
XX
XX
XX
DE 17-APR-2003 (first entry)
DE EST polymorphic DNA repeat polynucleotide #118.
XX
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPous;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
XX
XX US6472154-B1.
XX
XX 29-OCT-2002.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX 31-DEC-1999; 99US-0475947.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX

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DR WPI; 2003-208818/20.  
 XX  
 PT Identifying a candidate polymorphic repeat within a coding sequence,  
 PT for understanding or treating genetic disease, comprises detecting  
 PT tandem repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability -  
 XX  
 XX Examples; Column 483; 588pp; English.  
 XX  
 CC The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs.  
 XX

SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 828  
 AAV54171/c  
 ID AAV54171 standard; cDNA; 18 BP.  
 AC AAV54171;  
 XX

DT 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 8.

DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 KW immunohistological staining.  
 XX

OS Synthetic.

PN WO9839437-A1.

PD 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

PF 05-MAR-1997; 97JP-0050302.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,  
 PT preventing or treating diseases associated with apoptosis  
 XX

PS Example 1; Page 49; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method  
 CC of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for

CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.  
 XX

SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 829  
 AAV54172/c  
 ID AAV54172 standard; cDNA; 18 BP.

XX AAV54172;

DT 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 9.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 KW immunohistological staining.  
 XX

OS Synthetic.

PN WO9839437-A1.

PD 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.

PF 05-MAR-1997; 97JP-0050302.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis,  
 PT preventing or treating diseases associated with apoptosis  
 XX

PS Example 1; Page 50; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method  
 CC of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for  
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.  
 XX

SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 830  
 AAV54174/c  
 ID AAV54174 standard; cDNA; 18 BP.

XX AAV54174;

XX



DT 21-DEC-1998 (first entry)  
 XX Nucleotide sequence PCR primer 11.  
 DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 XX immunohistological staining.  
 KW Synthetic.  
 XX  
 OS WO9839437-A1.  
 XX  
 PN 11-SEP-1998.  
 XX  
 PD 05-MAR-1998; 98WO-JP00905.  
 XX  
 PF 05-MAR-1997; 97JP-0050302.  
 XX  
 PR (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Sakaki Y;  
 XX  
 DR WPI; 1998-495844/42.  
 XX  
 DT Novel apoptosis-related DNAs and proteins - for diagnosis,  
 XX preventing or treating diseases associated with apoptosis  
 PT Example 1; Page 50; 70pp; Japanese.  
 XX  
 PS This is the nucleotide sequence of a PCR primer used in the method  
 XX of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for  
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.  
 XX  
 XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;  
 SQ  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB |||||  
 16 AAAAAAAAAAAAAA 2  
 RESULT 831  
 ID AAV54175/c  
 XX  
 AC AAV54175 standard; cDNA; 18 BP.  
 XX  
 XX AAV54175;  
 XX  
 DT 21-DEC-1998 (first entry)  
 XX  
 DE Nucleotide sequence PCR primer 12.  
 XX  
 KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 XX immunohistological staining.  
 OS Synthetic.  
 XX  
 PN WO9839437-A1.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PF 05-MAR-1998; 98WO-JP00905.  
 XX  
 PR 05-MAR-1997; 97JP-0050302.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Sakaki Y;  
 XX

DR WPI; 1998-495844/42.  
 XX Novel apoptosis-related DNAs and proteins - for diagnosis,  
 PT preventing or treating diseases associated with apoptosis  
 XX Example 1; Page 51; 70pp; Japanese.  
 XX  
 PS This is the nucleotide sequence of a PCR primer used in the method  
 CC of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for  
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.  
 XX  
 XX Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;  
 SQ  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB |||||  
 16 AAAAAAAAAAAAAA 2  
 RESULT 832  
 ID AAV35391/c  
 XX  
 AC AAV35391 standard; DNA; 18 BP.  
 XX  
 XX AAV35391;  
 XX  
 DT 13-OCT-1998 (first entry)  
 XX  
 DE HIV-1 gag protein DNA primer #4.  
 XX  
 XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;  
 KW vaccines; infection; protection; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9822596-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PF 19-NOV-1997; 97WO-JP04216.  
 XX  
 PR 19-NOV-1996; 96JP-0323412.  
 XX  
 PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.  
 XX (JAPG ) NIPPON ZEON KK.  
 XX  
 PI Kojima A, Kurata T, Yasuda A;  
 XX  
 DR WPI; 1998-312481/27.  
 XX  
 PT Recombinant vaccinia virus containing fusion H1B gag gene - for  
 PT production in host cells of gag protein for use as vaccine  
 XX  
 PS Example 1; Page 64; 84pp; Japanese.  
 XX  
 CC AAV35388-V35414 are primers used in a method which results in a  
 CC recombinant vaccinia virus comprising of a gag gene from a retrovirus  
 CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope  
 CC region (30-300 bases in length) of a retroviral gene other than the gag  
 CC gene. The gag gene may be altered so as to produce a gag protein modified  
 CC from the natural sequence by the addition, deletion or substitution of at  
 CC least 1 amino acid residue. The fusion gene is inserted into a region of  
 CC a vaccinia virus not essential to its propagation, to give a recombinant  
 CC vaccinia virus vector which is used to transform a host cell (such as  
 CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon  
 CC culturing the host cell produces particulate structures containing the  
 CC fusion gag protein. The recombinant vaccinia virus or the fusion gag  
 CC protein particles may be used in the production of vaccines for

CC protecting against infection with retroviruses such as HIV.  
 XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;  
 SQ

Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 18 AAAAAAAAAAAAAA 4

## RESULT 833

AA58385  
 ID AAA58385 standard; DNA; 18 BP.

XX  
 AC AAA58385;

XX 01-NOV-2000 (first entry)

XX Polynucleotide # 1 used in a biomolecule detection system.

XX Nanocrystal; biomolecule detection; nonisotopic detection system; ss.  
 XX Synthetic.

XX WO200028088-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US26612.

XX 10-NOV-1998; 98US-0107828.

XX 09-NOV-1999; 99US-0437076.

XX (BIOC-) BIOCRYSTAL LTD.

XX Barbera-Guillem E, Nelson MB, Castro S;

XX WPI; 2000-376593/32.

XX Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal -

XX Example 3; Page 68; 72pp; English.

XX The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of nanocrystals, which have polynucleotides complementary to the first polynucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Adenine bases. This sequence may therefore be used with a polynucleotide composed mainly of Thymine bases (AAA58386).

XX Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 4 AAAAAAAAAAAAAA 18

## RESULT 834

AA58386/c  
 ID AAA58386 standard; DNA; 18 BP.

XX  
 AC AAA58386;

XX 01-NOV-2000 (first entry)

XX Polynucleotide # 2 used in a biomolecule detection system.

XX Nanocrystal; biomolecule detection; nonisotopic detection system; ss.  
 XX Synthetic.

XX WO200028088-A1.

XX 18-MAY-2000.

XX 10-NOV-1999; 99WO-US26612.

XX 10-NOV-1998; 98US-0107828.

XX 09-NOV-1999; 99US-0437076.

XX (BIOC-) BIOCRYSTAL LTD.

XX Barbera-Guillem E, Nelson MB, Castro S;

XX WPI; 2000-376593/32.

XX Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal -

XX Example 3; Page 69; 72pp; English.

XX The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of nanocrystals, which have polynucleotides complementary to the first polynucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Thymine bases. This sequence may therefore be used with a polynucleotide composed mainly of Adenine bases (AAA58385).

XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 |||||  
 Db 18 AAAAAAAAAAAAAA 4

## RESULT 835

AAZ90641/c

ID AAZ90641 standard; DNA; 18 BP.

XX  
 AC AAZ90641;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #2.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
 XX Homo sapiens.

```
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX (NISH ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 836
ID AAZ90642/c
XX AAZ90642 standard; DNA; 18 BP.
XX
XX AAZ90642;
XX
XX 13-JUN-2000 (first entry)
XX
XX Human adipose tissue gene amplifying primer #3.
XX
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX
XX JP2000037190-A.
XX
XX 08-FEB-2000.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX (NISH ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 836
ID AAZ90642/c
XX AAZ90642 standard; DNA; 18 BP.
XX
XX AAZ90642;
XX
XX 13-JUN-2000 (first entry)
XX
XX Human adipose tissue gene amplifying primer #3.
XX
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX
XX JP2000037190-A.
XX
XX 08-FEB-2000.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX (NISH ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 other;
SQ
```

```
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 837
ID AAZ90650/c
XX AAZ90650 standard; DNA; 18 BP.
XX
XX AAZ90650;
XX
XX 13-JUN-2000 (first entry)
XX
XX Human adipose tissue gene amplifying primer #11.
XX
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
XX
XX JP2000037190-A.
XX
XX 08-FEB-2000.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX 23-JUL-1998; 98JP-0225228.
XX
XX (NTSB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension,
CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic
CC diagnosis, prevention and treatment of adipose tissue related diseases.
CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
CC tissue genes.
XX
XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAA 1098
DB |||||
16 AAAAAAAAAAAAAA 2
RESULT 838
ID AAZ90651/c
XX AAZ90651 standard; DNA; 18 BP.
XX
XX AAZ90651;
XX
```

XX 13-JUN-2000 (first entry)  
 XX DE Human adipose tissue gene amplifying primer #12.  
 XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
 XX OS Homo sapiens.  
 XX PN JP2000037190-A.  
 XX PD 08-FEB-2000.  
 XX PF 23-JUL-1998; 98JP-0225228.  
 XX PR 23-JUL-1998; 98JP-0225228.  
 XX PA (NISR ) JAPAN TOBACCO INC.  
 XX PR WPI; 2000-306578/27.  
 XX PT A physiologically active protein specifically derived from mammal  
 XX PT tissue -  
 XX PS Example 2; Page 18; 50pp; Japanese.  
 XX CC The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension,  
 CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes  
 CC (AAZ90631-633) and the proteins (AAZ67598-Y67600) are used in the genetic  
 CC diagnosis, prevention and treatment of adipose tissue related diseases.  
 CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose  
 CC tissue genes.  
 XX SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 DB 16 AAAAAAAAAAAAAA 2  
 RESULT 839  
 ABT11136/c  
 ID ABT11136 standard; DNA; 18 BP.  
 AC ABT11136;  
 XX 05-DEC-2002 (first entry)  
 DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 24.  
 KW Human; polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis;  
 KW sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis;  
 KW rheumatoid arthritis; scleroderma; lupus; non-allergic rhinitis;  
 KW polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease;  
 KW atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;  
 ds.  
 XX OS Homo sapiens.  
 XX WO200262825-A2.  
 XX 15-AUG-2002.  
 XX 07-FEB-2002; 2002WO-US03546.  
 XX 08-FEB-2001; 2001US-267515P.

PR 21-AUG-2001; 2001US-314248P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX PI Barnes G, Meyer J;  
 XX PR WPI; 2002-627522/67.  
 XX New isolated nucleic acid molecule with an allelic variant of a  
 PT polymorphic region of an 5-LO gene, useful for diagnosing and/or  
 PT prognosticating disorders associated with an aberrant inflammatory  
 PT response such as asthma -  
 XX Claim 10; Page 237; 290pp; English.  
 XX The invention relates to an isolated human nucleic acid molecule  
 CC comprising an allelic variant of a polymorphic region of a 5-lipoxygenase  
 CC (5-LO) gene, where the allelic variant comprises one or more nucleotide  
 CC selected from any of 3, 20 or 21 base pair sequences, given in the  
 CC specification, or their complement. The compositions and methods of the  
 CC present invention are useful for diagnosing and/or prognosticating disorders  
 CC associated with an aberrant inflammatory response such as asthma,  
 CC bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis,  
 CC rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic  
 CC rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory  
 CC disease, atopic and contact dermatitis. The nucleic acid molecules can  
 CC also be useful for identifying an individual amongst other individuals  
 CC from the same species for use in forensic medicine and paternity testing.  
 CC This polynucleotide sequence represents DNA relating to the human 5-  
 CC lipoxygenase (5-LO) gene of the invention.  
 XX SQ Sequence 18 BP; 2 A; 3 C; 9 G; 4 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 ACAGCCAGCTACCGC 24  
 DB 17 ACAGCCAGCTACCGC 3  
 RESULT 840  
 AAT73293/c  
 ID AAT73293 standard; DNA; 20 BP.  
 XX AAT73293;  
 XX 12-DEC-1997 (first entry)  
 DT Primer for pUC19 DNA amplification.  
 DE primer; PCR; polymerase chain reaction; sequencing; walking;  
 KW complementary extension reaction; low redundancy; universal primer; ss.  
 XX Synthetic.  
 XX BP767240-A2.  
 XX 09-APR-1997.  
 XX 17-SEP-1996; 96EP-0114907.  
 XX 30-JAN-1996; 96JP-0013634.  
 XX 18-SEP-1995; 95JP-0238141.  
 XX (HITA ) HITACHI LTD.  
 XX Kambara H, Okano K;  
 XX WPI; 1997-205424/19.  
 XX Efficient sequencing of long DNA by fragment walking - with

PT simultaneous sequencing of restriction enzyme fragment and adjacent  
PT region of intact DNA, avoids the need for cloning and requires fewer  
PT primers  
XX  
XX Example 1; Page 23; 50pp; English.  
XX  
XX A method for DNA analysis based on a complementary extension reaction  
CC using a DNA polymerase, comprises a combination of fragment walking and  
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a  
CC restriction enzyme and the targeted DNA sequence can be determined  
CC directly from the digested DNA fragments. By exploring the overlapping  
CC sequence of the determined base sequence, the overall base sequence of a  
CC length DNA can be determined with low redundancy without cloning or  
CC subcloning. In addition, the method can be done with commercially  
CC available universal primers or with fewer primers than required in  
CC existing methods. AAT73291-92 are primers used in determination of the  
CC pUC19 sequence. Primer extension was carried out using 16 primers  
CC AAT73293.  
XX  
XX Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 2 other;

Query Match 1.4%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
Dd 15 AAAAAAAAAAAAAA 1

RESULT 841  
AA32003/c  
ID AAX32003 standard; DNA; 20 BP.  
XX  
XX AC AAX32003;  
XX  
XX 14-JUN-1999 (first entry)  
XX  
XX MSH2 gene specific primer.  
XX  
XX Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;  
KW CFTF; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;  
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;  
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;  
KW BAP1 gene; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9906598-A2.  
XX  
XX 11-FEB-1999.  
XX  
XX 04-AUG-1998; 98WO-US16574.  
XX  
XX 22-MAY-1998; 98US-0084471.  
XX  
XX 04-AUG-1997; 97US-0905772.  
XX  
XX (ONCO-) ONCORMED INC.  
XX  
XX Murphy PD;  
XX  
XX WPI; 1999-153820/13.

PT Determining common functional alleles in a population - useful in  
PT the diagnosis of disease associated with allelic heterogeneity  
XX  
XX Example 1; Page 24; 78pp; English.  
XX  
XX The invention relates to methods of determining a functional allele  
CC profile of a gene in a population. Functional allele profiles comprise  
CC the commonly occurring alleles in a population, and the relative  
CC frequencies at which such alleles of a given gene occur. The methods  
CC are used to identify and determine the frequency of the functional  
CC alleles of genes which display extensive allelic heterogeneity,  
CC particularly those implicated in disease or conditions, such as the  
CC BRCA1 gene associated with breast cancer, CFTF associated with cystic  
CC fibrosis, dystrophin associated with Duchenne muscular dystrophy and  
CC Becker muscular dystrophy, and p53 associated with Li-Fraumeni syndrome.

CC alleles of genes which display extensive allelic heterogeneity,  
CC particularly those implicated in disease or conditions, such as the  
CC BRCA1 gene associated with breast cancer, CFTF associated with cystic  
CC fibrosis, dystrophin associated with Duchenne muscular dystrophy and  
CC Becker muscular dystrophy, and p53 associated with Li-Fraumeni syndrome.  
CC The methods can also be employed for diseases where allelic and genetic  
CC heterogeneity exist, such as breast cancer, neurofibromatosis, and  
CC hereditary non-polyposis colorectal cancer. Identification of functional  
CC alleles is necessary for identification of mutations which may be  
CC implicated in the disease. Sequences AAX32001-172 represent primers for  
CC determining the functional allele profiles of various genes. The  
CC primers are specific for genes such as MSH2 gene, MLH1 gene, BRCA1 gene,  
CC BRCA2 gene and BAP1 gene.  
XX  
XX Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTTAAAAA 1096  
Dd 15 TTTAAAAA 1

RESULT 842  
AA32010/c  
ID AAX32010 standard; DNA; 20 BP.  
XX  
XX AC AAX32010;  
XX  
XX 14-JUN-1999 (first entry)  
XX  
XX MSH2 gene specific primer.  
XX  
XX Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;  
KW CFTF; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;  
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;  
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;  
KW BAP1 gene; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9906598-A2.  
XX  
XX 11-FEB-1999.  
XX  
XX 04-AUG-1998; 98WO-US16574.  
XX  
XX 22-MAY-1998; 98US-0084471.  
XX  
XX 04-AUG-1997; 97US-0905772.  
XX  
XX (ONCO-) ONCORMED INC.  
XX  
XX Murphy PD;  
XX  
XX WPI; 1999-153820/13.

PT Determining common functional alleles in a population - useful in  
PT the diagnosis of disease associated with allelic heterogeneity  
XX  
XX Example 1; Page 24; 78pp; English.

XX The invention relates to methods of determining a functional allele  
CC profile of a gene in a population. Functional allele profiles comprise  
CC the commonly occurring alleles in a population, and the relative  
CC frequencies at which such alleles of a given gene occur. The methods  
CC are used to identify and determine the frequency of the functional  
CC alleles of genes which display extensive allelic heterogeneity,  
CC particularly those implicated in disease or conditions, such as the  
CC BRCA1 gene associated with breast cancer, CFTF associated with cystic  
CC fibrosis, dystrophin associated with Duchenne muscular dystrophy and  
CC Becker muscular dystrophy, and p53 associated with Li-Fraumeni syndrome.

CC The methods can also be employed for diseases where allelic and genetic  
 CC heterogeneity exist, such as breast cancer, neurofibromatosis, and  
 CC hereditary non-polyposis colorectal cancer. Identification of functional  
 CC alleles is necessary for identification of mutations which may be  
 CC implicated in the disease. Sequences AAX32001-172 represent primers for  
 CC determining the functional allele profiles of various genes. The  
 CC primers are specific for genes such as MSH2 gene, MLH1 gene, BRCA1 gene,  
 CC BRCA2 gene and BAP1 gene.

XX Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1097  
 Db 15 TAAAAAATAAAAAA 1

RESULT 843  
 AAC82908/c  
 ID AAC82908 standard; DNA; 20 BP.

XX AC AAC82908;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #1.

XX Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.

XX OS Homo sapiens.

XX PN DE19923966-Al.

XX PD 30-NOV-2000.

XX PF 25-MAY-1999; 99DE-1023966.

XX PR 25-MAY-1999; 99DE-1023966.

XX PA (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX PI Boekenkamp D, Hoppe H, Burgstaller P;

XX WPI; 2001-050938/07.

XX Recognition system, e.g. for identifying nucleic acids, comprises at  
 PT least one recognition unit comprising a region with a defined structure  
 PT adjacent to a region with a randomized structure -

XX Examples; Fig 1; 8pp; German.

XX This invention describes a novel recognition system comprising at least  
 CC 1 recognition unit bound to a support, each recognition unit comprising a  
 CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.

XX Sequence 20 BP; 2 A; 0 C; 3 G; 15 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TAAAAAATAAAAAA 1096  
 Db 15 TAAAAAATAAAAAA 1

RESULT 844  
 AAC82909/c  
 ID AAC82909 standard; DNA; 20 BP.

XX AC AAC82909;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #2.

XX Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.

XX OS Homo sapiens.

XX PN DE19923966-Al.

XX PD 30-NOV-2000.

XX PF 25-MAY-1999; 99DE-1023966.

XX PR 25-MAY-1999; 99DE-1023966.

XX PA (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX PI Boekenkamp D, Hoppe H, Burgstaller P;

XX WPI; 2001-050938/07.

XX Recognition system, e.g. for identifying nucleic acids, comprises at  
 PT least one recognition unit comprising a region with a defined structure  
 PT adjacent to a region with a randomized structure -

XX Examples; Fig 1; 8pp; German.

XX This invention describes a novel recognition system comprising at least  
 CC 1 recognition unit bound to a support, each recognition unit comprising a  
 CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.

XX Sequence 20 BP; 2 A; 0 C; 4 G; 14 T; 0 other;

Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TAAAAAATAAAAAA 1096  
 Db 15 TAAAAAATAAAAAA 1

RESULT 845  
 AAC82910/c  
 ID AAC82910 standard; DNA; 20 BP.

XX AC AAC82910;

XX DT 21-MAR-2001 (first entry)

XX DE Human beta-actin derived oligonucleotide #3.



CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.  
 XX Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;  
 SQ Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1096  
 DB 15 TTAAAAA 1

RESULT 848  
 AAC82917/c  
 ID AAC82917 standard; DNA; 20 BP.  
 XX AAC82917;  
 AC  
 DT 21-MAR-2001 (first entry)  
 XX Human S-9 derived oligonucleotide #1.  
 DE Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.  
 XX Homo sapiens.  
 OS  
 XX DE19923966-A1.  
 PN 30-NOV-2000.  
 XX PD  
 XX PF 25-MAY-1999; 99DE-1023966.  
 XX PR 25-MAY-1999; 99DE-1023966.  
 DE (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
 XX Boekenkamp D, Hoppe H, Burgstaller P;  
 PI WPI; 2001-050938/07.  
 XX Recognition system, e.g. for identifying nucleic acids, comprises at  
 PT least one recognition unit comprising a region with a defined structure  
 PT adjacent to a region with a randomized structure -  
 XX Examples; Fig 1; 8pp; German.  
 PS This invention describes a novel recognition system comprising at least  
 CC 1 recognition unit bound to a support, each recognition unit comprising a  
 CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.  
 XX Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 other;  
 SQ Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1096  
 DB 15 TTAAAAA 1

RESULT 850  
 AAC82920/c  
 ID AAC82920 standard; DNA; 20 BP.  
 XX AAC82920;  
 AC  
 DT 21-MAR-2001 (first entry)  
 XX Human S-9 derived oligonucleotide #4.  
 DE Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW

DB 15 TTAAAAA 1

RESULT 849  
 AAC82919/c  
 ID AAC82919 standard; DNA; 20 BP.  
 XX AAC82919;  
 AC  
 DT 21-MAR-2001 (first entry)  
 XX Human S-9 derived oligonucleotide #3.  
 DE Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.  
 XX Homo sapiens.  
 OS  
 XX DE19923966-A1.  
 PN 30-NOV-2000.  
 XX PD  
 XX PF 25-MAY-1999; 99DE-1023966.  
 XX PR 25-MAY-1999; 99DE-1023966.  
 DE (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
 XX Boekenkamp D, Hoppe H, Burgstaller P;  
 PI WPI; 2001-050938/07.  
 XX Recognition system, e.g. for identifying nucleic acids, comprises at  
 PT least one recognition unit comprising a region with a defined structure  
 PT adjacent to a region with a randomized structure -  
 XX Examples; Fig 1; 8pp; German.  
 PS This invention describes a novel recognition system comprising at least  
 CC 1 recognition unit bound to a support, each recognition unit comprising a  
 CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.  
 XX Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 other;  
 SQ Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1096  
 DB 15 TTAAAAA 1

RESULT 850  
 AAC82920/c  
 ID AAC82920 standard; DNA; 20 BP.  
 XX AAC82920;  
 AC  
 DT 21-MAR-2001 (first entry)  
 XX Human S-9 derived oligonucleotide #4.  
 DE Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW





CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides.  
 XX

SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTTAAAAA 1096  
 DB 15 TTTAAAAA

RESULT 853  
 AAF87713/C  
 ID AAF87713 standard; DNA; 20 BP.

XX AAF87713;  
 DT 06-JUL-2001 (first entry)  
 DE Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.  
 KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;  
 KW hepatic cell proliferative disorder; liver cancer; anticancer;  
 KW tumorigenesis; detection; PCR primer; ss.  
 XX Homo sapiens.  
 OS WO200126536-A2.  
 PN 19-APR-2001.  
 PD 12-OCT-2000; 2000WO-US28427.  
 PF 13-OCT-1999; 99US-0159168.  
 PR (UJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Nelson WG, Lin X, Tchou JC, Bakker J;  
 XX WPI; 2001-290647/30.  
 XX Detecting hepatic cell proliferative disorder useful for detecting  
 PT hepatocellular carcinoma comprises detecting a methylated  
 FT CpG-containing glutathione-S-transferase nucleic acid -  
 XX Claim 83; Page 42; 64pp; English.

CC The present invention describes a method for detecting hepatic cell  
 CC proliferative disorders. The method comprises detecting a methylated  
 CC CpG-containing glutathione-S-transferase (GST) nucleic acid (I) in a  
 CC hepatic specimen or a biological fluid, where a methylated GST nucleic  
 CC acid is indicative of a hepatic cell proliferative disorder. The method  
 CC can be used to diagnose hepatocellular carcinoma, and to monitor  
 CC progress of its treatment. Increasing the level of GST is useful in the  
 CC treatment of liver cancer, in humans or animals. The method can detect  
 CC the early stages of tumorigenesis in liver cells simply. The present  
 CC sequence represents a PCR primer which is used in the amplification  
 CC of the human glutathione S-transferase pi gene (GSTP1) promoter in an  
 CC example from the present invention for mapping somatic GSTP1 CpG island  
 CC DNA hypermethylation changes by genomic sequencing after bisulfite  
 CC treatment.

SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTTAAAAA 1096  
 DB 19 TTTAAAAA

RESULT 854  
 AAD35095/C  
 ID AAD35095 standard; DNA; 20 BP.

XX AAD35095;  
 XX AAD35095;  
 DT 25-JUL-2002 (first entry)  
 DE HT15-C downstream PCR primer used for identification of genes.

XX Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;  
 KW sex separation; infertility treatment; chromosomal manipulation;  
 KW sperm separation; gene therapy; PCR; primer; ss.

XX Unidentified.  
 XX EP1195382-A2.  
 PN 10-APR-2002.  
 PD 02-OCT-2001; 2001EP-0123259.  
 PF 03-OCT-2000; 2000JP-0303994.  
 PR (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.  
 PA (UYGU-) UNIV GUNMA.

XX Aizawa A, Kawakami A, Kondo T;  
 XX WPI; 2002-354153/39.

XX New X-chromosome gene expressed in haploid cells of the testis, useful  
 PT for gene diagnosis, discrimination of sex, separation of sperm,  
 PT infertility treatment and chromosomal manipulation -  
 XX Example 1; Page 4; 28pp; English.

CC The present invention relates to genes located on the X-chromosome of  
 CC mammals. These genes are specifically expressed in haploid cells of the  
 CC testis and encode amino acid sequences having homology with the amino  
 CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences  
 CC of the invention are used for gene diagnosis, discrimination of sex,  
 CC separation of sperm, infertility treatment and chromosomal manipulation,  
 CC especially in livestock. They are also used in gene therapy. The present  
 CC DNA sequence is a PCR primer which is used for the identification of  
 CC genes by differential display method.

XX SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAA 1098  
 DB 19 AAAAAA

RESULT 855  
 ABL57070  
 ID ABL57070 standard; DNA; 20 BP.

XX ABL57070;  
 XX ABL57070;  
 DT 22-JUL-2002 (first entry)  
 DE Molecular beacon target sequence.

```

KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;
KW ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_binding 1..20
FT /*tag= a
FT /bound moiety= "Molecular beacon"
FT /note= "forms double-stranded region with bases
FT 1-20 of sequence in ABL57069"
XX
XX WO200218951-A2.
XX PN
XX PD
XX PD 07-MAR-2002.
XX PF 29-AUG-2001; 2001WO-US41941.
XX PF 29-AUG-2000; 2000US-228728P.
XX PR 30-MAR-2001; 2001US-280350P.
XX XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX PA
XX PI Dubertret B, Calame M, Libchaber A;
XX PI WPI; 2002-401727/43.
XX DR
XX XX
XX Sensitively detecting proximity changes in a system that utilizes an
XX interacting fluorophore and quencher, for high sensitivity
XX applications, involves utilizing a metal surface as quencher -
XX
XX Example 2; Page 26; 62pp; English.
XX
XX The present sequence is that of a perfectly matched target
XX sequence for a molecular beacon comprising an oligonucleotide probe
XX (see ABL57069) covalently attached at the 3' end to fluorescent
XX dye and at the 5' end to a nanoparticle. In the native state, the
XX probe forms a hairpin conformation with hybridised termini. The
XX proximity of the fluorophore and quencher (gold nanoparticle) in
XX the molecular beacon results in little or no detectable
XX fluorescence. Upon hybridisation of the central complementary
XX stretch of the probe to a target sequence, such as the present
XX sequence, the hairpin undergoes a conformational change resulting
XX in an increase in fluorescence, the extent of which is proportional
XX to the amount of target sequence present. Single mismatches can
XX be detected. The invention relates generally to the use of metal
XX surface quenchers such as particles or films for high sensitivity
XX applications in, for example, detection and diagnostic systems.
XX
XX Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1098
XX |||||
XX 1 AAAAAAAAAAAAAA 15
XX
XX RESULT 856
XX ABL58300
XX ID ABL58300 standard; DNA; 20 BP.
XX AC ABL58300;
XX XX
XX 15-JUL-2002 (first entry)
XX
XX Human GLUT 10 SSCP analysis primer GLUT10 ex2cF.
XX DE
XX XX
XX Glucose transporter; GLUT10; insulin; chromosome 20q12-13.3; human;
XX KW glucose metabolism; single strand conformational polymorphism; PCR;
XX KW type 2 diabetes; SSCP; primer; ss.

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XX Homo sapiens.
XX OS
XX WO200218621-A2.
XX PN
XX PD 07-MAR-2002.
XX PF 22-AUG-2001; 2001WO-US26184.
XX PF 31-AUG-2000; 2000US-0652292.
XX PR (UYWA-) UNIV WAKE FOREST.
XX PA
XX PI Bowden DW, Dawson PA, Fossey SC;
XX PI WPI; 2002-371828/40.
XX DR
XX XX
XX New glucose transporter gene and protein, designated GLUT10, useful for
XX studying and analyzing biological processes of glucose metabolism and
XX Type 2 diabetes, as well as for screening modulators of glucose
XX transporter activity -
XX
XX Example 4; Page 52; 85pp; English.
XX
XX The invention relates to a novel glucose transporter gene and protein,
XX designated GLUT10. GLUT 10 is an insulin-responsive glucose transporter
XX gene located in the type 2 diabetes linked region of chromosome
XX 20q12-13.3. The GLUT 10 polypeptide can be expressed by standard
XX recombinant methodology. The GLUT 10 glucose transporter gene and protein
XX are useful for studying and analysing biological processes of both
XX glucose metabolism and type 2 diabetes. These are also useful in drug
XX screening techniques, especially for screening modulators of glucose
XX transporter activity or compounds having the ability to be transported
XX across the cell membranes. Sequences ABL58290-315 represent primers
XX specific for the various regions of the human GLUT 10 glucose transporter
XX gene, used in single strand conformational polymorphism (SSCP) analysis
XX of the gene.
XX
XX Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 335 GGAGCAACTTGGTGC 349
XX |||||
XX 1 GGAGCAACTTGGTGC 15
XX
XX Db
XX
XX RESULT 857
XX ABL96929/c
XX ID ABL96929 standard; DNA; 20 BP.
XX AC ABL96929;
XX XX
XX 16-FEB-2002 (first entry)
XX
XX Capture oligonucleotide Zip ID#4016 oligo #9.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX KW environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX OS
XX WO200179548-A2.
XX PN
XX PD 25-OCT-2001.
XX PD 04-APR-2001; 2001WO-US10958.
XX PF
XX XX

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PR 14-APR-2000; 2000US-197271P.
XX (CORR ) CORNELL RES FOUND INC.
PA Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
PI WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
XX Example 5; Fig 23; 300bp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (II) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocyctotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
XX medineis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. ABI82074 to a
XX ABI97546 represent oligonucleotide sequences used in the exemplification
XX of the present invention.
XX
XX Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 23 GCGGCTAGGTCCTC 37
XX Db 18 GCGGCTAGGTCCTC 4
XX
XX RESULT 858
XX AAF96192
XX ID AAF96192 standard; DNA; 21 BP.
XX AC AAF96192;
XX XX
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #953.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.
XX

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PD 15-MAR-2001.
XX 07-SEP-2000; 2000WO-US24503.
XX 10-SEP-1999; 99US-0153357.
XX 26-JUL-2000; 2000US-0220947.
XX 16-AUG-2000; 2000US-0225724.
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis -
XX
XX Examples; Page 116; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification.
XX
XX Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 348 GCCAGCGCCACCTG 362
XX Db 7 GCCAGCGCCACCTG 21
XX
XX RESULT 859
XX ABS97669
XX ID ABS97669 standard; DNA; 21 BP.
XX AC ABS97669;
XX XX
XX DT 23-DEC-2002 (first entry)
XX DE Histamine N-methyl transferase (HNMT) PCR Primer #4.
XX KW Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
XX cytochrome P450 A2; CYP450A2; cytochrome P450 02B; CYP45002E1; LTF;
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile;
XX STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological.
XX OS Homo sapiens.

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XX WO200257410-A2.  
 XX PD 25-JUL-2002.  
 XX PF 28-NOV-2001; 2001WO-US44838.  
 XX PR 28-NOV-2000; 2000US-0724389.  
 XX PA (DNAS-) DNA SCI LAB INC.  
 XX PI Guida M, Hall J;  
 XX WPI; 2002-698522/75.  
 XX Isolated nucleic acid molecules having polymorphisms in known human  
 PT genes e.g. cytochrome p450 and catepsin S useful as genetic linkage  
 PT markers for locating, identifying and characterizing the genes  
 PT responsible for disorder-related traits -  
 XX Example 13; Page 123; 714pp; English.  
 XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase  
 CC activating protein (FLAP), glutathione-S-transferase 12 (GSTI2),  
 CC histamine-N-methyl transferase (HNMT), (kallikrein 2) KLK2, nicotinamide  
 CC -N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance  
 CC protein 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated  
 CC muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or  
 CC CHMR5) sequence. The polymorphisms in the human genes cited in the  
 CC invention are useful as genetic linkage markers for locating and  
 CC characterising the genes that are responsible for specific traits within  
 CC the genome and eventually identifying the genes responsible for a  
 CC variety of disorder-related traits as a result of their e.g.,  
 CC overexpression, constitutive expression, mutation or underexpression,  
 CC which may be used in diagnosing and/or treating the disorders. The  
 CC nucleic acid molecules comprising the polymorphic sequences contained  
 CC in CYP450A1, CYP450A2, CYP45002E1, AHR, MDR1 and/or MDR3 may  
 CC also be used to screen individuals for susceptibility to cancer.  
 CC Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered  
 CC cardiovascular function, in COX2 for altered susceptibility to  
 CC colorectal tumours, in DBI or CHMR1 for altered central nervous system  
 CC function, in FLAP and HNMT for altered pulmonary, immunological or  
 CC haematological function, in KLK2 for altered serine protease activity in  
 CC the prostate, in LTF for altered immunological or haematological  
 CC function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral  
 CC nervous system function. The present sequence represents a PCR  
 CC primer used to amplify the sequences of the invention.  
 XX Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;  
 SQ  
 Query Match 1-4%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1098  
 Db 3 AAAAAAAAAAAAAA 17  
 RESULT 860

ABS97681  
 ID ABS97681 standard; DNA; 21 BP.  
 XX AC ABS97681;  
 XX DT 23-DEC-2002 (first entry)  
 XX DE Histamine N-methyl transferase (HNMT) sequencing Primer #4.  
 XX Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS;  
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;  
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile;  
 KW STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW altered drug metabolism; cardiovascular function; colorectal tumour;  
 KW central nervous system; pulmonary; immunological; sequencing.  
 XX Homo sapiens.  
 OS WO200257410-A2.  
 PN 25-JUL-2002.  
 PD 28-NOV-2001; 2001WO-US44838.  
 PF 28-NOV-2000; 2000US-0724389.  
 XX (DNAS-) DNA SCI LAB INC.  
 PI Guida M, Hall J;  
 XX WPI; 2002-698522/75.  
 XX Isolated nucleic acid molecules having polymorphisms in known human  
 PT genes e.g. cytochrome p450 and catepsin S useful as genetic linkage  
 PT markers for locating, identifying and characterizing the genes  
 PT responsible for disorder-related traits -  
 XX Example 13; Page 124; 714pp; English.  
 XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase  
 CC activating protein (FLAP), glutathione-S-transferase 12 (GSTI2),  
 CC histamine-N-methyl transferase (HNMT), (kallikrein 2) KLK2, nicotinamide  
 CC -N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance  
 CC protein 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated  
 CC muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or  
 CC CHMR5) sequence. The polymorphisms in the human genes cited in the  
 CC invention are useful as genetic linkage markers for locating and  
 CC characterising the genes that are responsible for specific traits within  
 CC the genome and eventually identifying the genes responsible for a  
 CC variety of disorder-related traits as a result of their e.g.,  
 CC overexpression, constitutive expression, mutation or underexpression,  
 CC which may be used in diagnosing and/or treating the disorders. The  
 CC nucleic acid molecules comprising the polymorphic sequences contained  
 CC in CYP450A1, CYP450A2, CYP45002E1, AHR, MDR1 and/or MDR3 may  
 CC also be used to screen individuals for susceptibility to cancer.  
 CC Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered  
 CC cardiovascular function, in COX2 for altered susceptibility to  
 CC colorectal tumours, in DBI or CHMR1 for altered central nervous system  
 CC function, in FLAP and HNMT for altered pulmonary, immunological or  
 CC haematological function, in KLK2 for altered serine protease activity in  
 CC the prostate, in LTF for altered immunological or haematological  
 CC function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral  
 CC nervous system function. The present sequence represents a PCR  
 CC primer used to amplify the sequences of the invention.  
 XX Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;  
 SQ

CC in CYP4501A1, CYP4501A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2,  
 CC NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful  
 CC for screening individuals for altered drug metabolism. The polymorphic  
 CC sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may  
 CC also be used to screen individuals for susceptibility to cancer.  
 CC Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered  
 CC cardiovascular function, in COX2 for altered susceptibility to  
 CC colorectal tumours, in DBI or CHMR1 for altered central nervous system  
 CC function, in FIAP and HNMT for altered pulmonary, immunological or  
 CC haematological function, in KLK2 for altered serine protease activity in  
 CC the prostate, in LTR for altered immunological or haematological  
 CC function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral  
 CC nervous system function. The present sequence represents a sequencing  
 CC primer used to sequence the polymorphic genes of the invention.

SQ Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 Db 3 AAAAAAAAAAAAAA 17

RESULT 861  
 ABL57071  
 ID ABL57071 standard; DNA; 21 BP.  
 AC ABL57071;  
 DT 22-JUL-2002 (first entry)  
 DE Molecular beacon target sequence.  
 KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection;  
 KW ss.  
 KW Synthetic.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH misc\_binding 1..21  
 FT /\*tag= a  
 FT /bound moiety= "Molecular beacon"  
 FT /note= "forms double-stranded region with bases  
 1-21 of sequence in ABL57069"

XX PN WO200218951-A2.  
 XX PD 07-MAR-2002.  
 XX PF 29-AUG-2001; 2001WO-US41941.  
 XX PR 29-AUG-2000; 2000US-228728P.  
 XX PR 30-MAR-2001; 2001US-280350P.  
 XX PA (UVRQ ) UNIV ROCKEFELLER.  
 XX PI Dubertret B, Calame M, Libchaber A;  
 XX WP1; 2002-401727/43.  
 XX PT Sensitive detecting proximity changes in a system that utilizes an  
 PT interacting fluorophore and quencher, for high sensitivity  
 PT applications, involves utilizing a metal surface as quencher -  
 XX Example 3; Page 62; 62pp; English.  
 PS The present sequence is that of a perfectly matched target  
 CC sequence for a molecular beacon comprising an oligonucleotide probe  
 CC (see ABL57069) covalently attached at the 3' end to fluorescent  
 CC dye and at the 5' end to a nanoparticle. In the native state, the

CC probe forms a hairpin conformation with hybridised termini. The  
 CC proximity of the fluorophore and quencher (gold nanoparticle) in  
 CC the molecular beacon results in little or no detectable  
 CC fluorescence. Upon hybridisation of the central complementary  
 CC stretch of the probe to a target sequence, such as the present  
 CC sequence, the hairpin undergoes a conformational change resulting  
 CC in an increase in fluorescence, the extent of which is proportional  
 CC to the amount of target sequence present. Single mismatches can  
 CC be detected. The invention relates generally to the use of metal  
 CC surface quenchers such as particles or films for high sensitivity  
 CC applications in, for example, detection and diagnostic systems.

XX SQ Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 other;  
 Query Match 1.4%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1098  
 Db 2 AAAAAAAAAAAAAA 16

RESULT 862  
 AAZ73046  
 ID AAZ73046 standard; DNA; 18 BP.  
 AC AAZ73046;  
 DT 10-SEP-2001 (first entry)  
 DE Human biallelic marker upstream amplification primer SEQ ID NO:7402.  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX OS Homo sapiens.  
 XX PN WO9954500-A2.  
 XX PD 28-OCT-1999.  
 XX PF 21-APR-1999; 99WO-IB00822.  
 XX PR 21-APR-1998; 98US-0082614.  
 XX PR 23-NOV-1998; 98US-0109732.  
 XX PA (GEST ) GENSET.  
 XX PI Cohen D, Blumenfeld M, Chumakov I;  
 XX WP1; 2000-013267/01.  
 XX PT Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome -  
 XX Claim 9; Page 1809; 2745pp; English.  
 XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the  
 CC invention have a variety of uses: they can be used for high density  
 CC mapping of the human genome, and in complex association studies and  
 CC haplotyping studies which are useful in determining the genetic basis  
 CC for disease states. Compositions and methods of the invention can also  
 CC be useful for the identification of the targets for the development of  
 CC pharmaceutical agents and diagnostic methods, as well as the  
 CC characterisation of the differential efficacious responses to and side  
 CC effects from pharmaceutical agents acting on a disease as well as other

CC treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
 CC and 3367, are not actually given a sequence in the Sequence Listing  
 CC from the present invention.  
 XX  
 SQ Sequence 18 BP; 9 A; 1 C; 7 G; 1 T; 0 other;  
 Query Match 1.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 4.6e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 117 AAACGGGAGGAAGGATG 134  
 ||||| ||||| |||||  
 Db 1 AAACGAGAGGAAGGATG 18  
 RESULT 863  
 AAQ20030/c  
 ID AAQ20030 standard; DNA; 19 BP.  
 XX  
 AC AAQ20030;  
 DT 01-APR-1992 (first entry)  
 DE Cross-linking oligomer 116 for targetting HUM11B.  
 XX deoxyribonucleic acid; major groove; ethanoino group; IL-1;  
 KW aziridinylcytosine; cross-linking group; o-xylose linking group;  
 KW human interleukin-1 beta; inverted polarity region; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "N4M4-ethanocytosine"  
 FT modified\_base 4  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "N-methyl-8-oxo-2'-deoxyadenine"  
 FT misc\_feature 14..19  
 FT /tag= c  
 FT /label= inverted\_polarity\_region  
 FT /note= "see comments"  
 FT modified\_base 14  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "N-methyl-8-oxo-2'-deoxyadenine"  
 FT modified\_base 18  
 FT /tag= e  
 FT /mod\_base= OTHER  
 FT /note= "N-methyl-8-oxo-2'-deoxyadenine"  
 FT modified\_base 19  
 FT /tag= f  
 FT /mod\_base= OTHER  
 FT /note= "N-methyl-8-oxo-2'-deoxyadenine"  
 XX WO9118997-A.  
 XX  
 PD 12-DEC-1991.  
 XX  
 PF 24-MAY-1991; 91WO-1003680.  
 XX  
 PR 14-JAN-1991; 91US-0640654.  
 PR 25-MAY-1990; 90US-0529346.  
 XX  
 PA (GILE-) GILEAD SCIE INC.  
 XX  
 PI Matteucci MD, Krawczyk S;  
 XX  
 DR WPI; 1992-007480/01.  
 XX

PT New sequence-specific non-photo-activated crosslinking agents -  
 PT bind to the major groove of duplex DNA and are esp. useful for  
 PT treating latent infections e.g. HIV  
 XX  
 PS Example 4; Page 25; 42pp; English.  
 XX  
 CC This oligomer contains an inverted polarity region formed from an  
 CC o-xyloso dimer synthon. Residues 13 and 14 are linked via an  
 CC o-xyloso group (i.e. nucleotides that have xylose sugar linked via  
 CC the o-xyloso ring). The sequence is designed to target the Human  
 CC interleukin-1 beta gene beginning at nucleotide 7378 and will  
 CC covalently cross-link to it via the N4M4-ethanocytosine group.  
 CC See also AAQ20026-Q20029.  
 XX  
 SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;  
 Query Match 1.3%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1082 TTAATAAAAAAAAAAAAA 1099  
 ||||| ||||| |||||  
 Db 19 TTAATAAAAAAAAAATAA 2  
 RESULT 864  
 AAQ30373/c  
 ID AAQ30373 standard; DNA; 19 BP.  
 XX  
 AC AAQ30373;  
 DT 25-MAR-2003 (updated)  
 DT 07-DEC-1992 (first entry)  
 XX  
 DE Oligomer HUM beta 113 for forming triplex with IL-1 target duplex.  
 KW Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;  
 KW HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT modified\_base 4  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT modified\_base 14  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT modified\_base 18  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT modified\_base 19  
 FT /tag= e  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT misc\_feature 14..19  
 FT /tag= f  
 FT /label= inverted\_polarity\_region  
 FT /note= "see comments"  
 FT misc\_feature 13..14  
 FT /tag= g  
 FT /note= "O-xyloso dimer synthon linkage"  
 XX  
 XX WO9209705-A1.  
 XX  
 PD 11-JUN-1992.

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XX 25-NOV-1991; 91WO-US08811.
XX
XX 23-NOV-1990; 90US-0617907.
XX
XX 18-JAN-1991; 91US-0643382.
XX
XX 08-APR-1991; 91US-0683420.
XX
XX 17-APR-1991; 91US-0686544.
XX
XX 17-APR-1991; 91US-0686546.
XX
XX 17-APR-1991; 91US-0686547.
XX
XX 27-SEP-1991; 91US-0766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
XX hepatitis, herpes, malignancy and inflammation
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at
XX physiological pH with a purine rich target sequence by coupling
XX into the major groove of the duplex. The specific target sequence
XX of this oligomer is the human interleukin -1 beta gene beginning at
XX nucleotide 7378 contg. a purine rich sequence concd. on one strand
XX of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterised by specific DNA
XX duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant
XX tumours and inflammation. The triple helices form under mild conditions
XX thus assays may be carried out without subjecting the test specimen to
XX harsh conditions. The oligomer contains an inverted polarity region
XX formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
XX (nucleotides have the 3' positions of xylose sugars linked via the
XX o-xyline ring). Two nucleotides are coupled through a xyline residue
XX to form the dimer synthon. This additional modifications may render
XX the oligomer stable to nuclease activity. The oligomer is able to
XX inhibit gene expression, as verified by in vitro systems.
XX See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 0 C; 0 G; 14 T; 0 other;
XX
XX Query Match 1.3%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 4.9e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1082 TTAATAAAAAAAAAAAAAA 1099
XX ||||| ||||| ||||| |||||
XX 19 TTAATAAAAAAAAAAAAAATA 2
XX
XX RESULT 865
XX AAQ30376/c
XX ID AAQ30376 standard; DNA; 19 BP.
XX AC AAQ30376;
XX
XX DT 25-MAR-2003 (updated)
XX DT 07-DEC-1992 (first entry)
XX
XX Oligomer HUM beta 116 for forming triplex with IL-1 target duplex.
XX
XX Human interleukin - 1 beta gene; herpes simplex; AIDS; modified;
XX HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX

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FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT
FT 4
FT /*tag= b
FT /mod_base= OTHER
FT
FT 14
FT /mod_base= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT
FT /*tag= c
FT /mod_base= OTHER
FT
FT 18
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT
FT /*tag= d
FT /mod_base= OTHER
FT
FT 19
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT
FT /*tag= e
FT /mod_base= OTHER
FT
FT 14..19
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT
FT /*tag= f
FT /label= inverted_polarity_region
FT
FT 13..14
FT /note= "see comments"
FT
FT /*tag= g
FT /note= "o-xylosa dimer synthon linkage"
FT
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US08811.
XX
XX 23-NOV-1990; 90US-0617907.
XX
XX 18-JAN-1991; 91US-0643382.
XX
XX 08-APR-1991; 91US-0683420.
XX
XX 17-APR-1991; 91US-0686544.
XX
XX 17-APR-1991; 91US-0686546.
XX
XX 17-APR-1991; 91US-0686547.
XX
XX 27-SEP-1991; 91US-0766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,
XX hepatitis, herpes, malignancy and inflammation
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at
XX physiological pH with a purine rich target sequence by coupling
XX into the major groove of the duplex. The specific target sequence
XX of this oligomer is the human interleukin -1 beta gene beginning at
XX nucleotide 7378 contg. a purine rich sequence concd. on one strand
XX of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterised by specific DNA
XX duplex targets, e.g. HPV; HER; HIV, hepatitis B, herpes, malignant
XX tumours and inflammation. The triple helices form under mild conditions
XX thus assays may be carried out without subjecting the test specimen to
XX harsh conditions. The oligomer contains an inverted polarity region
XX formed from an o-xylosa dimer synthon. The linking gp. is o-xylosa
XX (nucleotides have the 3' positions of xylose sugars linked via the
XX o-xyline ring). Two nucleotides are coupled through a xyline residue
XX to form the dimer synthon. This additional modifications may render
XX the oligomer stable to nuclease activity. The oligomer is able to
XX inhibit gene expression, as verified by in vitro systems.
XX See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;
XX

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CC See also AAQ33501-34437.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 331
AAQ58578
ID AAQ58578 standard; RNA; 20 BP.
XX
AC AAQ58578;
XX
DT 25-MAR-2003 (updated)
DT 21-AUG-1994 (first entry)
XX
DE Sequence of synthetic RNA oligo which is a target nucleotide for
DE a novel receptor.
XX
KW Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS Synthetic.
XX
PN W09404194-A1.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993; 93WO-US07603.
XX
PR 14-AUG-1992; 92US-0930087.
XX
PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI De MENDOZA J, Rebek J, Usman N;
XX
DR WFI; 1994-082846/10.
XX
PT Transport of nucleic acid derivs. across membranes - using new
PT receptors which use salt bridging, aromatic stacking, hydrogen
PT bonding and chelation.
XX
PS Example; Table 1, page 38; 103pp; English.
XX
CC The inventors claim a method of transporting a nucleic acid deriv.
CC across a membrane which comprises using a receptor that uses salt
CC bridgin, aromatic stacking, H bonding and chelation to recognise
CC the nucleic acid deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs
CC used in the examples.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 332
AAQ4917/c
ID AAQ4917 standard; cDNA; 20 BP.
XX
AC AAQ4917;
XX
DT 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)

XX 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)

XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
XX 25-MAR-2003 (updated)
XX 15-MAY-1996 (first entry)

XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
XX EP676470-A1.
XX
XX 11-OCT-1995.
XX
XX 04-OCT-1990; 95EP-0105391.
XX
XX 01-OCT-1990; 90US-0589701.
XX 16-OCT-1989; 89US-0422383.
XX 11-JUN-1990; 90US-0537198.
XX 24-AUG-1990; 90US-0573616.
XX 28-SEP-1990; 90WO-US05548.
XX
PA (AMGE-) AMGEN INC.
XX
XX Bosselman RA, Martin FH, Suggs SV, Zsebo KM;
XX
XX WFI; 1995-346090/45.
XX
XX New stem cell factor polypeptide(s) - for stimulating the growth of
XX primitive progenitor cells, esp. for treating disorders involving
XX blood cells
XX
XX Example 3; Fig 12C; 127pp; English.
XX
XX AAQ04915-T04922 are oligonucleotide primers and probes used for the
XX amplification and sequencing of mammalian stem cell factor (SCF).
XX Non-naturally occurring SCF and C-terminally truncated polypeptides,
XX having amino acid sequences sufficiently duplicative of naturally
XX occurring SCF, stimulate growth of primitive progenitors such as
XX haematopoietic progenitor cells, neural stem cells and primordial
XX germ stem cells. The peptides can be used in a composition for
XX treating leucopenia, anaemia or thrombocytopenia, for enhancing
XX engraftment of bone marrow during transplantation or for bone marrow
XX recovery after chemotherapy or radiation-induced bone marrow aplasia
XX or myelosuppression. They can also be used for treating neoplasia,
XX nerve damage, infertility, intestinal damage or myeloproliferative
XX disorders. Antibodies may be raised against the peptides for use in
XX detection or neutralisation of SCF in serum. SCF may be useful for
XX the treatment of AIDS and severe combined immunodeficiency (SCID)
XX states alone or in combination with other factors such as IL-7.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 333
AAQ04918/c
ID AAQ04918 standard; cDNA; 20 BP.
XX
AC AAQ04918;
XX
XX 25-MAR-2003 (updated)
DT 15-MAY-1996 (first entry)

```

XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.  
 DE Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;  
 XX Thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;  
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.  
 XX Synthetic.  
 OS EP676470-A1.  
 XX 11-OCT-1995.  
 XX 04-OCT-1990; 95EP-0105391.  
 XX 01-OCT-1990; 90US-0589701.  
 PR 16-OCT-1989; 89US-0423383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 28-SEP-1990; 90WO-US05548.  
 XX (AMGE-) AMGEN INC.  
 PA Bosselman RA, Martin FH, Suggs SV, Zsebo KM;  
 XX WPI; 1995-346090/45.  
 DR New stem cell factor polypeptide(s) - for stimulating the growth of  
 XX primitive progenitor cells, esp. for treating disorders involving  
 PT blood cells  
 PT Example 3; Fig 12C; 127pp; English.  
 PS AA04915-T04922 are oligonucleotide primers and probes used for the  
 CC amplification and sequencing of mammalian stem cell factor (SCF).  
 CC Non-naturally occurring SCF and C-terminally truncated polypeptides,  
 CC having amino acid sequences sufficiently duplicative of naturally  
 CC occurring SCF, stimulate growth of primitive progenitors such as  
 CC haematopoietic progenitor cells, neural stem cells and primordial  
 CC germ stem cells. The peptides can be used in a composition for  
 CC treating leucopenia, anaemia or thrombocytopenia, for enhancing  
 CC engraftment of bone marrow during transplantation or for bone marrow  
 CC recovery after chemotherapy or radiation-induced bone marrow aplasia  
 CC or myelosuppression. They can also be used for treating neoplasia,  
 CC nerve damage, infertility, intestinal damage or myeloproliferative  
 CC disorders. Antibodies may be raised against the peptides for use in  
 CC detection or neutralisation of SCF in serum. SCF may be useful for  
 CC the treatment of AIDS and severe combined immunodeficiency (SCID)  
 CC states alone or in combination with other factors such as IL-7.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 334  
 AAQ90405/c  
 ID AAQ90405 standard; DNA; 20 BP.  
 AC AAQ90405;  
 XX 08-JAN-1996 (first entry)  
 DT T2 (synthetic DNA probe with 5' amino terminal #4).  
 DE T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;  
 XX

KW ss.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH misc\_feature 1  
 FT /\*tag= a  
 FT /note= "3' aminolink2 Thymine; allows binding to any  
 FT amine"  
 XX WO9512808-A1.  
 PN 11-MAY-1995.  
 XX 26-OCT-1994; 94WO-US12270.  
 XX 01-NOV-1993; 93US-0146504.  
 XX (NANO-) NANOGEN INC.  
 XX Heller MJ, Tu E;  
 XX WPI; 1995-185870/24.  
 DR New self-addressable electronic devices - used for multi-step and  
 XX multiplex reactions such as DNA hybridisation(s), clinical  
 PT diagnostics and bio:polymer synthesis  
 PT Example 1; Page 41; 86pp; English.  
 PS The sequences represented by, AAQ90402-15 are synthetic DNA probes  
 CC containing 5' amino termini. The sequences shown in AAQ90390-401 are  
 CC synthetic DNA probes with 3' ribonucleoside termini. These sequences  
 CC were specific for the polymorphisms of HLA gene dQa. The sequences  
 CC used in the device of the invention. This is a self-addressable  
 CC electronic device (SAED) that can be used to carry out multi-step and  
 CC multiplex reactions, such as nucleic acid hybridisations. The  
 CC advantages of this method are that these reactions can be carried out  
 CC with complete and precise electronic control, and that the rate,  
 CC specificity and sensitivity of these reactions are greatly improved at  
 CC micro-locations.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4  
 RESULT 335  
 AAQ94205/c  
 ID AAQ94205 standard; DNA; 20 BP.  
 XX AAQ94205;  
 AC 25-MAR-2003 (updated)  
 DT 24-AUG-1995 (first entry)  
 XX Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.  
 DE Oligonucleotide ligand; steroid hormone; hapten; immobilisation;  
 KW immunodetection; estradiol; alpha-anomer; ss.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH modified\_base 20  
 FT /\*tag= a  
 FT /mod\_base= OTHER

FT FT /note= "carries a group derived from  
FT misc\_feature 1..21 aminopropanediol"  
FT /\*tag= b  
FT /note= "the glycosidic bonds between nucleotides  
FT are all in the alpha-anomer form"  
XX  
PN WO9429723-A1.  
XX  
XX  
PD 22-DEC-1994.  
XX  
PF 10-JUN-1994; 94WO-FR00689.  
XX  
PR 11-JUN-1993; 93FR-0007093.  
XX  
PA (INMR ) BIO MERIEUX.  
PA (BATT/) BATTAIL N.  
PA (CROS/) CROS P.  
PA (KURE/) KURFURST R.  
PA (PIGA/) FIGA N.  
XX  
XX Battail N, Cros P, Kurfurst R, Piga N;  
XX WPI; 1995-036665/05.  
XX  
XX Assay device for hapten or its specific antibodies - comprises  
PT support having competitive reagent immobilised via nucleic acid  
PT ligand to improve orientation and accessibility  
XX  
PS Example 1; Page 10; 39pp; French.  
XX  
CC Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.  
CC The ligands are covalently linked to a hapten (esp. a steroid hormone).  
CC to form a conjugate which is then immobilised on a solid support for  
CC interaction with antibodies against the hapten. Nucleic acid ligands  
CC are less likely to be recognised by the antibodies than are peptide  
CC ligands and nucleic acids are also less likely to undergo  
CC intramolecular organisation which interferes with accessibility of the  
CC hapten to the antibodies. For immunodiagnosis of oestradiol, the  
CC active hapten oestradiol-6-carboxymethoxime-N-hydroxysuccinimide  
CC ester was used.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
SQ  
Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1100  
DB 20 AAAAAAAAAAAAAA 4  
RESULT 336  
AAQ75599/C  
ID AAQ75599 standard; DNA; 20 BP.  
AC AAQ75599;  
XX  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX JP06303997-A.  
PN  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
PT Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
PT Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAA 1  
RESULT 337  
AAQ75600/C  
ID AAQ75600 standard; DNA; 20 BP.  
XX  
XX AAQ75600;  
XX  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX Synthetic.  
XX  
XX JP06303997-A.  
PN  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
PT Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

CC separate lanes. The method can be used to analyse gene expression  
 XX rapidly and easily.

SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 17 AAAAAAAAAAAAAAAAAA 1

## RESULT 338

AAQ75601/C  
 ID AAQ75601 standard; DNA; 20 BP.

XX AC AAQ75601;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 17 AAAAAAAAAAAAAAAAAA 1

## RESULT 339

AAQ75602/C  
 ID AAQ75602 standard; DNA; 20 BP.

XX AC AAQ75602;

DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 17 AAAAAAAAAAAAAAAAAA 1

## RESULT 340

AAQ75603/C  
 ID AAQ75603 standard; DNA; 20 BP.

XX AC AAQ75603;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.





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RESULT 346
AAQ75593/c
ID AAQ75593 standard; DNA; 20 BP.
XX AC AAQ75593;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX DE aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 348
AAQ75567/c
ID AAQ75567 standard; DNA; 20 BP.
XX AC AAQ75567;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX DE aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 347
AAQ75594/c
ID AAQ75594 standard; DNA; 20 BP.
XX AC AAQ75594;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX DE aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.

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CC rapidly and easily.
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 349
AAQ75568/c
ID AAQ75568 standard; DNA; 20 BP.
XX
AC AAQ75568;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 351
AAQ75570/c
ID AAQ75570 standard; DNA; 20 BP.
XX
AC AAQ75570;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX

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PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 352  
 AAQ75571/c  
 ID AAQ75571 standard; DNA; 20 BP.

XX AAQ75571;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 353  
 AAQ75572/c  
 ID AAQ75572 standard; DNA; 20 BP.

XX AAQ75572;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 354  
 AAQ75573/c  
 ID AAQ75573 standard; DNA; 20 BP.

XX AAQ75573;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.  
 XX PN  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 355  
 AAQ75574/C  
 ID AAQ75574 standard; DNA; 20 BP.  
 AC AAQ75574;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 355  
 AAQ75574/C  
 ID AAQ75574 standard; DNA; 20 BP.  
 AC AAQ75574;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 356  
 AAQ75553/C  
 ID AAQ75553 standard; DNA; 20 BP.  
 AC AAQ75553;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 357

AAQ75560/c  
ID AAQ75560 standard; DNA; 20 BP.  
AC AAQ75560;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
FN JP06303997-A.  
XX  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-0112515.  
PF  
XX 16-APR-1993; 93JP-0112515.  
PR  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 358  
AAQ75561/c  
ID AAQ75561 standard; DNA; 20 BP.  
AC AAQ75561;  
XX  
XX 04-AUG-1995 (first entry)  
DT  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
FN JP06303997-A.  
XX  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-0112515.  
PF  
XX

PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 359  
AAQ75562/c  
ID AAQ75562 standard; DNA; 20 BP.  
AC AAQ75562;  
XX  
XX 04-AUG-1995 (first entry)  
DT  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
XX 01-NOV-1994.  
PD  
XX  
XX 16-APR-1993; 93JP-0112515.  
PF  
XX  
XX 16-APR-1993; 93JP-0112515.  
PR  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX

```
XX SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 360
AAT63649/c
ID AAT63649 standard; DNA; 20 BP.
XX AC AAT63649;
XX 06-JUN-1997 (first entry)
XX DE Anti-HTLV antisense reference oligonucleotide HT.
XX KW antisense; complementary; tax gene; inhibit; HTLV-1;
XX KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
XX OS Synthetic.
XX JP09052898-A.
XX 25-FEB-1997.
XX 09-AUG-1995; 95JP-0224606.
XX 09-AUG-1995; 95JP-0224606.
XX (SOYA-) SOYAKU GIUTSU KENKYUSHO KK.
XX WPI; 1997-197252/18.
XX Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region
PT of tax gene from human T-cell lymphotropic virus type 1 and inhibits
PT viral antigen expression
XX Example 1; Page 8; 10pp; Japanese.
XX Oligonucleotides having a partial sequence consisting of at least 15
CC bases of AAT63641 (an antisense oligo complementary to a region of the
CC tax gene which can inhibit human T-cell lymphotropic virus type 1
CC (HTLV-1) viral antigen expression) are claimed. In an example, six
CC antisense oligos were designed, T1-T6 (AAT63650-55) and were compared to
CC six oligos derived from other regions of HTLV-1, i.e. SJ1 (splice
CC junction), P1 (p21), R1 (rex), RR1 (rex response element), E1 (env) and
CC G1 (gag), four reference oligonucleotides T1S (tax-sense), HC (dc20), HT
CC (dt20) (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC expression inhibiting test. Oligonucleotide T1 gave the best results.
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 20 AAAAAAAAAAAAAAAAAA 4
RESULT 361
AAV34591
ID AAV34591 standard; DNA; 20 BP.
XX AC AAV34591;
XX
```

```
DT 25-AUG-1998 (first entry)
XX M. vaccae antigenic sequence hybridising oligo AD12.
XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX OS Synthetic.
XX OS Mycobacterium vaccae.
XX WO9808542-A2.
XX 05-MAR-1998.
XX 28-AUG-1997; 97WO-NZ00105.
XX 12-JUN-1997; 97US-0873970.
XX 29-AUG-1996; 96US-0705347.
XX (GENE-) GENESIS RES & DEV CORP.
XX PA Hiyaama J, Prestidge RL, Scott LM, Skinner MA, Tan P;
XX PI Visser E;
XX WPI; 1998-216926/19.
XX Mycobacterium vaccae polypeptides - used to develop products for use
PT in detection, therapy and prevention of mycobacteria infections or
PT as immune response enhancers
XX Example 8; Page 99; 153pp; English.
XX This oligonucleotide is used in the DNA cloning strategies of the
CC Mycobacterium vaccae antigens. The invention provides M. vaccae
CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC antigen, or a variant, where the antigen induces an immune response in
CC patients previously exposed to a mycobacterium. Such M. vaccae
CC polypeptides can be used in methods for enhancing non-specific immune
CC response. The methods and products can be used for the detection,
CC treatment and prevention of infectious diseases caused by mycobacteria
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC the ability to induce cell proliferation and cytokine production (e.g.
CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
CC B cells, or macrophages. They can be used for enhancing immune
CC responses for use in vaccines or immunotherapy of infectious diseases
CC and cancers.
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17
RESULT 362
AAT86606/c
ID AAT86606 standard; DNA; 20 BP.
XX AC AAT86606;
XX 04-JUN-1998 (first entry)
XX Oligonucleotide separated by capillary affinity gel electrophoresis.
XX Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX OS Synthetic.
```

XX WO9745721-A1.  
 XX 04-DEC-1997.  
 XX 23-MAY-1997; 97WO-EF02647.  
 XX 24-MAY-1996; 96CH-0001320.  
 XX (NOVS ) NOVARTIS AG.  
 XX Muscate A, Natt F, Paulus A;  
 XX WPI; 1998-041763/04.  
 XX Separation of electrically charged target molecules - by capillary  
 PT affinity gel electrophoresis using polymer-gel to which receptors  
 PT for target molecules are bound  
 XX  
 XX Example D3; Page 25; 41pp; English.  
 XX  
 CC A mixture of oligonucleotides (AAT96604-7) were separated by a new  
 CC process using capillary affinity gel electrophoresis. The invention  
 CC relates to selective separation of electrically charged target molecules  
 CC in an analytical mixture. It comprises capillary affinity gel  
 CC electrophoresis using a capillary tube which is at least partly filled  
 CC with a polymer gel. Receptors for target molecules are covalently bound  
 CC to the polymer. An electric field of at least 50 volts/cm is applied.  
 CC The capillary tube is charged with the analytical mixture. In a first  
 CC separation stage, the target molecules in the mixture are bound to the  
 CC receptors and the remaining components are eluted, optionally whilst  
 CC splitting open. In a second stage, the elution conditions are changed,  
 CC optionally in stages, so that the affinity of the target molecules for  
 CC the receptor is eliminated and the target molecules are eluted and  
 CC detected, optionally whilst splitting open. The process is useful for  
 CC selective separation and/or determination of charged organic compounds,  
 CC such as oligonucleotides, peptides or carbohydrates. It may be used,  
 CC e.g. for isolation of specific proteins and DNA molecules, purification  
 CC of antibodies, analysis of antisense compounds or screening for enzyme  
 CC inhibitors. The process achieves higher resolution and selectivity  
 CC than prior art processes, especially in the case of complex biological  
 CC analytical mixtures. It has high sensitivity, even with small amounts of  
 CC samples. The derivatised polymers may be synthesised specifically using  
 CC standard methods.  
 XX  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4  
 RESULT 363  
 AA211326  
 ID AA211326 standard; DNA; 20 BP.  
 XX  
 XX AA211326;  
 AC  
 DT 25-OCT-1999 (first entry)  
 XX  
 XX Mycobacterial 16S rRNA specific oligo AD12.  
 DE  
 XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;  
 XX dendritic cell maturation; infectious disease; immune disorder; cancer;  
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;  
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;  
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;  
 KW squamous cell carcinoma; melanoma; PCR primer; ss.

OS Synthetic.  
 OS Mycobacterium vaccae.  
 XX  
 PN WO9932634-A2.  
 XX  
 PD 01-JUL-1999.  
 XX  
 XX 23-DEC-1998; 98WO-NZ00189.  
 XX  
 PR 04-DEC-1998; 98US-0205426.  
 PR 23-DEC-1997; 97US-0996624.  
 PR 23-DEC-1997; 97US-0997080.  
 PR 23-DEC-1997; 97US-0997362.  
 PR 11-JUN-1998; 98US-0095855.  
 PR 17-SEP-1998; 98US-0156181.  
 XX  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA  
 XX Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;  
 XX WPI; 1999-430163/36.  
 XX  
 XX Enhancing immune response to an antigen  
 XX  
 XX Example 15; Page 177; 243pp; English.  
 XX  
 CC The invention provides heat-killed Mycobacterium vaccae, or recombinant  
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate  
 CC T cells and natural killer cells, to stimulate the production of  
 CC cytokines, to enhance the expression of co-stimulatory molecules on  
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation  
 CC and function. The proteins can be expressed by standard recombinant  
 CC methodology. Pharmaceutical compositions comprising the proteins or  
 CC nucleic acid sequences encoding the proteins can be used for the  
 CC treatment, prevention, and detection of disorders including infectious  
 CC diseases, immune disorders and cancer. In particular, the compounds and  
 CC methods are used for treatment of diseases of the respiratory system,  
 CC such as mycobacterial infections, asthma, allergies, tuberculosis,  
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as  
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,  
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell  
 CC carcinoma and melanoma.  
 XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17  
 RESULT 364  
 AAX27533/c  
 ID AAX27533 standard; RNA; 20 BP.  
 XX  
 XX AAX27533;  
 AC  
 DT 27-MAY-1999 (first entry)  
 XX  
 XX Synthetic RNA sequence produced by the method of the invention.  
 DE  
 XX Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;  
 KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.  
 XX  
 XX Synthetic.  
 OS  
 PN WO9909044-A1.  
 XX  
 XX 25-FEB-1999.  
 XX

PF 17-AUG-1998; 98WO-EP05215.  
 XX  
 PR 18-AUG-1997; 97CH-0001931.  
 XX  
 PA (JENN/) JENNY L.  
 PA (PITS/) FITSCH S.  
 PA (WEIS/) WEISS P A.

XX Jenny L, Pitsch S, Weiss PA;  
 XX WPI; 1999-180963/15.

XX 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives  
 PT - have high purity, use in machine synthesis of ribonucleic acids,  
 PT enable longer oligonucleotide chain construction, and larger amounts  
 XX

PS Example 6; Page 25; 38pp; English.

CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides  
 CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are  
 CC intermediates for synthesis of RNA-oligonucleotides with predetermined  
 CC nucleotide sequence, particularly by machine synthesis. The groups  
 CC specified above, apart from those on silyl, are those particularly for  
 CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide  
 CC products in diagnosis, therapy, and as research tools, are well known,  
 CC and are not dealt with in detail. (II) is an intermediate for (I). The  
 CC silyloxymethyl halide reagent is easy to prepare, and yields are high.  
 CC Introduction of the silyloxymethyl group into the ribonucleoside is  
 CC simple and rapid, and the acetal bond formed does not migrate,  
 CC eliminating particularly the prior art problem of 2' to 3' isomerisation.  
 CC The methylenedioxy group spacer between the silyl group and nucleoside  
 CC ring results in less steric hindrance than bulky direct silyloxy  
 CC linkages, enabling first, a range of choices for the silyl substituents,  
 CC to provide, e.g., acid or base stability; and second, higher yields in  
 CC coupling. Purer products are therefore obtained than in prior art,  
 CC enabling larger quantities and longer chains of oligoribonucleotides to  
 CC be synthesised successfully, and in shorter times.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB |||||  
 20 AAAAAAAAAAAAAAAAAA 4

RESULT 365  
 AAA40448/C  
 ID AAA40448 standard; DNA; 20 BP.  
 XX  
 AC AAA40448;

DT 13-NOV-2000 (first entry)

XX Electrochemical detection method fixed probe DNA.

XX Electrochemical detection; glucose; cholesterol; urea nitrogen;  
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;  
 KW plasma; serum; urine; lymph diagnosis; probe; ss.

OS Synthetic.

XX EPI018646-A2.

XX 12-JUL-2000.

XX 07-JAN-2000; 2000EP-0100126.

XX 06-JAN-1999; 99JP-0001111.

XX 24-MAY-1999; 99JP-0143599.

XX (FUJF ) FUJI PHOTO FILM CO LTD.  
 XX Ogawa M, Takenaka S, Takagi M;  
 XX WPI; 2000-444372/39.

XX Quantitative analysis of a biochemical compound such as glucose, in  
 PT body a body fluid such as blood, comprising detecting enhanced electron  
 PT transfer between an oxidase and a DNA-immobilized electrode, useful for  
 PT diagnosis of disease -

XX Example 1; Page 7; 14pp; English.

XX This invention describes a novel method for quantitatively analysing a  
 CC biochemical compound (I) which comprises contacting (I) with double  
 CC stranded DNA fixed to the surface of an electrode at their terminals in  
 CC which electrochemically active threading intercalators are intercalated,  
 CC in an aqueous medium under application of electric potential to the  
 CC electrode in the presence of an oxidase which oxidizes the biochemical  
 CC compound and becomes reduced, and detecting electric current flowing  
 CC between the electrode and a second electrode in the aqueous medium. The  
 CC method is useful for detection of biochemical compounds such as glucose,  
 CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
 CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
 CC for diagnosis of various diseases. The method allows detection of  
 CC biochemical compounds quickly and easily with a high sensitivity using a  
 CC simple apparatus. This sequence represents DNA fragment used as fixed  
 CC probe DNA in the method of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB |||||  
 20 AAAAAAAAAAAAAAAAAA 4

RESULT 366  
 AAA40449  
 ID AAA40449 standard; DNA; 20 BP.  
 XX  
 AC AAA40449;

DT 13-NOV-2000 (first entry)

XX Electrochemical detection method sample DNA target.

XX Electrochemical detection; glucose; cholesterol; urea nitrogen;  
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;  
 KW plasma; serum; urine; lymph diagnosis; ss.

OS Synthetic.

XX EPI018646-A2.

XX 12-JUL-2000.

XX 07-JAN-2000; 2000EP-0100126.

XX 06-JAN-1999; 99JP-0001111.

XX 24-MAY-1999; 99JP-0143599.

XX (FUJF ) FUJI PHOTO FILM CO LTD.

XX Ogawa M, Takenaka S, Takagi M;

XX WPI; 2000-444372/39.

XX Quantitative analysis of a biochemical compound such as glucose, in

PT body a body fluid such as blood, comprising detecting enhanced electron  
PT transfer between an oxidase and a DNA-immobilized electrode, useful for  
PT diagnosis of disease -

XX Example 1; Page 8; 14pp; English.

XX This invention describes a novel method for quantitatively analysing a  
CC biochemical compound (I) which comprises contacting (I) with double  
CC stranded DNA fixed to the surface of an electrode at their terminals in  
CC which electrochemically active threading intercalators are intercalated,  
CC in an aqueous medium under application of electric potential to the  
CC electrode in the presence of an oxidase which oxidizes the biochemical  
CC compound and becomes reduced, and detecting electric current flowing  
CC between the electrode and a second electrode in the aqueous medium. The  
CC method is useful for detection of biochemical compounds such as glucose,  
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
CC for diagnosis of various diseases. The method allows detection of  
CC biochemical compounds quickly and easily with a high sensitivity using a  
CC simple apparatus. This sequence represents DNA fragment used as a target  
CC sample in the method of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 367

AAA50193/c  
ID AAA50193 standard; DNA; 20 BP.

XX AAA50193;

XX 07-NOV-2000 (first entry)

XX 2'-Methoxyethoxy-modified oligonucleotide.

XX Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..19

FT /\*tag= a

FT /note= "2'-methoxyethoxy modified thymidine"

XX WO200047593-A1.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US03543.

XX 12-FEB-1999; 99US-0250075.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Maier MA;

XX WPI; 2000-558188/51.

XX Preparation of mixed backbone oligomeric compounds useful as e.g.

PT primers for diagnostic tests, involves oxidation of H-phosphonate

PT internucleoside linkages to phosphodiester internucleoside linkages -

XX Example 12; Page 34; 49pp; English.

XX The present sequence is that of a phosphodiester oligonucleotide

CC containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group  
CC on its 5' ribose sugar moiety. It is an example of an oligomeric  
CC compound produced according to the methods of the invention. The  
CC invention provides compounds and methods for the preparation of  
CC mixed backbone oligomeric, or chimeric, compounds having  
CC phosphodiester internucleoside linkages in addition to  
CC phosphorothioate and/or phosphoramidate internucleoside linkages.  
CC The methods also include incorporation of boranophosphate  
CC internucleoside linkages. The methods utilize H-phosphonate  
CC intermediates that are coupled together forming contiguous regions  
CC of 1 or more H-phosphonate internucleoside linkages. Each  
CC contiguous region is subsequently oxidized to phosphodiester,  
CC phosphorothioate, phosphoramidate or boranophosphate  
CC internucleoside linkages prior to further elongation. Mixed  
CC backbone oligomeric compounds are prepared in this manner by  
CC oxidizing adjacent regions with different reagents. Oligomeric  
CC compounds of the invention are prepared using novel oxidation steps  
CC that oxidize a region of 1 or more H-phosphonate internucleoside  
CC linkages without degrading existing linkages that have been  
CC previously oxidized. The oligonucleotides obtained are useful as  
CC primers in PCR, probes, linkers, gene fragments and for other  
CC diagnostic tests on e.g. biological tissue, fluid, cells etc., as  
CC research reagents, and as antiviral agents.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 368

AAA13752/c

ID AAA13752 standard; DNA; 20 BP.

XX AAA13752;

XX 27-JUL-2000 (first entry)

XX Stem cell factor universal oligonucleotide 220-3.

XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;  
XX primitive progenitor cell; haematopoietic disorder; syngeneic;  
XX allogeneic; autologous bone marrow transplant; gene therapy;  
XX transfection; haematopoietic stem cell; acute blood loss; neoplasia;  
XX cancer; ss.

XX Synthetic.

XX EP992579-A1.

XX 12-APR-2000.

XX 04-OCT-1990; 99EP-0122861.

XX 16-OCT-1989; 89US-0422383.

XX 11-JUN-1990; 90US-0537198.

XX 24-AUG-1990; 90US-0573616.

XX 28-SEP-1990; 90WO-US05548.

XX 01-OCT-1990; 90US-0589701.

XX 04-OCT-1990; 90EP-0310699.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX WPI; 2000-259135/23.

PT Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell  
 XX factor -  
 PS Example 3; Fig 12C; 123pp; English.  
 XX  
 CC A method has been developed of making haematopoietic cells suitable for  
 CC administration to a subject. The method comprises: (a) obtaining the  
 CC haematopoietic progenitor cells from a donor; and (b) expanding the  
 CC cells by adding to the cells a haematopoietically effective dose of a  
 CC polypeptide product having at least part of the primary structural  
 CC confirmation and one or more of the biological properties of naturally  
 CC occurring stem cell factor (SCF). The method is useful for stimulating  
 CC primitive progenitor cells including early haematopoietic progenitor  
 CC cells which are capable of maturing to erythroid, megakaryocyte,  
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute  
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.  
 CC SCF is useful for treating haematopoietic disorders. The method is  
 CC useful for expanding early haematopoietic progenitors in syngeneic,  
 CC allogeneic or autologous bone marrow transplant. SCF is useful for  
 CC enhancing the efficiency of gene therapy based on transfecting the  
 CC haematopoietic stem cells. SCF is also useful for combating the  
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing  
 CC haematopoietic recovery after acute blood loss and as a boost to the  
 CC immune system for fighting neoplasia (cancer). The present sequence  
 CC represents a universal oligonucleotide which is used in an example from  
 CC the present invention.

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAA 2

RESULT 369  
 AAA13754/C  
 ID AAA13754 standard; DNA; 20 BP.

AC AAA13754;  
 XX  
 XX 27-JUL-2000 (first entry)  
 XX  
 DE Stem cell factor universal oligonucleotide 220-11.  
 XX  
 KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;  
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;  
 KW allogeneic; autologous bone marrow transplant; gene therapy;  
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;  
 KW cancer; ss.

XX Synthetic.  
 OS  
 XX EP992579-A1.  
 PN  
 XX 12-APR-2000.  
 PD  
 XX 04-OCT-1990; 99EP-0122861.  
 XX  
 PF 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 28-SEP-1990; 90WO-US05548.  
 PR 01-OCT-1990; 90US-0589701.  
 PR 04-OCT-1990; 90EP-0310899.  
 XX  
 XX (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

DR WPI; 2000-259135/23.  
 XX  
 PT Production of hematopoietic cells suitable for administration to a  
 PT subject using progenitor cells and expanding the cells using stem cell  
 PT factor -  
 XX  
 PS Example 3; Fig 12C; 123pp; English.

XX A method has been developed of making haematopoietic cells suitable for  
 CC administration to a subject. The method comprises: (a) obtaining the  
 CC haematopoietic progenitor cells from a donor; and (b) expanding the  
 CC cells by adding to the cells a haematopoietically effective dose of a  
 CC polypeptide product having at least part of the primary structural  
 CC confirmation and one or more of the biological properties of naturally  
 CC occurring stem cell factor (SCF). The method is useful for stimulating  
 CC primitive progenitor cells including early haematopoietic progenitor  
 CC cells which are capable of maturing to erythroid, megakaryocyte,  
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute  
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.  
 CC SCF is useful for treating haematopoietic disorders. The method is  
 CC useful for expanding early haematopoietic progenitors in syngeneic,  
 CC allogeneic or autologous bone marrow transplant. SCF is useful for  
 CC enhancing the efficiency of gene therapy based on transfecting the  
 CC haematopoietic stem cells. SCF is also useful for combating the  
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing  
 CC haematopoietic recovery after acute blood loss and as a boost to the  
 CC immune system for fighting neoplasia (cancer). The present sequence  
 CC represents a universal oligonucleotide which is used in an example from  
 CC the present invention.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1084 AAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAA 2

RESULT 370  
 AAZ91117/C  
 ID AAZ91117 standard; DNA; 20 BP.

XX AAZ91117;  
 AC  
 XX 06-JUN-2000 (first entry)  
 DT  
 XX Oligonucleotide #5 for conjugation to abietane derivative.  
 DE  
 XX Abietane derivative; labelling; diagnostic test; biotin substitute; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX FR2781802-A1.  
 PN  
 XX 04-FEB-2000.  
 PD  
 XX 31-JUL-1998; 98FR-0010084.  
 PF  
 XX 31-JUL-1998; 98FR-0010084.  
 PR  
 XX (INMR) BIO MERIEUX.  
 PA  
 XX Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;  
 PI  
 XX WPI; 2000-239603/21.

XX Saturated and unsaturated derivatives of abietic acid and their  
 PT conjugated derivatives with natural and synthetic polymers, having use  
 PT in diagnostics, chemical reactions and analysis -  
 XX



PS Example 5; Page 20; 39pp; French.

XX The invention relates to novel saturated and unsaturated abietane derivatives. The new compounds may be used directly or indirectly in the development of new diagnostic tests, to follow infections, CC especially viral infections, to follow and/or measure chemical products, CC especially potential pollutants. In diagnostic tests they may be used CC as markers, or to form a universal solid phase after immobilization CC on a solid support, to produce monoclonal antibodies or polyclonal CC antibodies having diagnostic uses. The oligonucleotides AA291113-Z91117 CC represent examples of sequences that can be labeled with the CC new abietane derivatives. The new derivatives may be used to substitute CC for biotin in diagnostic tests, but because they are not found naturally CC in humans the risk of potential interactions with biological molecules CC is eliminated.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
|||||  
DB 20 AAAAAAAAAAAAAA 4

RESULT 371

AA563428

ID AAS63428 standard; DNA; 20 BP.

AC AAS63428;

XX 29-JAN-2002 (first entry)

DE Oligonucleotide-nanoparticle probe #52.

XX Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;

KW nucleic acid detection; nanostructure; biochip; biofilter;

KW drug delivery; ss.

XX Synthetic.

XX WO200173123-A2.

PN 04-OCT-2001.

PD 28-MAR-2001; 2001WO-US10071.

PF 28-MAR-2000; 2000US-192699P.

PR 26-APR-2000; 2000US-200161P.

PR 26-JUN-2000; 2000US-213906P.

PR 26-JUN-2000; 2000US-0603830.

PR 08-DEC-2000; 2000US-254392P.

PR 11-DEC-2000; 2000US-25235P.

PR 12-JAN-2001; 2001US-0760500.

PR 28-MAR-2001; 2001US-0820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Park S, Li Z;

XX WPI; 2001-656926/75.

DR Detecting and separating nucleic acid, useful e.g. for diagnosis,

XX comprises reaction with nanoparticles that carry oligonucleotides

PT complementary to parts of the target

XX Example 18; Page 158; 404pp; English.

PS The invention relates to a method for detection of nucleic acid (I)

XX having at least 2 portions, comprising treatment with nanoparticles that

CC carry oligonucleotides complementary to at least 2 parts of (I), where  
CC detectable change caused by hybridisation of the oligonucleotide to (I)  
CC is observed. The method is used to detect (or to separate) specific (I),  
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic  
CC analysis etc., and generally to detect analytes other than (I). The  
CC oligonucleotide-derivatised nanoparticles are also useful for preparing  
CC nanostructures useful, for example, as biochips, biofilters, mechanical  
CC devices, separation membranes, chemical sensors, in computers, and for  
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates  
CC can be produced, allowing their direct use (as probes) in polymerase  
CC chain reaction, i.e. they survive multiple heating/cooling cycles so do  
CC not need to be added after amplification. (I) are detected by simple  
CC colour change, without the need for special equipment, making possible  
CC rapid field testing for e.g. pathogens. AAS63374-AAS63448 represent  
CC oligonucleotide-nanoparticle probes, and related sequences, used in the  
CC method of the invention.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
|||||  
DB 1 AAAAAAAAAAAAAA 17

RESULT 372

AAH78547

ID AAH78547 standard; cDNA; 20 BP.

XX AAH78547;

XX 10-DEC-2001 (first entry)

XX Nucleotide sequence of a cDNA sequence.

XX Nucleic acid identification; DNA library screening; ss.

XX Synthetic.

XX US6274321-B1.

XX 14-AUG-2001.

XX 03-DEC-1999; 99US-0454704.

XX 03-DEC-1999; 99US-0454704.

XX (REGC ) UNIV CALIFORNIA.

XX Blumberg B;

XX WPI; 2001-588900/66.

XX Screening nucleic acids (NA) in pool of interest comprises pooling,

PT expressing NA to form expression product pool and identifying NA in NA

PT pool corresponding to expression product pool having interaction with

PT target moiety

XX Disclosure; Column 22; 19pp; English.

XX The specification describes a method for identifying a nucleic acid

CC in a pool of interest. The method comprises pooling individually

CC identifiable nucleic acids into at least two pools of one nucleic acid

CC each; expressing nucleic acid pools to obtain protein expression product

CC pools; assaying protein expression product pools for products having

CC interaction with target molecule; selecting nucleic acid pools

CC corresponding to identified protein expression product pools; and

CC identifying individual nucleic acids in identified nucleic acid

CC pools. The method is useful for identifying a nucleic acid (e.g. cDNA)

CC in a pool of interest and for functionally screening several nucleic

CC acids. The method is also useful for screening genomic DNA libraries  
 CC or other source of individual cDNAs, mRNAs, synthetic libraries of  
 CC nucleic acids e.g. combinatorial libraries. The present sequence  
 CC was used in the course of the invention.  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17  
 RESULT 373  
 AAS10371  
 ID AAS10371 standard; DNA; 20 BP.  
 AC AAS10371;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE Oligonucleotide-cyclic disulphide linker, d.  
 DE  
 KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
 KW DNA isolation; genetic disease; bacterial disease; viral disease;  
 KW forensic science; paternity testing; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1  
 FT /\*tag= a  
 FT /note= "A is covalently linked to a  
 FT cyclic-disulphide moiety"  
 XX  
 FN WO200151665-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US01190.  
 XX  
 PR 13-JAN-2000; 2000US-0176409.  
 PR 26-APR-2000; 2000US-0200161.  
 PR 26-JUN-2000; 2000US-0603830.  
 PR 12-JAN-2001; 2001US-0760500.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Li Z;  
 XX  
 DR WPI; 2001-451868/48.  
 XX  
 PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial  
 PT or viral diseases, by contacting the nucleic acid with oligonucleotides  
 PT attached to nanoparticles and having sequences complementary a portion  
 PT of the nucleic acid -  
 XX  
 PS Example 24; Fig 44; 323pp; English.  
 XX  
 CC The sequence represents a cyclic disulphide linked oligonucleotide  
 CC which may be coupled with colloidal gold particles (nanoparticles) and  
 CC used to demonstrate the method of the invention. The invention relates to  
 CC isolating or detecting a nucleic acid of interest, in a mixture of  
 CC nucleic acids, by binding it to 2 or more complementary nucleotides which  
 CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.  
 CC colloidal gold) are used to both isolate and detect (e.g. by linking the  
 CC particle to a fluorescent probe) the resultant complex. The methods are  
 CC useful for detecting nucleic acids, natural or synthetic, and modified or  
 CC unmodified. The methods may also be applied in the diagnosis of genetic,

CC bacterial and viral diseases, in forensics, in DNA sequencing, for  
 CC paternity testing, for cell line authentication, and for monitoring gene  
 CC therapy. The methods are further useful in research and analytical  
 CC laboratories in DNA sequencing, in the field to detect the presence of  
 CC specific pathogens, for quick identification of an infection to assist in  
 CC drug prescription, and in homes and health centres for inexpensive  
 CC first-line screening. The methods, which are based on observing  
 CC colour change with the naked eye, are cheap, fast, simple, robust  
 CC (reagents are stable), do not require specialised or expensive equipment,  
 CC and little or no instrumentation is required.  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17  
 RESULT 374  
 AAS10402/c  
 ID AAS10402 standard; DNA; 20 BP.  
 XX  
 AC AAS10402;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE DNA template for 3' end labeling of an RNA molecule, #14.  
 DE  
 KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US6238865-B1.  
 XX  
 PD 29-MAY-2001.  
 XX  
 PF 16-OCT-1998; 98US-0173936.  
 XX  
 PR 17-OCT-1997; 97US-0063757.  
 XX  
 PA (CHEN/) CHEN G.  
 PA (HUAN/) HUANG Z.  
 PA (SZOS/) SZOSTAK J W.  
 XX  
 PI Huang Z, Szostak JW;  
 XX  
 DR WPI; 2001-366470/38.  
 XX  
 PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for  
 PT labeling and modifying 3'-termini of other nucleic acids, comprises  
 PT using a synthetic nucleotide template with a defined overhang  
 PT nucleotide -  
 XX  
 PS Example 5; Column 13; 22pp; English.  
 XX  
 CC The sequence represents a synthetic DNA template molecule used to  
 CC demonstrate the method of the invention. The invention relates to a  
 CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3'  
 CC terminus of an RNA molecule by providing a DNA oligonucleotide,  
 CC complementary to the 3' end of the RNA molecule, with an overhang at the  
 CC 5' end which allows incorporation of the labeling nucleotide into the  
 CC RNA molecule. The method, based on the synthesis of Okazaki fragments, is  
 CC useful for labeling and modifying the 3'-termini of other nucleic acids  
 CC such as DNA fragments. The method is a simple and efficient way of  
 CC labeling or modifying RNA 3'-termini using DNA polymerase and a synthetic  
 CC template with defined overhang nucleotides.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 375  
 AAS10447/c  
 ID AAS10447 standard; DNA; 20 BP.  
 XX  
 AC AAS10447;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-3.  
 XX  
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;  
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN USG248319-B1.  
 XX  
 PD 19-JUN-2001.  
 XX  
 PF 24-MAY-1995; 95US-0449653.  
 XX  
 PR 10-APR-1991; 91US-0684535.  
 PR 25-NOV-1992; 92US-0982255.  
 PR 16-OCT-1989; 89US-0423283.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 PR 21-DEC-1993; 93US-0172329.  
 XX  
 PA (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX  
 DR WPI; 2001-407312/43.  
 XX  
 PT Increasing the number of early haematopoietic progenitor cells in the  
 PT peripheral blood useful for the treatment of blood disorders including  
 PT Hodgkin's disease comprises the administration of human stem cell  
 PT factor -  
 XX  
 PS Example 3; Fig 12C; 210pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-3 is 1 of 19  
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of  
 CC the human SCF cDNA sequence. The sequence is described in an  
 CC invention relating to novel stem cell factors, the polynucleotides  
 CC encoding them and methods for producing the stem cell factors. The  
 CC methods involve increasing the number of early haematopoietic progenitor  
 CC cells in human peripheral blood by administering a haematopoietically  
 CC effective human stem cell factor polypeptide. The methods are useful for  
 CC the treatment of blood disorders, including myelofibrosis,  
 CC myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,  
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,  
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic  
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral  
 CC induced disorders, including AIDS.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 376  
 AAS10449/c  
 ID AAS10449 standard; DNA; 20 BP.  
 XX  
 AC AAS10449;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.  
 XX  
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;  
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN USG248319-B1.  
 XX  
 PD 19-JUN-2001.  
 XX  
 PF 24-MAY-1995; 95US-0449653.  
 XX  
 PR 10-APR-1991; 91US-0684535.  
 PR 25-NOV-1992; 92US-0982255.  
 PR 16-OCT-1989; 89US-0423283.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 PR 21-DEC-1993; 93US-0172329.  
 XX  
 PA (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX  
 DR WPI; 2001-407312/43.  
 XX  
 PT Increasing the number of early haematopoietic progenitor cells in the  
 PT peripheral blood useful for the treatment of blood disorders including  
 PT Hodgkin's disease comprises the administration of human stem cell  
 PT factor -  
 XX  
 PS Example 3; Fig 12C; 210pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-11 is 1 of 19  
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of  
 CC the human SCF cDNA sequence. The sequence is described in an  
 CC invention relating to novel stem cell factors, the polynucleotides  
 CC encoding them and methods for producing the stem cell factors. The  
 CC methods involve increasing the number of early haematopoietic progenitor  
 CC cells in human peripheral blood by administering a haematopoietically  
 CC effective human stem cell factor polypeptide. The methods are useful for  
 CC the treatment of blood disorders, including myelofibrosis,  
 CC myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia,  
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,  
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic  
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral  
 CC induced disorders, including AIDS.  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;



DT 21-AUG-2001 (first entry)  
 XX Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.  
 XX Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;  
 KW gene therapy; PCR primer; mutagenesis; probe; ss.  
 XX Synthetic.  
 OS  
 XX US6207454-B1.  
 PN 27-MAR-2001.  
 XX 31-DEC-1998; 98US-0224681.  
 XX 21-DEC-1993; 93US-0172329.  
 PR 24-MAY-1995; 95US-0449653.  
 PR 12-JAN-1998; 98US-0005893.  
 PR 25-NOV-1992; 92US-0982255.  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-366062/38.  
 XX Enhancing efficiency of transfer of polynucleotide into a target  
 PT mammalian cell in vitro, involves exposing cell that expresses a stem  
 PT cell factor receptor to stem cell factor, and introducing  
 PT polynucleotide into cell in vitro -  
 XX Example 3; Fig 12C; 210pp; English.  
 PS The present invention describes a method for enhancing (E) the  
 CC efficiency of transfer of a polynucleotide (I) into a target mammalian  
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell  
 CC factor (SCF) receptor to a biologically active SCF, its analogue or  
 CC fragment, which induces cell proliferation, and introducing (I) to (II)  
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)  
 CC into the cell. The method is useful for enhancing the efficiency of the  
 CC transfer of a polynucleotide into a target mammalian cell in vitro.  
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364  
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification  
 CC of the present invention.  
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 380  
 AAS04111/C  
 ID AAS04111 standard; DNA; 20 BP.  
 XX AAS04111;  
 AC AAS04111;  
 XX 29-AUG-2001 (first entry)  
 DT Human SCF (stem cell factor) cDNA universal PCR primer 220-3.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

KW PCR primer; ss.  
 XX Homo sapiens.  
 XX US6207417-B1.  
 PN 27-MAR-2001.  
 XX 07-JUN-1995; 95US-0482918.  
 XX 21-DEC-1993; 93US-0172329.  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-298941/31.  
 DR Novel nucleic acids encoding stem cell factor useful for treating  
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's  
 PT disease, Kala azar, anaemia and septicemia -  
 XX Example 3; Fig 12C; 209pp; English.  
 PS The present sequence for universal PCR primer 220-3 is 1 of 8  
 CC universal oligonucleotides (AAS04110-AAS04117) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAU02462-AAU02481) and the oligonucleotides  
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC Pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 381  
 AAS04113/C  
 ID AAS04113 standard; DNA; 20 BP.  
 XX AAS04113;  
 AC AAS04113;  
 XX 29-AUG-2001 (first entry)  
 DT Human SCF (stem cell factor) cDNA universal PCR primer 220-11.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 XX US6207417-B1.  
 XX 27-MAR-2001.  
 XX 07-JUN-1995; 95US-0482918.  
 XX 21-DEC-1993; 93US-0172329.  
 XX 16-OCT-1989; 89US-0422383.  
 XX 11-JUN-1990; 90US-0537198.  
 XX 24-AUG-1990; 90US-0573616.  
 XX 01-OCT-1990; 90US-0589701.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-298941/31.  
 DR Novel nucleic acids encoding stem cell factor useful for treating  
 XX disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's  
 PT disease, kala azar, anaemia and septicemia -  
 PS Example 3; Fig 12C; 203pp; English.  
 CC The present sequence for universal PCR primer 220-11 is 1 of 8  
 CC universal oligonucleotides (AAS04110-AAS04117) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAU02462-AAU02481) and the oligonucleotides  
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 382  
 AAS04212/C  
 ID AAS04212 standard; DNA; 20 BP.  
 XX AC AAS04212;  
 XX 29-AUG-2001 (first entry)  
 DT Human SCF (stem cell factor) cDNA universal PCR primer 220-3.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 XX PCR primer; ss.  
 XX Homo sapiens.  
 XX US6218148-B1.  
 XX 17-APR-2001.  
 XX 21-DEC-1993; 93US-0172329.  
 XX 25-NOV-1992; 92US-0982255.  
 XX 16-OCT-1989; 89US-0422383.  
 XX 11-JUN-1990; 90US-0537198.  
 XX 24-AUG-1990; 90US-0573616.  
 XX 01-OCT-1990; 90US-0589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-281051/29.  
 DR Isolated DNA sequence, encoding polypeptide product useful for  
 XX stimulating growth of early haematopoietic progenitor cells -  
 PT Example 3; Fig 12C; 167pp; English.  
 CC The present sequence for universal PCR primer 220-3 is 1 of 8  
 CC universal oligonucleotides (AAS04211-AAS04218) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAU02777-AAU02794) and the oligonucleotides  
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 383  
 AAS04214/C  
 ID AAS04214 standard; DNA; 20 BP.  
 XX AC AAS04214;  
 XX 29-AUG-2001 (first entry)  
 DT Human SCF (stem cell factor) cDNA universal PCR primer 220-11.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.

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XX OS Homo sapiens.
XX PN US6218148-B1.
XX PD 17-APR-2001.
XX PF 21-DEC-1993; 93US-0172329.
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-281051/29.
XX DR Isolated DNA sequence, encoding polypeptide product useful for
XX PT stimulating growth of early haematopoietic progenitor cells -
XX PT
XX PS Example 3; Fig 12C; 167pp; English.
XX CC The present sequence for universal PCR primer 220-11 is 1 of 8
XX CC universal oligonucleotides (AAS04211-AAS04218) used in the
XX CC isolation of the human SCF (stem cell factor) cDNA sequence. The
XX CC present invention relates to novel stem cell factors
XX CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides
XX CC encoding them. SCF stimulate primitive progenitor cells including early
XX CC haematopoietic progenitor cells. The invention also describes SCF
XX CC peptides (AAU02777-AAU02794) and the oligonucleotides
XX CC (AAS04182-AAS04210) used in the isolation of human and rat SCF
XX CC sequences. The polynucleotide encoding SCF is useful for producing SCF
XX CC and useful in gene therapy. It is useful for treating disorders
XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
XX CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX CC pyridoxine deficiency, and hypopigmentation disorders such as
XX CC piebaldism and vitiligo.
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2
RESULT 384
AAH23889/c
ID AAH23889 standard; DNA; 20 BP.
XX AC AAH23889;
XX DT 07-AUG-2001 (first entry)
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN US6204363-B1.
XX PD 20-MAR-2001.
XX PF 25-NOV-1992; 92US-0982255.
XX PR 10-APR-1991; 91US-0684535.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-256683/26.
XX DR New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors, useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX PT disease -
XX PS Example 3; Fig 12C; 166pp; English.
XX CC The present sequence for universal PCR primer 220-3 is 1 of 8
XX CC universal oligonucleotides (AAH23888-AAH23895) used in the
XX CC isolation of the human SCF (stem cell factor) cDNA sequence. The
XX CC present invention relates to novel stem cell factors
XX CC (AAB73561-AAB73568, AAB73571-AAB73576) and the polynucleotides
XX CC encoding them. SCF stimulate primitive progenitor cells including early
XX CC haematopoietic progenitor cells. The invention also describes SCF
XX CC peptides (AAB73578-AAB73597) and the oligonucleotides
XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF
XX CC sequences. The polynucleotide encoding SCF is useful for producing SCF
XX CC and useful in gene therapy. It is useful for treating disorders
XX CC involving blood cells such as myelofibrosis, metastatic carcinoma,
XX CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,
XX CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,
XX CC sarcoidosis, military tuberculosis, disseminated fungus disease,
XX CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,
XX CC pyridoxine deficiency, and hypopigmentation disorders such as
XX CC piebaldism and vitiligo.
XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 18 AAAAAAAAAAAAAAAAAA 2
RESULT 385
AAH23891/c
ID AAH23891 standard; DNA; 20 BP.
XX AC AAH23891;
XX DT 07-AUG-2001 (first entry)
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN US6204363-B1.

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PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids -  
 XX Claim 101; Page 49; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells.  
 CC Note: the present sequence may have a phosphorothioate backbone.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
 SQ Query Match 1-5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4  
 RESULT 388  
 AAF99431  
 ID AAF99431 standard; DNA; 20 BP.  
 AC AAF99431;  
 XX 12-JUN-2001 (first entry)  
 DT Immunostimulatory nucleic acid #547.  
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 OS WO200122972-A2.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US26383.  
 XX 25-SEP-1999; 99US-0156113.  
 PR 27-SEP-1999; 99US-0156135.  
 PR 23-AUG-2000; 2000US-0227436.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids -  
 XX Claim 101; Page 49; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells.  
 CC Note: the present sequence may have a phosphorothioate backbone.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
 SQ Query Match 1-5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4  
 RESULT 389  
 AAF60896  
 ID AAF60896 standard; DNA; 20 BP.  
 AC AAF60896;  
 XX 15-MAY-2001 (first entry)  
 DT Conjugate forming oligonucleotide ON5 SEQ ID 5.  
 DE Transport; membrane; cytostatic; virucide; vasotropic; dermatological;  
 KW antiparasitic; antiasthmatic; gene therapy; tumor cell; antitense;  
 KW tumor therapy; drug; phosphodiester linkage; ss.  
 OS Unidentified.  
 OS DE19935302-A1.  
 XX 08-FEB-2001.  
 XX 28-JUL-1999; 99DE-1035302.  
 XX 28-JUL-1999; 99DE-1035302.  
 XX (AVET ) AVENTIS PHARMA DEUT GMBH.  
 XX Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;  
 PI WPI; 2001-203679/21.  
 DR New substituted aryl conjugates of parent molecules, especially  
 XX oligonucleotides, having improved transmembrane and intracellular  
 PT transport properties, useful as medicaments or diagnostic agents -  
 XX Disclosure; Page 9; 28pp; German.  
 XX This invention describes a novel conjugate (I) which consists of (A) a  
 CC molecule to be transported and (B) at least one aryl residue of formula  
 CC -Ar-(X-C(Y)-R.1) n (II). Ar = group containing at least one aromatic  
 CC ring; X = O or N (sic); Y = O, S or NH-R.2 (sic); R.1 = optionally  
 CC substituted 1-23C alkyl (optionally containing double and/or triple  
 CC bonds); R.2 = optionally substituted 1-18C alkyl (optionally containing  
 CC double and/or triple bonds); n = integer of 1 or more. (A) is bonded to

CC (B) directly or via a chemical group, provided that the chemical group is  
 CC other than CH<sub>2</sub>-S if the bond is via a phosphodiester linkage of (A). The  
 CC invention also describes (i) the preparation of a conjugate (I') of (A')  
 CC a molecule to be transported and (B') at least one aryl residue (not  
 CC restricted to (ii)), by preparing (A') containing a reactive function at  
 CC the position at which (B') is to be bonded, preparing (B') and reacting  
 CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded  
 CC via a chemical group) for transporting (A) across biological membranes.  
 CC The products of the invention have cytostatic, virucide, vasotropic,  
 CC dermatological, antipsoriatic and antiasthmatic activity and can be used  
 CC for gene therapy. Conjugation of (A) with (B) is useful for transporting  
 CC (A) across biological membranes or into eukaryotic or prokaryotic cells  
 CC (specifically bacterial, yeast or mammalian cells, including human cells,  
 CC particularly tumor cells). Medicaments, diagnostic agents and test kits  
 CC containing (I) are also claimed. Typically (I) are antisense  
 CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for  
 CC treating viral infections or diseases associated with integrins or  
 CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);  
 CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ  
 CC hybridization. Conjugation with (B) markedly improves the cellular uptake  
 CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,  
 CC in which case the conjugates (I) are fluorescently labeled, allowing  
 CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)  
 CC is superior to that obtained using other conjugated groups related to  
 CC (ii); e.g. oligonucleotides conjugated with fluorescein diacetate (within  
 CC the scope of (B)) have superior uptake to corresponding fluorescein  
 CC conjugates.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 390  
 AAF28351  
 ID AAF28351 standard; DNA; 20 BP.  
 AC AAF28351;  
 DT 02-APR-2001 (first entry)  
 DE DNA oligomer #1.  
 KW Deoxynucleic S-Methylthiouracil; DNmt; antisense therapy;  
 KW cardiovascular disease; inflammatory disease; neurocellular disease;  
 KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;  
 KW influenza; herpes; infection; ss.

OS Unidentified.  
 EN US6169176-B1.  
 XX 02-JAN-2001.  
 XX 28-SEP-1999; 99US-0407675.  
 XX 02-JUL-1998; 99US-0091481.  
 XX 11-DEC-1998; 99US-0111800.  
 XX 02-JUL-1999; 99US-0347443.  
 XX (REGC) UNIV CALIFORNIA.  
 XX Dev AP, Bruce TC;  
 XX WPI; 2001-122276/13.  
 XX Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in

PT antisense therapy, by synthesizing oligonucleotides comprising backbone  
 of alkyl or alkoxy thiourea linkages in solution or on solid phase -  
 XX Example 7; Fig 16; 48pp; English.

XX The present sequence was used to demonstrate the ability of deoxynucleic  
 S-Methylthiouracil (DNmt) compounds to form triplexes with DNA oligomers. An  
 increase in the C content of the oligos resulted in a large decrease in  
 binding. This experiment was performed as an example of a method for  
 preparing oligonucleotides comprising a backbone of alkyl or alkoxy  
 thiourea linkages. The method is useful for preparing oligonucleotides  
 for use in antisense or antigenic therapy, to inhibit production of  
 proteins associated with genetic diseases, cardiovascular, inflammatory  
 and neurocellular diseases, and for antiviral therapy, e.g. to treat  
 human immunodeficiency virus, human-cytomegalovirus, influenza and  
 herpes infections. The compounds are also useful as diagnostic reagents  
 to detect the presence or absence of the target DNA or RNA sequences to  
 which they specifically bind and by antagonizing the normal biological  
 activity of a target protein, they can be used in the manipulation of  
 tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue  
 cultures. The method provides an efficient and rapid solid-phase method  
 for the synthesis of thiourea and S-methylthiouracil.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 391  
 AAF28481  
 ID AAF28481 standard; DNA; 20 BP.  
 AC AAF28481;  
 DT 03-APR-2001 (first entry)  
 DE Random oligonucleotide, SEQ ID NO: 53.  
 KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
 KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;  
 KW cell line authentication; gene therapy; ss.

OS Synthetic.

FN WO200100876-A1.

PD 04-JAN-2001.

PF 26-JUN-2000; 2000WO-US17507.

PR 25-JUN-1999; 99US-0344667.

PR 26-APR-2000; 2000US-0200161.

PA (MIRK/) MIRKIN C A.

PA (LETS/) LETSINGER R L.

PA (MUCI/) MUCIC R C.

PA (STOR/) STORHOFF J J.

PA (ELGH/) ELGHANIAN R.

PA (TATO/) TATON T A.

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX WPI; 2001-061976/07.

XX Detecting nucleic acid, useful for e.g. diagnosis of diseases,  
 PT forensics and DNA sequencing, comprises observing detectable change

PT brought about by hybridization of nucleic acid with substrate or  
PT particle bound oligonucleotides -

PS Disclosure; Page 199; 205pp; English.

XX The present sequence is an oligonucleotide used in a method for detecting  
CC a nucleic acid having at least 2 portions. The method comprises  
CC hybridizing the nucleic acid with oligonucleotides, such as the present  
CC sequence, attached to a substrate and/or particle and detecting a change  
CC in colour, conductivity or optical density. The method is useful for the  
CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,  
CC for paternity testing, for cell line authentication and for monitoring  
CC gene therapy. Detecting nucleic acids based upon observing a colour  
CC change is cheap, fast, simple, and does not require specialised or  
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain  
CC stable for at least 6 months. A single base mismatch and as little as 20  
CC femtomoles (fm) of target can be detected using the conjugates.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 392

AAC87230/C

ID AAC87230 standard; DNA; 20 BP.

AC AAC87230;

DT 09-MAR-2001 (first entry)

DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.

XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW immunostimulatory DNA-binding protein; nucleolin; hRNP D; AUF1;  
KW hRNP A1; lupus La protein; functional modifier identification;  
KW agonist; antagonist; mimic; inhibitor; drug screening;  
KW cellular target identification; oligonucleotide optimisation;  
KW immunotherapy; ss.

XX Synthetic.

XX WO200067023-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11697.

XX 29-APR-1999; 99US-0131830.

XX 03-MAR-2000; 2000US-0186845.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

XX WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory  
PT DNA functional modifiers, immunostimulatory DNA binding competitors and  
PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -

XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded  
CC DNA-binding protein in screening assays to identify compounds which bind  
CC to it and thereby act as functional modifiers of immunostimulatory

CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.

CC Immunostimulatory DNA-binding proteins can also be used in  
CC screening methods to identify immunostimulatory DNA binding competitors,  
CC and to optimize an immunostimulatory ODN for immune stimulation.

CC Isolated complexes of an immunostimulatory DNA-binding protein bound to  
CC an immunostimulatory ODN can additionally be used to screen a panel of  
CC candidate target molecules to identify the cellular target molecules of  
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins

CC used in the methods of the invention are the RNA-binding proteins  
CC nucleolin, hRNP D, AUF1, hRNP A1 and lupus La protein. The screening  
CC methods are useful for identifying a compound that inhibits interaction  
CC between immunostimulatory DNA and an immunostimulatory DNA-binding

CC protein and for identifying agonists useful in immunotherapy. The  
CC complex is useful in screening for immunostimulatory DNA cellular target  
CC molecules. The candidate immunostimulatory ODN competitors allow the

CC investigation of structure/activity relationships of immunostimulatory  
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
CC represents an oligonucleotide used in an exemplification of the

CC invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 393

AAC87238/C

ID AAC87238 standard; DNA; 20 BP.

XX AAC87238;

XX 09-MAR-2001 (first entry)

DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.

XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW immunostimulatory DNA-binding protein; nucleolin; hRNP D; AUF1;  
KW hRNP A1; lupus La protein; functional modifier identification;  
KW agonist; antagonist; mimic; inhibitor; drug screening;  
KW cellular target identification; oligonucleotide optimisation;  
KW immunotherapy; ss.

XX Synthetic.

XX WO200067023-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11697.

XX 29-APR-1999; 99US-0131830.

XX 03-MAR-2000; 2000US-0186845.

XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Noll BO, Schetter C, Krieg AM;

XX WPI; 2001-016002/02.

XX Immunostimulatory DNA binding proteins to identify immunostimulatory  
PT DNA functional modifiers, immunostimulatory DNA binding competitors and  
PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -  
XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded  
 CC DNA-binding protein in screening assays to identify compounds which bind  
 CC to it and thereby act as functional modifiers of immunostimulatory  
 CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.  
 CC Immunostimulatory DNA-binding proteins can also be used in  
 CC screening methods to identify immunostimulatory DNA binding competitors,  
 CC and to optimize an immunostimulatory ODN for immune stimulation.  
 CC Isolated complexes of an immunostimulatory DNA-binding protein bound to  
 CC an immunostimulatory ODN can additionally be used to screen a panel of  
 CC candidate target molecules to identify the cellular target molecules of  
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins  
 CC used in the methods of the invention are the RNA-binding proteins  
 CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening  
 CC methods are useful for identifying a compound that inhibits interaction  
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding  
 CC protein and for identifying agonists useful in immunotherapy. The  
 CC complex is useful in screening for immunostimulatory DNA cellular target  
 CC molecules. The candidate immunostimulatory ODN competitors allow the  
 CC investigation of structure/activity relationships of immunostimulatory  
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
 CC represents an oligonucleotide used in an exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAA 4

## RESULT 394

AAAC87241/C  
 ID AAC87241 standard; DNA; 20 BP.  
 AC AAC87241;  
 XX  
 XX 09-MAR-2001 (first entry)  
 DT Poly T oligonucleotide, SEQ ID NO:20.  
 XX  
 XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
 KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;  
 KW hnRNP A1; lupus La protein; functional modifier identification;  
 KW agonist; antagonist; mimic; inhibitor; drug screening;  
 KW cellular target identification; oligonucleotide optimisation;  
 KW immunotherapy; ss.  
 KW  
 OS Synthetic.  
 XX  
 XX WO200067023-A1.  
 EN  
 XX  
 XX 09-NOV-2000.  
 PD  
 XX  
 XX 28-APR-2000; 2000WO-US11697.  
 PF  
 XX  
 XX 29-APR-1999; 99US-0131830.  
 PR  
 XX 03-MAR-2000; 2000US-0186845.  
 XX  
 XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 XX  
 XX Noll BO, Schetter C, Krieg AM;  
 PI  
 XX WPI; 2001-016002/02.  
 DR  
 XX Immunostimulatory DNA binding proteins to identify immunostimulatory  
 PI

PT DNA functional modifiers, immunostimulatory DNA binding competitors and  
 PT to optimize immunostimulatory oligodeoxynucleotides for stimulation -  
 XX  
 XX Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded  
 CC DNA-binding protein in screening assays to identify compounds which bind  
 CC to it and thereby act as functional modifiers of immunostimulatory  
 CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
 CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
 CC DNA mimics, and immunostimulatory DNA agonists and antagonists.  
 CC Immunostimulatory DNA-binding proteins can also be used in  
 CC screening methods to identify immunostimulatory DNA binding competitors,  
 CC and to optimize an immunostimulatory ODN for immune stimulation.  
 CC Isolated complexes of an immunostimulatory DNA-binding protein bound to  
 CC an immunostimulatory ODN can additionally be used to screen a panel of  
 CC candidate target molecules to identify the cellular target molecules of  
 CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins  
 CC used in the methods of the invention are the RNA-binding proteins  
 CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening  
 CC methods are useful for identifying a compound that inhibits interaction  
 CC between immunostimulatory DNA and an immunostimulatory DNA-binding  
 CC protein and for identifying agonists useful in immunotherapy. The  
 CC complex is useful in screening for immunostimulatory DNA cellular target  
 CC molecules. The candidate immunostimulatory ODN competitors allow the  
 CC investigation of structure/activity relationships of immunostimulatory  
 CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
 CC represents an oligonucleotide used in an exemplification of the  
 CC invention.  
 XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAA 4

## RESULT 395

AAF89091/C  
 ID AAF89091 standard; DNA; 20 BP.  
 XX  
 XX AAF89091;  
 XX  
 XX 13-JUL-2001 (first entry)  
 DT Mammalian stem cell factor PCR primer SEQ ID NO: 32.  
 XX  
 XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
 KW severe combined immunodeficiency; PCR primer; ss.  
 KW  
 OS Mammalia.  
 XX  
 XX US6207802-B1.  
 EN  
 XX  
 XX 27-MAR-2001.  
 PD  
 XX  
 XX 09-NOV-1994; 94US-0336728.  
 PF  
 XX  
 XX 25-NOV-1992; 92US-0982255.  
 PR  
 XX 16-OCT-1989; 89US-0422383.  
 PR  
 XX 11-JUN-1990; 90US-0537198.  
 PR  
 XX 24-AUG-1990; 90US-0573616.  
 PR  
 XX 01-OCT-1990; 90US-0589701.  
 XX  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI

XX DR WPI; 2001-353108/37.

XX PT Novel isolated non-human mammalian stem cell factor polypeptide

XX PT stimulating growth of early haematopoietic progenitor cells, useful for

XX PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,

XX PT sarcoidosis -

XX PS Example 3; Fig 12C; 209pp; English.

XX CC The present invention provides the protein and coding sequences of

XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the

XX CC growth of early haematopoietic progenitor cells, neural stem cells and

XX CC primordial germ stem cells. The sequences are useful in the treatment of

XX CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal

XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological

XX CC and intestinal damage, infertility, AIDS and severe combined

XX CC immunodeficiency (SCID). The present sequence is primer used to amplify

XX CC an SCF in the exemplification of the invention.

XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e-02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 396

AAF89093/c

ID AAF89093 standard; DNA; 20 BP.

XX AC AAF89093;

XX DT 13-JUL-2001 (first entry)

XX DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.

XX KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;

XX KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;

XX KW neurological damage; intestinal damage; infertility; AIDS; SCID;

XX KW severe combined immunodeficiency; PCR primer; ss.

XX OS Mammalia.

XX PN US6207802-B1.

XX PD 27-MAR-2001.

XX PF 09-NOV-1994; 94US-0336728.

XX PR 25-NOV-1992; 92US-0982255.

XX PR 16-OCT-1989; 89US-0422383.

XX PR 11-JUN-1990; 90US-0537198.

XX PR 24-AUG-1990; 90US-0573616.

XX PR 01-OCT-1990; 90US-0589701.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX PT WPI; 2001-353108/37.

XX PT Novel isolated non-human mammalian stem cell factor polypeptide

XX PT stimulating growth of early haematopoietic progenitor cells, useful for

XX PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,

XX PT sarcoidosis -

XX PS Example 3; Fig 12C; 209pp; English.

XX CC The present invention provides the protein and coding sequences of

XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the

XX CC growth of early haematopoietic progenitor cells, neural stem cells and

XX CC primordial germ stem cells. The sequences are useful in the treatment of

XX CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal

XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological

XX CC and intestinal damage, infertility, AIDS and severe combined

XX CC immunodeficiency (SCID). The present sequence is primer used to amplify

XX CC an SCF in the exemplification of the invention.

XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e-02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 397

AA016997/c

ID AAD16997 standard; DNA; 20 BP.

XX AC AAD16997;

XX DT 29-NOV-2001 (first entry)

XX DE Capture probe CP5'.

XX KW Scaffold protein; antibody mimic; fibronectin type III domain;

XX KW randomised loop; randomised beta-sheet; diagnostic purpose;

XX KW protein designing; probe; tenth module of human Fn3; 10Fn3;

XX KW fibronectin module of type III; Fn3; ss.

XX OS Unidentified.

XX PN WO200164942-A1.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US06414.

XX PR 29-FEB-2000; 2000US-0515260.

XX PA (PHYL-) PHYLLOS INC.

XX PI Lipovsek D, Wagner RW, Kuimelis RG;

XX PT WPI; 2001-557782/62.

XX PT Fibronectin scaffold protein array for obtaining a protein/compound

XX PT which binds to a compound/protein, comprises a fibronectin type III

XX PT domain having a randomised loop, a randomised beta-sheet or their

XX PT combination -

XX PS Disclosure; Page 41; 67pp; English.

XX CC The present invention relates to an array of proteins (antibody mimics)

XX CC comprising a fibronectin type III domain having a randomised loop, a

XX CC randomised beta-sheet, or their combination, and has the capacity to

XX CC bind to a compound that is not bound by a corresponding naturally-

XX CC occurring fibronectin, immobilised onto a solid support. The antibody

XX CC mimics is useful for detecting a compound preferably a protein, in a

XX CC biological sample. It is also useful to detect one or more different

XX CC analytes simultaneously in a sample. Hence is useful for diagnostic

XX CC purposes. It is also useful for the purpose of designing proteins

XX CC capable of binding to virtually any compound of interest. The present

XX CC sequence is a capture probe used to self-assemble and anchor the tenth

XX CC module of human fibronectin module of type III (Fn3) (10Fn3) which is

XX CC used in an exemplification of the invention.

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 398  
 ABSQ79871/c  
 ID ABQ79871 standard; DNA; 20 BP.  
 AC ABQ79871;  
 XX  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 XX Nucleotide sequence of a PCR primer #1.  
 DE Polymerase chain reaction; thermal cycle; immobilisation;  
 KW genetic engineering; PCR; primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX JP2002191369-A.  
 PN  
 XX  
 XX  
 PD 09-JUL-2002.  
 XX  
 XX 27-DEC-2000; 2000JP-0399573.  
 PF  
 XX  
 XX 27-DEC-2000; 2000JP-0399573.  
 PR  
 XX  
 XX (TOJO ) TOYO KOHAN CO LTD.  
 PA (TAKA/) TAKAHASHI K.  
 XX  
 XX WPI; 2002-630904/68.  
 DR  
 XX  
 XX Carrying out a thermal cycle of polymerase chain reaction (PCR) by  
 PT using a substrate on which a DNA is immobilized used in medical,  
 PT biochemical, molecular biological and gene engineering fields -  
 XX  
 XX Examples; Page 9; 13pp; Japanese.  
 PS  
 XX The invention relates to performing a thermal cycle of PCR by using a  
 CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
 CC method is useful in the medical, biochemical, molecular biological and  
 CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
 CC used in the method of the invention.  
 XX  
 SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 399  
 ABS73848/c  
 ID ABS73848 standard; DNA; 20 BP.  
 AC ABS73848;  
 XX  
 XX  
 DT 05-DEC-2002 (first entry)  
 XX  
 XX SCF universal oligonucleotide 220-3.  
 DE  
 XX Stem cell factor; SCF; blood-forming system; blood cell disorder;  
 KW

KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
 KW disseminated fungus disease; haematopoietic; tuberculostatic;  
 KW antianemic; antifungal; antimalarial; dermatological; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX EP1241258-A2.  
 PN  
 XX  
 XX 18-SEP-2002.  
 PD  
 XX  
 XX 04-OCT-1990; 2002EP-0008587.  
 PF  
 XX  
 XX 16-OCT-1989; 89US-042383.  
 PR  
 XX 11-JUN-1990; 90US-0537198.  
 PR  
 XX 24-AUG-1990; 90US-0573616.  
 PR  
 XX 28-SEP-1990; 90WO-US05548.  
 PR  
 XX 01-OCT-1990; 90US-0589701.  
 PR  
 XX 04-OCT-1990; 90EP-0310899.  
 PR  
 XX 04-OCT-1990; 95EP-0105391.  
 XX  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX  
 XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
 PI  
 XX  
 XX WPI; 2002-684093/74.  
 DR  
 XX  
 XX Production of a human stem cell factor (SCF) polypeptide for treating  
 PT disorders involving blood cells, such as leukaemia, comprises culturing  
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
 PT encoding the human SCF -  
 XX  
 XX Example 3; Fig 12C; 120pp; English.  
 PS  
 XX The present invention relates to novel stem cell factors (SCFs),  
 CC polynucleotide sequences encoding the SCFs, and methods of producing  
 CC them. SCFs are involved in the blood-forming (haematopoietic)  
 CC system in mammals, particularly humans. The method of the invention  
 CC is useful for the production of human SCF. The stem cell factors are  
 CC useful to treat disorders involving blood cells e.g. metastatic  
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
 CC lymphoma, refractory erythroblastic anaemia, miliary tuberculosis,  
 CC disseminated fungus disease, malaria, and vitiligo. The present  
 CC sequence representing a universal oligonucleotide for SCF DNA is  
 CC used in the examples of the present invention.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 400  
 ABS73850/c  
 ID ABS73850 standard; DNA; 20 BP.  
 AC  
 XX  
 XX ABS73850;  
 XX  
 XX  
 DT 05-DEC-2002 (first entry)  
 XX  
 XX SCF universal oligonucleotide 220-11.  
 DE  
 XX  
 XX Stem cell factor; SCF; blood-forming system; blood cell disorder;  
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
 KW disseminated fungus disease; haematopoietic; tuberculostatic;

KW antianaemic; antifungal; antimalarial; dermatological; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN EP1241258-A2.  
 XX  
 XX  
 PD 18-SEP-2002.  
 XX  
 XX  
 PF 04-OCT-1990; 2002EP-0008587.  
 XX  
 XX  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 28-SEP-1990; 90WO-US05548.  
 PR 01-OCT-1990; 90US-0589701.  
 PR 04-OCT-1990; 90EP-0310899.  
 PR 04-OCT-1990; 95EP-0105391.  
 XX  
 XX  
 PA (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
 XX WPI; 2002-684093/74.  
 DR  
 XX  
 XX Production of a human stem cell factor (SCF) polypeptide for treating  
 PT disorders involving blood cells, such as leukaemia, comprises culturing  
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
 PT encoding the human SCF -  
 XX  
 XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),  
 CC polynucleotide sequences encoding the SCFs, and methods of producing  
 CC them. SCFs are involved in the blood-forming (haematopoietic)  
 CC system in mammals, particularly humans. The method of the invention  
 CC is useful for the production of human SCF. The stem cell factors are  
 CC useful to treat disorders involving blood cells e.g. metastatic  
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
 CC lymphoma, refractory erythroidlastic anaemia, myeloid leukaemia,  
 CC disseminated fungus disease, malaria, and vitiligo. The present  
 CC sequence representing a universal oligonucleotide for SCF DNA is  
 CC used in the examples of the present invention.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 401  
 ABS77742/c  
 ID ABS77742 standard; DNA; 20 BP.  
 XX  
 AC ABS77742;  
 XX  
 XX 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #226.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;  
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;  
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;  
 KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation;  
 KW haemophilic joint; angiofibroma; wound granulation;  
 KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

OS Synthetic.  
 XX WO200253141-A2.  
 PN  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX  
 PF 14-DEC-2001; 2001WO-US48458.  
 XX  
 XX  
 PR 14-DEC-2000; 2000US-255534P.  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA  
 XX Bratzler RL;  
 XX  
 XX WPI; 2002-566690/60.  
 DR  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least  
 PT one antiangiogenic nucleic acid molecule to the subject -  
 PT  
 XX  
 XX Claim 2; Page 23; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule.  
 CC Also included is a kit comprising a first container housing the  
 CC antiangiogenic nucleic acids, and instructions for administering them to  
 CC a subject having a condition characterised by unwanted angiogenesis.  
 CC The method is useful for inhibiting angiogenesis associated with solid  
 CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid  
 CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,  
 CC macular degeneration, corneal graft rejection, neovascular glaucoma,  
 CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial  
 CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic  
 CC joints, angiofibroma, wound granulation, intestinal adhesions,  
 CC atherosclerosis, scleroderma and hypertrophic scars. The present  
 CC sequence is an antiangiogenic nucleic acid of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 402  
 ABS78072/c  
 ID ABS78072 standard; DNA; 20 BP.  
 XX  
 AC ABS78072;  
 XX  
 XX 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #556.

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;  
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;  
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;  
 KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation;  
 KW haemophilic joint; angiofibroma; wound granulation;  
 KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX Synthetic.

OS WO200253141-A2.

PN 11-JUL-2002.

PD 14-DEC-2001; 2001WO-US48458.

```

XX PR 14-DEC-2000; 2000US-255534P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PI Bratzler RL;
XX XX WPI; 2002-566890/60.
XX PT Inhibiting angiogenesis in a subject, involves administering at least
XX PT one antiangiogenic nucleic acid molecule to the subject -
XX PS Claim 2; Page 29; 276pp; English.
XX CC The invention relates to inhibiting angiogenesis in a subject, comprising
XX CC administering at least one antiangiogenic nucleic acid molecule.
XX CC Also included is a kit comprising a first container housing the
XX CC antiangiogenic nucleic acids, and instructions for administering them to
XX CC a subject having a condition characterised by unwanted angiogenesis.
XX CC The method is useful for inhibiting angiogenesis associated with solid
XX CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
XX CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
XX CC macular degeneration, corneal graft rejection, neovascular glaucoma,
XX CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial
XX CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic
XX CC joints, angiofibroma, wound granulation, intestinal adhesions,
XX CC atherosclerosis, scleroderma and hypertrophic scars. The present
XX CC sequence is an antiangiogenic nucleic acid of the invention.
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;
    Query Match 1.5%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred.No. 2.1e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 11111111111111111111
   20 AAAAAAAAAAAAAAAAAA 4

RESULT 403
ABS78076
ID ABS78076: standard; DNA; 20 BP.
AC
XX AC ABS78076;
XX DT 13-DEC-2002 (first entry)
XX DE
XX DE Angiogenesis inhibitory oligonucleotide #560.
XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
XX KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
XX KW macular degeneration; corneal graft rejection; neovascular glaucoma;
XX KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;
XX KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
XX KW haemophilic joint; angiofibroma; wound granulation;
XX KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX OS Synthetic.
XX OS WO200253141-A2.
XX PN 11-JUL-2002.
XX PD
XX XX 14-DEC-2001; 2001WO-US48458.
XX XX 14-DEC-2000; 2000US-255534P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PI Bratzler RL;
XX XX

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nanoparticles to allow hybridization, and observing detectable change

Example 18; Page 437; 442pp; English.

The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. (I) and (II) are useful for fabrication, and for separating a selected nucleic acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (especially polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1084 AAAAAAAAAAAAAAAAAA 1100
Db      |||||
        1 AAAAAAAAAAAAAAAAAA 17

RESULT 405
ABS64688
ID ABS64688 standard; DNA; 20 BP.
XX AC ABS64688;
XX DT 15-NOV-2002 (first entry)
XX Nucleic acid detection method associated polynucleotide #70.
XX DE XX
XX DE XX
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX KW nanoparticle; viral RNA detection; bacterial DNA detection;
XX KW fungal DNA detection; nanoprobe conjugate; ss.
XX OS Synthetic.
XX WO200246472-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46418.
XX PP 08-DEC-2000; 2000US-254392P.
XX PR 08-DEC-2000; 2000US-254418P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 11-DEC-2000; 2000US-255236P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR 09-APR-2001; 2001US-282640P.
XX PR 10-AUG-2001; 2001US-0927777.
XX (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PPI Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-608256/65.

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The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. (II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. (I) and (II) are useful for fabrication, and for separating a selected nucleic acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (especially polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

```

Query Match      1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1084 AAAAAAAAAAAAAAAAAA 1100
DB      1 AAAAAAAAAAAAAAAAAA 17
|||||
|||||

RESULT 406
ID AEN87103/c
ID AEN87103 standard; DNA; 20 BP.
XX AC AEN87103;
XX AC
DT 30-JUL-2002 (first entry)
XX XX
DE DE
XX XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX Synthetic.
XX WO200232925-A2.
XX PN
XX PD 25-APR-2002.
XX XX
XX PF 16-OCT-2001; 2001WO-US32233.
XX XX
XX PR 16-OCT-2000; 2000US-0688566.
XX XX
XX PA (PHYL-) PHYL0S INC.
XX XX
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX XX
XX PPT New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds
XX for designing proteins with specific properties, e.g. for binding any
XX antigen of interest -
XX

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New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest -

Thu Jan 8 16:51:41 2004

PS Disclosure; Page 58; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that  
 CC is not bound as tightly by the reference protein. The non-antibody  
 CC protein is useful as scaffolds for selecting or designing a protein  
 CC framework with specific and favourable properties, e.g. for binding any  
 CC antigen of interest, or for destroying or inactivating antibody  
 CC molecules. The non-antibody protein is also useful in all areas where  
 CC antibodies are used, e.g. research, therapeutic or diagnostic fields,  
 CC and for screening novel binding proteins useful in the above-mentioned  
 CC fields. The present proteins have thermodynamic properties superior to  
 CC those of natural antibodies, and can be evolved rapidly in vitro. The  
 CC present proteins or antibody mimics exhibit improved biophysical  
 CC properties, such as stability under reducing conditions and solubility  
 CC at high concentrations. In addition, these molecules are readily  
 CC expressed and folded in prokaryotic systems (e.g. Escherichia coli), in  
 CC eukaryotic systems (e.g. yeast), or in in vitro translation systems  
 CC (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins  
 CC are extremely amenable to affinity maturation techniques involving  
 CC multiple cycles of selection, e.g. in vitro selection using RNA-protein  
 CC fusion technology, phage display or yeast display systems. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

SQ Query Match 1.5%; Score 17; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-02; Indels 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 407

ID AAD35464/c

XX AAD35464 standard; DNA; 20 BP.

AC AAD35464;

XX 25-JUL-2002 (first entry)

XX Rat SCF 5' cdna amplifying PCR primer, 220-3.

XX Rat; stem cell factor; SCF protein; leucopaemia; thrombocytopaenia;  
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;  
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;  
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;  
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;  
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;  
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;  
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;  
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;  
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;  
 KW primer; ss.

XX Rattus sp.

OS US2002018763-A1.

PN 14-FEB-2002.

XX 12-JAN-1998; 98US-0005243.

XX 24-MAY-1995; 95US-0449653.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zeebo KM, Bosseelman RA, Suggs SV, Martin FH;

XX WPI; 2002-350789/38.

XX Novel non-naturally-occurring stem cell factor polypeptide, useful for  
 CC treating leucopenia, thrombocytopenia, anemia and for enhancing  
 CC engraftment of bone marrow during transplantation in a mammal -

XX Example 3; Fig 12C; 217pp; English.

XX The present invention relates to novel non-naturally-occurring stem cell  
 CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
 CC duplicative of that of naturally-occurring SCF to allow possession of  
 CC haematopoietic biological activity of naturally occurring SCF. Sequences  
 CC of the invention are useful for treating leucopaemia, thrombocytopaenia,  
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
 CC engraftment of bone marrow during transplantation in mammals and chemical  
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
 CC are also useful for treating acquired immune deficiency in a human, nerve  
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
 CC damage in a mammal. SCF sequences are useful for preparing biologically  
 CC active polymer polypeptide adducts, for enhancing transfection of early  
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
 CC a mammal. They are useful for treating myelofibrosis, myelocytosis,  
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
 CC splenic pancytopenia, disseminated fungus disease, malaria, military  
 CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin  
 CC B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
 CC and vitiligo. The present sequence is a PCR primer which is used for  
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
 CC exemplification of the invention.

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-02; Indels 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 408

AAD35466/c

ID AAD35466 standard; DNA; 20 BP.

XX AAD35466;

XX 25-JUL-2002 (first entry)

XX Rat SCF 5' cdna amplifying PCR primer, 220-11.

XX Rat; stem cell factor; SCF protein; leucopaemia; thrombocytopaenia;  
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;  
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;  
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;  
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;  
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;  
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;  
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;  
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;  
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;  
 KW primer; ss.

XX Rattus sp.

Thu Jan 8 16:51:41 2004

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XX OS Synthetic.
XX PN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PA 08-DEC-2000; 2000US-254392P.
XX PA 11-DEC-2000; 2000US-255235P.
XX PA 12-JAN-2001; 2001US-0760500.
XX PA 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 18; Page 410; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analyses such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABR64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 409
ABK65035
ID ABK65035 standard; DNA; 20 BP.
XX AC ABK65035;
XX XX 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #55.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX NW nucleic acid detection; ss.

Novel non-naturally-occurring stem cell factor polypeptide, useful for
treating leucopenia, thrombocytopenia, anemia and for enhancing
engraftment of bone marrow during transplantation in a mammal -
Example 3; Fig 12C; 217pp; English.

The present invention relates to novel non-naturally-occurring stem cell
factor (SCF) polypeptides having an amino acid sequence sufficiently
duplicative of that of naturally-occurring SCF to allow possession of
haematopoietic biological activity of naturally occurring SCF. Sequences
of the invention are useful for treating leucopenia, thrombocytopenia,
anemia and for enhancing bone marrow recovery in treatment of radiation,
engraftment of bone marrow during transplantation in mammals and chemical
or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
are also useful for treating acquired immune deficiency in a human, nerve
damage, neoplasia, infertility, myeloproliferative disorder, intestinal
damage in a mammal. SCF sequences are useful for preparing biologically
active polymer polypeptide adjuvant, for enhancing transfection of early
haematopoietic progenitor cells with a gene, and transfer of a gene into
a mammal. They are useful for treating myelofibrosis, myeloclerosis,
osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
splenic pancytopenia disseminated fungus disease, malaria, military
tuberculosis, fulminating septicemia, pyridoxine deficiency, vitamin
B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
and vitiligo. The present sequence is a PCR primer which is used for
amplifying the 5' end of rat SCF cDNA. This sequence is used in the
exemplification of the invention.

Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 410
ABK65050
ID ABK65050 standard; DNA; 20 BP.
XX AC ABK65050;
XX XX 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #70.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX NW nucleic acid detection; ss.

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```

XX OS Synthetic.
XX PN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PA 08-DEC-2000; 2000US-254392P.
XX PA 11-DEC-2000; 2000US-255235P.
XX PA 12-JAN-2001; 2001US-0760500.
XX PA 28-MAR-2001; 2001US-0820279.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-258024/30.
XX PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 18; Page 410; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analyses such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABR64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 410
ABK65050
ID ABK65050 standard; DNA; 20 BP.
XX AC ABK65050;
XX XX 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #70.
XX KW Nanoparticle-oligonucleotide; nanofabrication;

```

KW nucleic acid detection; ss.

XX Synthetic.

OS WO200218643-A2.

FN 07-MAR-2002.

XX 10-AUG-2001; 2001WO-US25237.

XX 11-AUG-2000; 2000US-224631P.

PR 08-DEC-2000; 2000US-254392P.

PR 11-DEC-2000; 2000US-255235P.

PR 12-JAN-2001; 2001US-0760500.

PR 28-MAR-2001; 2001US-0820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Garimella V, Li Z, Park S;

XX WPI; 2002-258024/30.

XX Detecting nucleic acid, useful for diagnosis of genetic, viral or

PT bacterial disease, comprises hybridising nanoparticles with attached

PT oligonucleotides to nucleic acid and detecting change brought about by

PT hybridisation -

XX Example 24; Figure 44; 412pp; English.

XX The invention relates to a method of detecting a nucleic acid (NA) having

CC at least 2 portions comprising: (a) providing nanoparticles (NP) with

CC attached oligonucleotides (OGN), where OGN has a sequence complementary

CC to the sequence of NA; (b) contacting NA and NP under conditions

CC effective to allow hybridisation of OGN with NA; and (c) observing a

CC detectable change brought about by hybridisation of OGN with NA.

CC The method is useful for detecting a nucleic acid, separating a

CC selected nucleic acid from others and methods of nanofabrication.

CC Detecting analytes such as nucleic acids and proteins are useful for the

CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates

CC that use cyclic disulphide linkers improve the sensitivity of diagnostic

CC assays. In particular assays using OGN-NP conjugates prepared using

CC linkers comprising a steroid residue attached to a cyclic disulphide have

CC been found to be approximately 10 times more sensitive than assays

CC employing conjugates prepared using alkanethiols or acyclic disulphides

CC as the linker. The OGN-NP conjugates are stable allowing them to be used

CC directly in PCR solutions. Therefore conjugates added as probes to a DNA

CC target to be PCR amplified can be carried through the 30 or 40 heating

CC cooling cycles of the PCR and are still able to detect the amplicons

CC without opening the tubes and causing contamination. ABK64981-ABK65055

CC represent nanoparticle-oligonucleotides of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 411

ABL54775/c

ID ABL54775 standard; DNA; 20 BP.

XX ABL54775;

XX 10-JUN-2002 (first entry)

XX CD14 receptor PCR primer SEQ ID NO 9.

XX

KW Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;

XX single-nucleotide polymorphism; PCR; primer; ss.

OS Synthetic.

XX JP2002034599-A.

XX 05-FEB-2002.

XX 26-JUL-2000; 2000JP-0225354.

XX 26-JUL-2000; 2000JP-0225354.

XX (TOYM) TOYOCO KK.

XX WPI; 2002-275727/32.

XX Detecting 1 base polymorphism on a sequence of a chromosome or it's

PT fragment -

XX Example 2; Page 10; 10pp; Japanese.

XX The invention relates to a method for detecting 1 base polymorphism on

CC the sequence of a chromosome or its fragment in which a sample nucleic

CC acid is reacted with a reaction liquor containing a nucleic acid primer

CC having a base adjacent to the polymorphic base at its 3'-end, one

CC dideoxynucleotide corresponding to a polymorphic base having a

CC distinguishable feature or its mixture, DNA polymerase and a composition

CC required for its activity expression to detect the presence of taking

CC dideoxynucleotide in the nucleic acid primer and to detect the type of

CC the base to be specified. The method is used for detecting 1 base

CC polymorphism on the sequence of a chromosome or its fragment. The present

CC sequence is that of a PCR primer, useful in examples of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 412

AAL45122/c

ID AAL45122 standard; DNA; 20 BP.

XX AAL45122;

XX 24-MAY-2002 (first entry)

XX Oligonucleotide synthesis method related DNA #1.

XX Oligonucleotide synthesis; polynucleotide array; protecting group;

XX oxidation; ss.

XX Synthetic.

XX EP1176151-A1.

XX 30-JAN-2002.

XX 27-JUL-2001; 2001EP-0118360.

XX 28-JUL-2000; 2000US-0627249.

XX (AGIL-) AGILENT TECHNOLOGIES INC.

XX Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;

XX WPI; 2002-156732/21.

XX Synthesis of polynucleotide useful during fabrication of an array  
PT involves coupling nucleoside phosphoramidite and a solid-supported  
PT nucleoside and treating the product with an oxidation/deprotection  
PT composition -  
XX  
PS Example 1; Page 15; 36pp; English.  
XX  
CC The present invention relates to a method for the synthesis of a  
CC polynucleotide which involves coupling a second nucleoside to a first  
CC nucleoside through a phosphate linkage, where the second nucleoside has a  
CC non-carbonate protecting group protecting a hydroxyl, and exposing the  
CC product to a composition which concurrently oxidizes the phosphate formed  
CC to a phosphate and deprotects the protected hydroxyl of the second  
CC nucleoside. The method is useful for synthesizing the polynucleotides,  
CC for carrying out either 3', to 5', or 5', to 3' synthesis and for  
CC fabricating an addressable array of polynucleotides on a substrate. The  
CC present sequence is an oligonucleotide produced to demonstrate the method  
CC of the invention.  
XX  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAA 1100  
DB 20 AAAAAAAAAAAAAAAA 4

RESULT 413  
ABL36232  
ID ABL36232 standard; DNA; 20 BP.  
XX  
AC ABL36232;  
XX  
XX 08-APR-2002 (first entry)  
XX  
DE M tuberculosis rRNA probe SEQ ID NO: 83.  
XX  
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;  
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;  
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;  
KW Th2 immune response; immunomodulatory; probe; ss.  
XX  
OS Mycobacterium tuberculosis.  
XX  
XX USG328978-B1.  
XX  
PD 11-DEC-2001.  
XX  
XX 02-JUN-1999; 99US-0324542.  
XX  
XX 23-DEC-1997; 97US-0997080.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
XX Watson JD, Tan PLJ, Prestidge R;  
XX  
XX WPI; 2002-138361/18.  
XX  
XX Inhibiting skin inflammation associated with skin disorder e.g.  
PT psoriasis, by administering composition comprising delipidated and  
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae  
PT culture filtrate -  
XX  
XX Example 5; Column 99-100; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation  
XX associated with a skin disorder selected from psoriasis, atopic  
XX dermatitis and allergic contact dermatitis, which involves administering  
XX a composition containing delipidated and deglycolipidated Mycobacterium

CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be  
CC treated may also include alopecia areata, and skin cancers such as basal  
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition  
CC acts by inhibiting the Th2 immune response. The present sequence is a  
CC probe described in the exemplification of the invention.  
XX  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAA 17

RESULT 414  
ABL38648  
ID ABL38648 standard; DNA; 20 BP.  
XX  
AC ABL38648;  
XX  
XX 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 2.  
XX  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
OS Synthetic.  
XX  
XX WO200197843-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US20154.  
XX  
XX 22-JUN-2000; 2000US-213346P.  
XX  
XX (IOWA) UNIV IOWA RES FOUND.  
XX  
XX Weiner G, Hartmann G;  
XX  
XX WPI; 2002-154611/20.  
XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer -  
XX  
PS Disclosure; Page 95; 312pp; English.  
XX  
CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,  
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in  
CC the exemplification of the invention.  
XX

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAA 17

RESULT 414  
ABL38648  
ID ABL38648 standard; DNA; 20 BP.  
XX  
AC ABL38648;  
XX  
XX 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 2.  
XX  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
OS Synthetic.  
XX  
XX WO200197843-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US20154.  
XX  
XX 22-JUN-2000; 2000US-213346P.  
XX  
XX (IOWA) UNIV IOWA RES FOUND.  
XX  
XX Weiner G, Hartmann G;  
XX  
XX WPI; 2002-154611/20.  
XX

XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
XX administering immunostimulatory nucleic acids that induce expression of  
XX cell surface antigens and antibodies to a subject having or at risk of  
XX developing cancer -  
XX  
PS Disclosure; Page 95; 312pp; English.  
XX  
CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,  
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in  
CC the exemplification of the invention.  
XX

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAA 17

```
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 415
ABL39402/c
ID ABL39402 standard; DNA; 20 BP.
XX
AC ABL39402;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 838.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 417
ABX92177
ID ABX92177 standard; DNA; 20 BP.
XX
AC ABX92177;
XX
DT 12-MAY-2003 (first entry)
XX
DE Nanoparticle-associated oligonucleotide SEQ ID 55.
XX
```

KW Nonparticle; nucleic acid detection; hybridisation; diagnosis; KW  
 KW sequencing; viral infection; human immunodeficiency virus; HIV; KW  
 KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus; KW  
 KW bacterial infection; sexually transmitted disease; inherited disorder; KW  
 KW forensic; paternity testing; cell line authentication; gene therapy; ss. KW  
 OS Synthetic. XX  
 XX US2002155458-A1. XX  
 XX 24-OCT-2002. XX  
 XX 28-SEP-2001; 2001US-0967409. XX  
 XX 29-JUL-1996; 96US-031809P. XX  
 XX 26-APR-2000; 2000US-200161P. XX  
 XX 26-JUN-2000; 2000US-0603830. XX  
 XX 21-JUL-1997; 97WO-US12783. XX  
 XX 29-JAN-1999; 99US-0240755. XX  
 XX 25-JUN-1999; 99US-0344667. XX  
 XX (NANO-) NANOSPHERE INC. XX  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R; XX  
 XX Taton TA; XX  
 XX WPI; 2003-182627/18. XX  
 XX Detecting nucleic acids having at least two portions involves use of XX  
 XX nanoparticles which have oligonucleotides attached to them that are XX  
 XX complementary to portions of the nucleic acid sequence - XX  
 XX Disclosure; Page 59; 130pp; English. XX  
 XX This invention describes a novel method of detecting nucleic acid having XX  
 XX at least two portions. The method involves providing nanoparticles XX  
 XX attached to oligonucleotides, where the oligonucleotide on each XX  
 XX nanoparticle have a sequence complementary to a sequence of at least two XX  
 XX portions of nucleic acid, contacting nucleic acid and nanoparticle to XX  
 XX allow hybridisation of the oligonucleotide on the nanoparticle with two XX  
 XX or more portions of nucleic acid and observing a detectable change XX  
 XX brought about by hybridisation of the oligonucleotide nanoparticle with XX  
 XX nucleic acid. The method is useful for separating a selected nucleic XX  
 XX acid having at least two portions, from other nucleic acids and for XX  
 XX detecting nucleic acids having at least two portions. The method is XX  
 XX useful for detecting any type of nucleic acids which may be used for XX  
 XX diagnosis of disease and in sequencing of nucleic acids. Preferably, the XX  
 XX method is useful for detecting nucleic acids for diagnosis and/or XX  
 XX monitoring of viral infections (human immunodeficiency virus (HIV), XX  
 XX hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus), XX  
 XX bacterial diseases, sexually transmitted diseases, inherited disorders, XX  
 XX in forensics, in DNA sequencing, for paternity testing, for cell line XX  
 XX authentication, and for monitoring gene therapy. The method is useful in XX  
 XX research and analytical laboratories in DNA sequencing, in the field to XX  
 XX detect the presence of specific pathogens. Detecting nucleic acids based XX  
 XX on observing a colour change with the naked eye is cheap, fast, simple XX  
 XX and robust and does not require specialised expensive equipment. XX  
 XX ABX92123-ABX92186 and ABQ77356 represent oligonucleotides used to XX  
 XX illustrate the method of the invention. XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; XX

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAA 17

RESULT 418  
 ABX79181

ID ABX79181 standard; DNA; 20 BP. XX  
 XX ABX79181; XX  
 XX 15-APR-2003 (first entry) XX  
 XX Thio-modified 20dA oligonucleotide. XX  
 XX Nanoparticle; ss; nucleic acid detection; viral disease; probe; XX  
 XX human immunodeficiency virus infection; hepatitis virus infection; XX  
 XX herpes virus infection; cytomegalovirus infection; forensic science; XX  
 XX Epstein-Barr virus infection; bacterial disease; gene therapy; XX  
 XX sexually transmitted disease; inherited disorder; DNA sequencing; XX  
 XX paternity testing; cell line authentication. XX  
 XX Synthetic. XX  
 XX US2002155462-A1. XX  
 XX 24-OCT-2002. XX  
 XX 12-OCT-2001; 2001US-0976577. XX  
 XX 29-JUL-1996; 96US-031809P. XX  
 XX 26-APR-2000; 2000US-200161P. XX  
 XX 26-JUN-2000; 2000US-0603830. XX  
 XX 21-JUL-1997; 97WO-US12783. XX  
 XX 29-JAN-1999; 99US-0240755. XX  
 XX 25-JUN-1999; 99US-0344667. XX  
 XX (NANO-) NANOSPHERE INC. XX  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R; XX  
 XX Taton TA; XX  
 XX WPI; 2003-198491/19. XX  
 XX Detecting nucleic acids having at least 2 portions comprises use of XX  
 XX nanoparticles which have oligonucleotides attached to them that are XX  
 XX complementary to portions of the nucleic acid sequence - XX  
 XX Example 18; Page 44; 130pp; English. XX  
 XX The invention relates to detecting a nucleic acid (NA) having at least XX  
 XX 2 portions, comprises providing a type of nanoparticles (NP) having XX  
 XX attached to oligonucleotides (O) (O) on each NP has a sequence XX  
 XX complementary to sequence of at least 2 portions of NA), contacting NA XX  
 XX and NP to allow hybridisation of (O) on NP with 2 or more portions of NA, XX  
 XX and observing a detectable change brought about by hybridisation of (O) XX  
 XX on NP with NA. The nanoparticle is useful for separating a selected XX  
 XX nucleic acid having at least 2 portions, from other nucleic acids, and XX  
 XX for detecting nucleic acids having at least 2 portions. The method of XX  
 XX using NP is useful for detecting any type of nucleic acids which may be XX  
 XX used for diagnosis of disease and in sequencing of nucleic acids. XX  
 XX Preferably, the method is useful for detecting nucleic acids for XX  
 XX diagnosis and/or monitoring of viral diseases (human immunodeficiency XX  
 XX virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr XX  
 XX virus), bacterial diseases, sexually transmitted diseases, inherited XX  
 XX disorders, in forensics, in DNA sequencing, for paternity testing, for XX  
 XX cell line authentication and for monitoring gene therapy. The method is XX  
 XX useful in research and analytical laboratories in DNA sequencing and in XX  
 XX the field to detect the presence of specific pathogens. Detecting nucleic XX  
 XX acids based on observing a colour change with the naked eye is cheap, XX  
 XX fast, simple and robust, and do not require specialised expensive XX  
 XX equipment. The present sequence is a nanoparticle (e.g. gold XX  
 XX particles) labelled probe used to demonstrate the method of the XX  
 XX invention. XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 U; 0 other; XX

Query Match 1.5%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1.5%; Score 17; DB 1; Length 20;



QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 20 AAAAAAAAAAAAAAAAAA 4

RESULT 421  
 AAQ90391  
 ID AAQ90391 standard; DNA; 21 BP.  
 XX AC AAQ90391;  
 XX 08-JAN-1996 (first entry)  
 XX DT  
 XX DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).  
 XX KW CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;  
 XX KW SAED; hybridisation; ss.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT misc\_feature 21  
 XX FT /tag= a  
 XX FT /note= "3' ribonucleoside terminal"  
 XX PN W09512808-A1.  
 XX PD 11-MAY-1995.  
 XX PF 26-OCT-1994; 94WO-US12270.  
 XX PR 01-NOV-1993; 93US-0146504.  
 XX PA (NANO-) NANOGEN INC.  
 XX PI Heller MJ, Tu E;  
 XX DR WPI; 1995-185870/24.  
 XX PT New self-addressable electronic devices - used for multi-step and  
 PT multiplex reactions such as DNA hybridisation(s), clinical  
 PT diagnostics and bio-polymer synthesis  
 XX PS Example 1; Page 40; 86pp; English.  
 XX CC The sequences represented by, AAQ90390-90401 are synthetic DNA probes  
 CC containing 3' ribonucleoside termini. The sequences shown in  
 CC AAQ90402-15 are synthetic DNA probes with 5' amino termini. These  
 CC sequences were specific for the polymorphisms of HLA gene dQa. The  
 CC self-addressable electronic device (SAED) that can be used to carry out  
 CC multi-step and multiplex reactions, such as nucleic acid hybridisations.  
 CC The advantages of this method are that these reactions can be carried out  
 CC with complete and precise electronic control, and that the rate,  
 CC specificity and sensitivity of these reactions are greatly improved at  
 CC micro-locations.  
 XX SQ Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 422  
 AAQ75665/c  
 ID AAQ75665 standard; DNA; 21 BP.  
 XX AC AAQ75665;

XX 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 423  
 AAQ75735/c  
 ID AAQ75735 standard; DNA; 21 BP.  
 XX AC AAQ75735;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS
XX FS
XX Disclosure; Page 8; 11pp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 424
AAQ75736/C
ID AAQ75736 standard; DNA; 21 BP.
AC AAQ75736;
XX
XX 04-AUG-1995 (first entry)
DT
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 426
AAQ75738/C
ID AAQ75738 standard; DNA; 21 BP.
XX
XX AAQ75738;
AC
XX
XX 04-AUG-1995 (first entry)
DT
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
```





CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB |||||||  
17 AAAAAAAAAAAAAAAAAA 1

RESULT 432

AAQ75745/C  
ID AAQ75745 standard; DNA; 21 BP.

XX AC

XX AAQ75745;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.

XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB |||||||  
17 AAAAAAAAAAAAAAAAAA 1

RESULT 433

AAQ75746/C  
ID AAQ75746 standard; DNA; 21 BP.

XX AC

XX AAQ75746;

DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.

XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

XX Query Match 1.5%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB |||||||  
17 AAAAAAAAAAAAAAAAAA 1

RESULT 434

AAQ75747/C  
ID AAQ75747 standard; DNA; 21 BP.

XX AC

XX AAQ75747;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 435  
AAQ75748/c  
ID AAQ75748 standard; DNA; 21 BP.  
XX AC AAQ75748;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
DE Analysis of cDNA and gene expression - by amplification of mRNA  
DE followed by digestion with restriction enzymes  
XX  
KW Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 437  
AAQ75750/c  
ID AAQ75750 standard; DNA; 21 BP.  
XX AC AAQ75750;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 436  
AAQ75749/c  
ID AAQ75749 standard; DNA; 21 BP.  
XX AC AAQ75749;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
DE Analysis of cDNA and gene expression - by amplification of mRNA  
DE followed by digestion with restriction enzymes  
XX  
KW Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 437  
AAQ75750/c  
ID AAQ75750 standard; DNA; 21 BP.  
XX AC AAQ75750;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX

OS Synthetic.  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;  
 XX  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 OS Synthetic.  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 PS Disclosure; Page 9; 11pp; Japanese.  
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 CC A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;  
 XX  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 XX  
 RESULT 439  
 AAQ75788/C  
 ID AAQ75788 standard; DNA; 21 BP.  
 XX  
 AC AAQ75788;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 PS Disclosure; Page 9; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;  
 XX  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 XX

RESULT 440  
AAQ75789/C  
ID AAQ75789 standard; DNA; 21 BP.  
XX  
XX AC AAQ75789;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-0112515.  
XX  
XX PR 16-APR-1993; 93JP-0112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX DR WPI; 1995-018287/03.  
XX  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes  
XX  
XX PS Disclosure; Page 9; 11pp; Japanese.  
XX  
XX CC A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX  
XX SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 441  
AAQ75790/C  
ID AAQ75790 standard; DNA; 21 BP.  
XX  
XX AC AAQ75790;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-0112515.  
XX

XX  
XX PR 16-APR-1993; 93JP-0112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX DR WPI; 1995-018287/03.  
XX  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes  
XX  
XX PS Disclosure; Page 9; 11pp; Japanese.  
XX  
XX CC A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX  
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 442  
AAQ75791/C  
ID AAQ75791 standard; DNA; 21 BP.  
XX  
XX AC AAQ75791;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-0112515.  
XX  
XX PR 16-APR-1993; 93JP-0112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX DR WPI; 1995-018287/03.  
XX  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes  
XX  
XX PS Disclosure; Page 9; 11pp; Japanese.  
XX  
XX CC A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX  
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 443  
AAQ75792/C  
ID AAQ75792 standard; DNA; 21 BP.  
XX  
XX AC AAQ75792;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-0112515.  
XX  
XX PR 16-APR-1993; 93JP-0112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX DR WPI; 1995-018287/03.  
XX  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes  
XX  
XX PS Disclosure; Page 9; 11pp; Japanese.  
XX  
XX CC A method for the analysis of cDNA comprises (a) preparing an  
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX and a plural type of labelled reverse transcription primers  
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
XX template for each reverse transcription primer; (b) digesting each of  
XX the prepared aggregates of the double-stranded cDNAs with restriction  
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX  
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 444  
AAQ75793/C  
ID AAQ75793 standard; DNA; 21 BP.  
XX  
XX AC AAQ75793;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-0112515.  
XX



CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 443  
 AAQ75793/c  
 ID AAQ75793 standard; DNA; 21 BP.  
 AC AAQ75793;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
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 XX Analysis of cDNA and gene expression - by amplification of mRNA  
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 XX Disclosure; Page 9; 11pp; Japanese.  
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 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 444  
 AAQ75794/c  
 ID AAQ75794 standard; DNA; 21 BP.  
 AC AAQ75794;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
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 PA WPI; 1995-018287/03.  
 DR  
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 DE Reverse transcription primer used in cDNA analysis technique.  
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 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
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 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
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 XX Disclosure; Page 9; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 445  
 AAQ75795/c  
 ID AAQ75795 standard; DNA; 21 BP.  
 AC AAQ75795;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR  
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS  
XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 446

AAQ75796/c  
ID AAQ75796 standard; DNA; 21 BP.

XX AC AAQ75796;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes

XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 447

AAQ75797/c  
ID AAQ75797 standard; DNA; 21 BP.

XX AC AAQ75797;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes

XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 448

AAQ75798/c  
ID AAQ75798 standard; DNA; 21 BP.

XX AC AAQ75798;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 449  
 AAQ75773/c  
 ID AAQ75773 standard; DNA; 21 BP.  
 XX AAQ75773;  
 XX 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 451  
 AAQ75773/c  
 ID AAQ75773 standard; DNA; 21 BP.  
 XX AAQ75773;  
 XX 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 450  
 AAQ75774/c  
 ID AAQ75774 standard; DNA; 21 BP.  
 XX AAQ75774;  
 XX 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 451

XX

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a physical type of labelled reverse transcription primers (GENESQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

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XX SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;
      Query Match      1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 454
AAQ75779/c
ID AAQ75779 standard; DNA; 21 BP.
XX AC AAQ75779;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 455
AAQ75780/c
ID AAQ75780 standard; DNA; 21 BP.
XX AC AAQ75780;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 456
AAQ75781/c
ID AAQ75781 standard; DNA; 21 BP.
XX AC AAQ75781;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA

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DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 456
AAQ75781/c
ID AAQ75781 standard; DNA; 21 BP.
XX AC AAQ75781;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA

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PT followed by digestion with restriction enzymes
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 457
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
XX
AC AAQ75782;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PS WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 459
AAQ75784/c
ID AAQ75784 standard; DNA; 21 BP.
XX
AC AAQ75784;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
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SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAA 1  
 RESULT 465  
 AAQ75770/c  
 ID AAQ75770 standard; DNA; 21 BP.  
 AC AAQ75770;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 9; 11pp; Japanese.  
 PS  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAA 1  
 RESULT 466  
 AAQ75666/c  
 ID AAQ75666 standard; DNA; 21 BP.  
 AC AAQ75666;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 9; 11pp; Japanese.  
 PS  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAA 1  
 RESULT 467  
 AAQ75667/c  
 ID AAQ75667 standard; DNA; 21 BP.  
 AC AAQ75667;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT

XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 7; 11pp; Japanese.  
 PS  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAA 1  
 RESULT 467  
 AAQ75667/c  
 ID AAQ75667 standard; DNA; 21 BP.  
 AC AAQ75667;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT

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XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 468
XX AAQ75668/c
XX ID AAQ75668 standard; DNA; 21 BP.
XX AC AAQ75668;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 470
XX AAQ75670/c
XX ID AAQ75670 standard; DNA; 21 BP.
XX AC AAQ75670;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 469
XX AAQ75669/c
XX ID AAQ75669 standard; DNA; 21 BP.
XX AC AAQ75669;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 470
XX AAQ75670/c
XX ID AAQ75670 standard; DNA; 21 BP.
XX AC AAQ75670;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
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XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX FT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAA 1
RESULT 471
AAQ75607/c
ID AAQ75607 standard; DNA; 21 BP.
AC AAQ75607;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAA 1
RESULT 471
AAQ75607/c
ID AAQ75607 standard; DNA; 21 BP.
AC AAQ75607;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

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CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAA 1
RESULT 472
AAQ75608/c
ID AAQ75608 standard; DNA; 21 BP.
XX AAQ75608;
AC AAQ75608;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-0112515.
XX 16-APR-1993; 93JP-0112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAA 1
RESULT 473
AAQ75609/c
ID AAQ75609 standard; DNA; 21 BP.

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Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 476  
 AAQ75639/C  
 ID AAQ75639 standard; DNA; 21 BP.  
 AC AAQ75639;  
 XX 04-AUG-1995 (first entry)  
 DT Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 PN 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 PF 16-APR-1993; 93JP-0112515.  
 PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 DE Disclosure; Page 6; 11pp; Japanese.  
 PS A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;  
 SQ

Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 477  
 AAQ75640/C  
 ID AAQ75640 standard; DNA; 21 BP.  
 AC AAQ75640;  
 XX 04-AUG-1995 (first entry)  
 DT Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 PN 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 PF 16-APR-1993; 93JP-0112515.  
 PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 DE Disclosure; Page 6; 11pp; Japanese.  
 PS A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;  
 SQ

KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 PN 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 PF 16-APR-1993; 93JP-0112515.  
 PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 DE Disclosure; Page 6; 11pp; Japanese.  
 PS A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ

Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 478  
 AAQ75641/C  
 ID AAQ75641 standard; DNA; 21 BP.  
 AC AAQ75641;  
 XX 04-AUG-1995 (first entry)  
 DT Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 PN 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 PF 16-APR-1993; 93JP-0112515.  
 PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 DE Disclosure; Page 6; 11pp; Japanese.  
 PS A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ

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Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 480
AAQ75612/c
ID      AAQ75612 standard; DNA; 21 BP.
XX
XX      AAQ75612;
AC
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX
DE
DE
XX
XX      Reverse transcription primer used in cDNA analysis technique.
KW
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX
XX      JPO6303997-A.
PN
XX
XX
XX      01-NOV-1994.
PD
XX
XX      16-APR-1993; 93JP-0112515.
PF
XX
XX      16-APR-1993; 93JP-0112515.
PR
XX
XX      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX      WPI; 1995-018287/03.
DR
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA
PT      followed by digestion with restriction enzymes
PT
XX
XX      Disclosure; Page 5; 11pp; Japanese.
PS
XX
XX      A method for the analysis of cDNA comprises (a) preparing an
CC      aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC      and a plural type of labelled reverse transcription primers
CC      (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the
CC      template for each reverse transcription primer; (b) digesting each of
CC      the prepared aggregates of the double-stranded cDNAs with restriction
CC      enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC      separate lanes. The method can be used to analyse gene expression
CC      rapidly and easily.
XX
XX      Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
SQ      Query Match 1.5%; Score 17; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2.3e+02;
      Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1084 AAAAAAAAAAAAAAAAAA 1100
      |||||||
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 481
AAQ75613/c
ID      AAQ75613 standard; DNA; 21 BP.
XX
XX      AAQ75613;
AC
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX      Reverse transcription primer used in cDNA analysis technique.
DE
DE
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
KW
XX
XX      Synthetic.
OS
XX
XX      JPO6303997-A.
FN
XX

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PD 01-NOV-1994.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75614-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 482  
 AAQ75614/C  
 ID AAQ75614 standard; DNA; 21 BP.  
 XX  
 XX AAQ75614;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
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 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 482  
 AAQ75614/C  
 ID AAQ75614 standard; DNA; 21 BP.  
 XX  
 XX AAQ75614;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 XX WPI; 1995-018287/03.  
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 XX Analysis of cDNA and gene expression - by amplification of mRNA  
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 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
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 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 483  
 AAQ75615/C  
 ID AAQ75615 standard; DNA; 21 BP.  
 XX  
 XX AAQ75615;  
 AC  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 484  
 AAQ75617/C  
 ID AAQ75617 standard; DNA; 21 BP.  
 XX







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RESULT 491
AAQ75661/c
ID AAQ75661 standard; DNA; 21 BP.
XX AC
XX AAQ75661;
XX DT
XX 04-AUG-1995 (first entry)
XX DE
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX KW
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WP1; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
FT followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNA
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNA
CC template for each reverse transcription primer; (b) digesting e
CC the prepared aggregates of the double-stranded cDNAs with restr
CC enzyme and; (c) electrophoresing the digested aggregate of cDNA
CC separate lanes. The method can be used to analyse gene expressi
CC rapidly and easily.
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
QY 1084 AAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAA 1
RESULT 492
AAQ75662/c
ID AAQ75662 standard; DNA; 21 BP.
XX AC
XX AAQ75662;
XX DT
XX 04-AUG-1995 (first entry)
XX DE
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX KW
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.

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XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX XX
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 493
AAQ75663/c
ID AAQ75663 standard; DNA; 21 BP.
XX AC AAQ75663;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
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CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 494
AAQ75645/c
ID AAQ75645 standard; DNA; 21 BP.
XX AC AAQ75645;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JP06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-0112515.
XX XX
XX PR 16-APR-1993; 93JP-0112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX XX
XX SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 495
AAQ75646/c
ID AAQ75646 standard; DNA; 21 BP.
XX AC AAQ75646;
```



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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 498
AAQ75650/c
ID AAQ75650 standard; DNA; 21 BP.
AC AAQ75650;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 500
AAQ75652/c
ID AAQ75652 standard; DNA; 21 BP.
XX
AC AAQ75652;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 499
AAQ75651/c
ID AAQ75651 standard; DNA; 21 BP.
AC AAQ75651;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

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CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 501  
 AAQ75653/c  
 ID AAQ75653 standard; DNA; 21 BP.  
 XX  
 AC AAQ75653;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 502  
 AAQ75654/c  
 ID AAQ75654 standard; DNA; 21 BP.  
 XX  
 AC AAQ75654;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 503  
 AAQ75655/c  
 ID AAQ75655 standard; DNA; 21 BP.  
 XX  
 AC AAQ75655;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX



DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 XX  
 RESULT 507  
 AAQ75659/c  
 ID AAQ75659 standard; DNA; 21 BP.  
 XX  
 XX AC AAQ75659;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 17 AAAAAAAAAAAAAAAAAA 1  
 XX  
 RESULT 508  
 AAAT10743  
 ID AAAT10743 standard; RNA; 21 BP.  
 XX  
 XX AC AAAT10743;  
 XX  
 XX 09-SEP-1996 (first entry)  
 XX  
 XX Oligonucleotide probe, CP-1.  
 DE Electronically self-addressable device; ED; electrode;  
 KW current source; attachment layer; permeable; counterion;  
 XX genetic typing; probe; detection; ss.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT modified\_base 21  
 FT /\*tag= a  
 FT /note= "3'-ribonucleoside terminus"  
 XX  
 XX WO9601836-A1.  
 XX  
 XX 25-JAN-1996.  
 XX  
 XX 05-JUL-1995; 95WO-US08570.  
 XX  
 XX 07-JUL-1994; 94US-0271882.  
 XX  
 XX (NANO-) NANOGEN INC.  
 XX  
 XX Evans GA, Heller MJ, Sosnowski RG, Tu E;  
 XX WPI; 1996-097582/10.  
 XX  
 XX Electronically self-addressable device - used for electronic control  
 PT of, e.g. nucleic acid hybridisation  
 XX  
 XX Example 1; Page 60; 155pp; English.  
 XX  
 CC The sequences given in AAAT10742-67 are synthetic oligonucleotides  
 CC which are used in the construction of the electronically self-  
 CC addressable device (ED) of the invention. The ED comprises a  
 CC substrate, an electrode or opt. a number of electrodes supported by  
 CC the substrate, a current source operatively connected to the  
 CC electrode and an attachment layer adjacent to the electrode which is



permeable to a counterion but not permeable to a molecule capable of insulating or binding to the electrode. The attachment layer is capable of attaching a macromolecule. The EP is used for genetic typing and comprises a number of electronically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence.

Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 509  
AAZ26268/c  
ID AAZ26268 standard; DNA; 21 BP.  
XX AC AAZ26268;  
XX DT 30-NOV-1999 (first entry)  
XX DE Human polymorphic region 457.  
XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
XX KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX OS Homo sapiens.  
XX PN WO9841648-A2.  
XX PD 24-SEP-1998.  
XX PF 19-MAR-1998; 98WO-US05419.  
XX PR 20-MAR-1997; 97US-0041057.  
XX PA (VARI-) VARIAGENICS INC.  
XX PI Housman D, Ledley FD, Stanton VP;  
XX PS WPI; 1998-521232/44.  
XX PT Identifying target genes for allele-specific drugs - used for  
XX PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic  
XX PT plaque, dysplastic lesions, endometriosis or graft versus host disease  
XX PS Disclosure; Figure 7; 605pp; English.  
XX CC This invention describes a novel method for identifying an inhibitor  
XX CC potentially useful for treatment of cancer, where the inhibitor is  
XX CC active on a gene vital for cell growth or viability, and where the gene  
XX CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
XX CC used for preventing the development of cancer in a patient having a  
XX CC precancerous condition, by administering to the patient a first allele  
XX CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
XX CC present in cells of the precancerous condition, where the normal somatic  
XX CC cells of the patient are heterozygous for the first gene, the inhibitor  
XX CC is active on at least one but less than all allelic forms of the gene  
XX CC present in a population and targets only one allelic form present in the  
XX CC normal somatic cells, and the first gene. The products and methods can  
XX CC be used in the diagnosis, prevention and treatment of LOH disorders,  
XX CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or  
XX CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney

disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ5812-226825  
CC represent human polymorphic sites described in the method of the  
CC invention.  
XX Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 other;  
SQ Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAATAAAAAAAAAA 1097  
DB 19 ATTAATAAAAAAAAAA 3

RESULT 510  
AAV35395  
ID AAV35395 standard; DNA; 21 BP.  
XX AC AAV35395;  
XX DT 13-OCT-1998 (first entry)  
XX DE HIV-1 gag protein DNA primer #8.  
XX KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;  
XX KW vaccines; infection; protection; primer; ss.  
XX OS Synthetic.  
XX PN WO9822596-A1.  
XX PD 28-MAY-1998.  
XX PF 19-NOV-1997; 97WO-JP04216.  
XX PR 19-NOV-1996; 96JP-0323412.  
XX PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.  
XX PA (JAPG) NIPPON ZEON KK.  
XX PI Kojima A, Kurata T, Yasuda A;  
XX PS WPI; 1998-312481/27.  
XX PT Recombinant vaccinia virus containing fusion HIB gag gene - for  
XX PT production in host cells of gag protein for use as vaccine  
XX PS Example 1; Page 66; 84pp; Japanese.  
XX CC AAV35388-V35414 are primers used in a method which results in a  
XX CC recombinant vaccinia virus comprising of a gag gene from a retrovirus  
XX CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope  
XX CC region (30-300 bases in length) of a retroviral gene other than the gag  
XX CC gene. The gag gene may be altered so as to produce a gag protein modified  
XX CC from the natural sequence by the addition, deletion or substitution of at  
XX CC least 1 amino acid residue. The fusion gene is inserted into a region of  
XX CC a vaccinia virus not essential to its propagation, to give a recombinant  
XX CC vaccinia virus vector which is used to transform a host cell (such as  
XX CC HeLa, vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon  
XX CC culturing the host cell produces particulate structures containing the  
XX CC fusion gag protein. The recombinant vaccinia virus or the fusion gag  
XX CC protein particles may be used in the production of vaccines for  
XX CC protecting against infection with retroviruses such as HIV.  
XX SQ Sequence 21 BP; 19 A; 2 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 3 AAAAAAAAAAAAAAAAAA 19  
|||||

## RESULT 511

AAZ81302  
ID AAZ81302 standard; DNA; 21 BP.

XX AC AAZ81302;

XX DT 20-AUG-1999 (first entry)

XX DE 3' ribonucleoside oligonucleotide probe CP-1.

XX KW Microelectronic device; multi-step reaction; microscopic format;  
XX KW ion-permeable permeation layer; electrode; electrical control;  
XX KW transport; attachment; binding; DNA/RNA hybrid; probe; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT misc\_RNA 21  
XX PT /\*tag= a

XX PN WO929711-A1.

XX PD 17-JUN-1999.

XX PF 01-DEC-1998; 98WO-US25475.

XX PR 05-DEC-1997; 97US-0986065.

XX PA (NANO-) NANOGEN INC.

XX PI Butler WF, Edman CF, Heller MJ, Nerenberg MI, Sosnowski RG;  
XX PI Tu E;

XX DR WPI; 1999-385567/32.

XX PT New microelectronic device designed to carry out and control  
XX PT multi-step and multiplex molecular biological reactions in  
XX PT microscopic format

XX PS Example 1; Page 89; 179pp; English.

XX CC The specification describes a self-addressable, self-assembling  
XX CC microelectronic device which is designed to actively carry out and  
XX CC control multi-step and multiplex molecular biological reactions in  
XX CC microscopic formats. A key aspect of this invention is played by the  
XX CC ion-permeable permeation layer which overlies the electrode. This  
XX CC permeation layer allows attachment of nucleic acids to permit  
XX CC immobilization but also separates the attached oligonucleotides and  
XX CC hybridized target DNA sequences from the highly reactive electrochemical  
XX CC environment generated immediately at the electrode surface. The  
XX CC microelectronic device is designed and fabricated to actively carry  
XX CC out and control reactions such as nucleic acid hybridizations,  
XX CC antibody/antigen reactions, sample preparation, diagnostics and  
XX CC biopolymer synthesis. The device can electronically control the  
XX CC transport and attachment of specific binding entities, such as nucleic  
XX CC acids and polypeptides, to specific micro-locations. The device can  
XX CC subsequently control the transport and reaction of analytes or reactants  
XX CC at the addressed specific micro-locations. The device is able to  
XX CC concentrate analytes and reactants, remove non-specifically bound  
XX CC molecules, provide stringency control for DNA hybridization reactions  
XX CC and improve the detection of analytes. The present sequence  
XX CC represents a probe used to exemplify the invention.

XX SQ Sequence 21 BP; 20 A; 0 C; 0 G; 1 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 1 AAAAAAAAAAAAAAAAAA 17  
|||||

## RESULT 512

AAZ26973/C  
ID AAZ26973 standard; cDNA; 21 BP.

XX AC AAZ26973;

XX DT 25-JUN-1999 (first entry)

XX DE Primer used to reverse transcribe mamaglobin RNA.

XX KW Human; mammary-specific protein; mamaglobin; antigen; vaccine;  
XX KW mamaglobin-expressing cancer; breast cancer;  
XX KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.

XX OS Synthetic.

XX PN WO9914230-A1.

XX PD 25-MAR-1999.

XX PF 18-SEP-1998; 98WO-US17991.

XX PR 18-SEP-1997; 97US-0933149.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Fleming TP, Watson MA;

XX DR WPI; 1999-244021/20.

XX PT Mamaglobin, secreted protein overexpressed in breast cancer

XX PS Example 2; Page 55; 60pp; English.

XX CC The present primer was used to reverse transcribe RNA encoding a human  
XX CC mammary-specific protein, designated mamaglobin. The specification  
XX CC describes a protein comprising a mamaglobin antigen that is recognized  
XX CC by B and/or Tc cells specific for the natural, secreted and glycosylated  
XX CC form of mamaglobin polypeptide. This protein, or recombinant vectors  
XX CC that express it, are used in vaccines for treating mamaglobin-  
XX CC expressing cancers, specifically of the breast. Such cancers can  
XX CC also be treated using autologous tumor lymphocytes activated  
XX CC ex vivo with an mamaglobin antigen, then returned to the  
XX CC patient. Expression of mamaglobin is elevated in 27% of stage I  
XX CC primary breast cancers, so it represents a marker useful for  
XX CC diagnosis of this disease.

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 21 AAAAAAAAAAAAAAAAAA 5  
|||||

## RESULT 513

AAZ44350/C  
ID AAZ44350 standard; DNA; 21 BP.

XX AC AAZ44350;

XX DT 04-APR-2000 (first entry)

XX DE Protein kinase inhibiting primer #12.

XX XX

KW Antimicrobial; cytostatic; immunosuppressive; protein kinase;  
 KW prophylactic; therapy; treatment; cancer; autoimmune disease;  
 KW pathogenic microorganism; primer; ss.

OS Unidentified.

PN US998596-A.

XX 07-DEC-1999.

XX 04-APR-1995; 95US-0416214.

XX 04-APR-1995; 95US-0416214.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Bergan R, Neckers L;

XX WPI; 2000-104623/09.

XX Oligonucleotides inhibiting protein kinase, useful for treating  
 PT diseases such as cancer and autoimmune disease -

XX Example 8; Column 27-28; 26pp; English.

XX This invention describes novel purified aptameric oligonucleotides  
 CC which have antimicrobial, cytostatic and immunosuppressive activity.  
 CC The oligonucleotides are useful for binding to and preventing or  
 CC inhibiting the biological function of a protein kinase or a target  
 CC molecule and for detecting the presence or absence of a target molecule  
 CC in biological samples. The oligonucleotides are also useful for  
 CC prophylactic and therapeutic treatment of diseases such as cancer,  
 CC autoimmune diseases and diseases caused by pathogenic microorganisms.  
 CC This sequence represents a primer used in the method of the invention.

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 514

AAH42480/c

ID AAH42480 standard; DNA; 21 BP.

XX AC AAH42480;

XX 01-OCT-2001 (first entry)

XX Oligonucleotide used to produce branched chain compounds.

XX Branched chain compound; nucleic acid synthesis; primer extension;  
 KW reverse transcription; nucleic acid hybridization;  
 KW nucleic acid amplification; ss.

XX Synthetic.

XX Key modified\_base 1 Location/Qualifiers

FT /\*tag= a

FT /\*note= "NH2-C6 attached"

FT /\*tag= b

FT /\*note= "NH2-C6 attached"

FT /\*tag= c

FT /\*note= "branch present"

PN EP1111068-A1.

XX 27-JUN-2001.

XX 21-DEC-1999; 99EP-0125484.

XX 21-DEC-1999; 99EP-0125484.

XX (LION-) LION BIOSCIENCE AG.

XX (VBCG-) VBC GENOMICS GMBH.

XX Schmidt W, Hiller R, Huber M, Mueller M;

XX WPI; 2001-466959/51.

XX Branched compounds useful in e.g. nucleic acid synthesis reaction  
 PT comprises nucleic acid moieties optionally extended by a polymerase -

XX Example 1; Page 10; 31pp; English.

XX The specification describes branched compounds containing nucleic  
 CC acid moieties optionally extended by a polymerase. The branched chain  
 CC compounds of the invention are used in nucleic acid synthesis reaction,  
 CC primer extension reaction, reverse transcription reaction of RNA into  
 CC DNA, nucleic acid hybridization experiment (for identifying sequence  
 CC of a nucleic acid), and nucleic acid amplification experiment (for  
 CC analysing the expression pattern of genes). The compounds are also used  
 CC in solid-phase enzymatic reactions. The present sequence was used  
 CC in the course of the invention to produce branched chain compounds.

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 515

AAF99707/c

ID AAF99707 standard; DNA; 21 BP.

XX AC AAF99707;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #823.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US26383.

XX 25-SEP-1999; 99US-0156113.

XX 27-SEP-1999; 99US-0156135.

XX 23-AUG-2000; 2000US-0227436.

XX (IOWA ) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

DR WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids -  
 XX  
 PS Claim 101; Page 56; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells.  
 CC Note: the present sequence may have a phosphorothioate backbone.  
 XX  
 SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 21 AAAAAAAAAAAAAAAAAA 5  
 RESULT 516  
 ABS78428/C  
 ID ABS78428 standard; DNA; 21 BP.  
 AC ABS78428;  
 DT 13-DEC-2002 (first entry)  
 XX  
 XX Angiogenesis inhibitory oligonucleotide #912.  
 DE  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;  
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;  
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;  
 KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;  
 KW haemophilic joint; angiofibroma; wound granulation;  
 KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200253141-A2.  
 FN  
 XX  
 PD 11-JUL-2002.  
 PD  
 XX  
 PF 14-DEC-2001; 2001WO-US48458.  
 PF  
 XX  
 PR 14-DEC-2000; 2000US-255534P.  
 PR  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA  
 XX  
 PI Bratzler RL;  
 PI  
 XX  
 XX WPI; 2002-566690/60.  
 DR  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least  
 PT one antiangiogenic nucleic acid molecule to the subject -  
 PT  
 XX  
 PS Claim 2; Page 35; 276pp; English.  
 XX

CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule.  
 CC Also included is a kit comprising a first container housing the  
 CC antiangiogenic nucleic acids, and instructions for administering them to  
 CC a subject having a condition characterised by unwanted angiogenesis.  
 CC The method is useful for inhibiting angiogenesis associated with solid  
 CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid  
 CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,  
 CC macular degeneration, corneal graft rejection, neovascular glaucoma,  
 CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial  
 CC angiogenesis, plaque neovascularisation, telangiectasia, haemophilic  
 CC joints, angiofibroma, wound granulation, intestinal adhesions.  
 CC atherosclerosis, scleroderma and hypertrophic scars. The present  
 CC sequence is an antiangiogenic nucleic acid of the invention.  
 XX  
 SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 21 AAAAAAAAAAAAAAAAAA 5  
 RESULT 517  
 ABL39404/C  
 ID ABL39404 standard; DNA; 21 BP.  
 AC ABL39404;  
 XX  
 XX 16-APR-2002 (first entry)  
 DT  
 XX  
 XX Immunostimulatory nucleic acid SEQ ID NO: 840.  
 DE  
 XX  
 DE Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 XX  
 XX WO200197843-A2.  
 PN  
 XX 27-DEC-2001.  
 PD  
 XX  
 XX 22-JUN-2001; 2001WO-US20154.  
 PF  
 XX  
 PR 22-JUN-2000; 2000US-213346P.  
 PR  
 XX  
 PA (IOWA) UNIV IOWA RES FOUND.  
 PA  
 XX  
 PI Weiner G, Hartmann G;  
 PI  
 XX WPI; 2002-154611/20.  
 DR  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer -  
 PT  
 XX  
 PS Disclosure; Page 309; 312pp; English.  
 XX  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,  
 CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in  
 CC the exemplification of the invention.

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
 DB 21 AAAAAAAAAAAAAA 5

RESULT 518  
 AAD51323/c  
 ID AAD51323 standard; DNA; 21 BP.  
 XX  
 AC AAD51323;  
 DT 16-APR-2003 (first entry)  
 DE Regular oligo dT primer used to illustrate the method of the invention.  
 XX  
 KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;  
 KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;  
 KW musculoskeletal damage; ss.  
 OS Unidentified.  
 XX  
 PN W0200290579-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 03-MAY-2002; 2002WO-AU00553.  
 XX  
 PR 04-MAY-2001; 2001AU-0004809.  
 PR 29-JUN-2001; 2001US-0896941.  
 XX  
 PA (GENO-) GENOMICS RES PARTNERS PTY LTD.  
 XX  
 PI Brandon RB;  
 XX  
 DR WPI; 2003-120558/11.  
 XX  
 PT Assessing condition e.g. athletic ability, stage of disease, presence  
 PT of drugs, response to exercise, response to vaccines, therapies,  
 PT nutritional states, of performance animal involves analyzing nucleic  
 PT acid expression  
 XX  
 PS Disclosure; Page 46; 87pp; English.  
 XX  
 CC The invention relates to a method for assessing a condition of a  
 CC performance animal. The method involves determining in sample abundance  
 CC of expressed target nucleic acid; transmitting digital sample signal to  
 CC remote diagnostic server; processing digital sample signal at remotely  
 CC located database to correlate digital signal with digital information  
 CC and returning report of particular condition of animal. The method is  
 CC useful for assessing a condition of a performance animal preferably  
 CC human, dog or camel. The condition can be an athletic ability and a  
 CC condition that enhances, hinders, impedes or does not change an expected  
 CC ability of the performance animal; and also normal, pre-clinical, overt  
 CC progress and/or stage of disease, undiagnosed or unclassified conditions,  
 CC presence of drugs, response to exercise, response to vaccines, therapies,  
 CC nutritional states and response to environmental conditions. Diseases  
 CC assessed by the invention include laminitis, lameness, viral or bacterial

CC disease, gastritis, gastric ulcers, respiratory ailments, fractures,  
 CC epistaxis, musculoskeletal damage or disorders and joint diseases. The  
 CC present sequence is a primer used to illustrate the method of the  
 CC invention.

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
 DB 21 AAAAAAAAAAAAAA 5

RESULT 519  
 AAQ64706/c  
 ID AAQ64706 standard; cDNA to mRNA; 22 BP.  
 XX  
 AC AAQ64706;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 04-JAN-1995 (first entry)  
 XX  
 DE 2', 5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.  
 XX  
 KW antisense; 2', 5'-tetraadenylate; 2-5A dependent RNase activator;  
 KW RNA cleavage; antiviral therapy; chimeric molecule; ss.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT misc\_feature 1...4  
 FT /\*tag= a  
 FT /label= 2', 5'-linked tetraadenylate  
 FT /note= "nucleotides linked through phosphodiester  
 FT bonds at hydroxyl groups of 2' and 5'  
 FT carbons"  
 FT misc\_feature 5..22  
 FT /\*tag= b  
 FT /note= "antisense region"  
 XX  
 PN W09409129-A2.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 20-OCT-1993; 93WO-US10103.  
 XX  
 PR 21-OCT-1992; 92US-0965666.  
 PR 17-SEP-1993; 93US-0123449.  
 XX  
 PA (CLEV-) CLEVELAND CLINIC RES INST.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Lesiak K, Maitra R, Silverman R, Torrence P;  
 XX  
 DR WPI; 1994-151315/18.  
 XX  
 FT Specific cleavage of RNA, useful partic. for treating viral  
 FT infection, cancers, etc. - by using anti-sense oligo:nucleotide  
 FT coupled to activator of 2-5A dependent RNase  
 XX  
 PS Example 1; Page 68; 86pp; English.  
 XX  
 CC This sequence is an example of a 2-5A-antisense oligonucleotide  
 CC chimeric molecule. The antisense region targets the chimeric  
 CC molecule to a particular region of RNA to be specifically  
 CC cleaved and the 2', 5'-linked tetraadenylate tail activates  
 CC the 2-5A RNase. Typical applications are treatment of viral  
 CC infections (esp. for cleavage of an RNA virus genome), cancer;  
 CC leukaemia, cardiovascular disorders (e.g. restenosis after  
 CC angioplasty), genetic disorders, osteoarthritis or rheumatoid

CC AAQ64711 and AAQ64724 all lacked cytotoxicity. In the novel  
CC 2-5A-antisense oligonucleotide chimeric molecules, the antisense  
CC region targets the chimeric molecule to a particular region of RNA  
CC to be specifically cleaved and the 2',5'-linked tetraadenylate tail  
CC activates the 2-5A RNase. Typical applications are treatment of viral  
CC infections (esp. for cleavage of an RNA virus genome), cancer;  
CC leukaemia, cardiovascular disorders (e.g. restenosis after  
CC angioplasty), genetic disorders, osteoarthritis or rheumatoid  
CC arthritis.  
CC CC (Updated on 25-MAR-2003 to correct PN field.)  
XX XX  
SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 other;  
  
Query Match 1.5%; Score 17; DB 1: Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAA 1100  
DB 1 AAAAAAAAAAAAAAAAAA 17  
|||||||  
  
RESULT 521  
AAA98276/c  
ID ID AAA98276 standard; DNA; 22 BP.  
XX AC AAA98276;  
XX AC  
DT 02-FEB-2001 (first entry)  
DE DE Human mismatch repair gene hMSH6 intron 9 DNA fragment.  
XX DE  
XX DE  
KW Human mismatch repair gene; hMSH6; disease predisposition; genotype;  
KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;  
KW neoplastic disease; drug development; ss.  
XX KW  
XX KW Homo sapiens.  
OS OS  
SS DE19909878-A1.  
PN PN  
PD PD 07-SEP-2000.  
XX PD  
PF PF 06-MAR-1999; 99DE-1009878.  
XX PF  
PR PR 06-MAR-1999; 99DE-1009878.  
XX PR  
XX XX (UYDR ) UNIV DRESDEN TECH.  
PA PA  
XX PA Plaschke J, Kruppa C, Schackert H,  
PI PI  
XX PI WFI; 2000-588378/56.  
DR DR  
XX XX  
PT PT Novel variants of the human mismatch repair gene, MSH6, useful e.g. for  
PT determining predisposition to cancer and for development of drugs -  
XX XX  
PS Claim 1; Page 4; 14pp; German.  
XX XX  
XX XX This invention describes a novel method of determining a predisposition  
CC to disease by genotyping a subject's DNA sequence (A) of the human  
CC mismatch repair gene, MSH6 at specified positions and comparing with  
CC reference DNA sequences, optionally taking into account all possible  
CC combinations of variations of the individual mutations, including any  
CC chosen absolute number of variations. (A), and analysis of their  
CC sequences, are useful for the following: (i) determining a predisposition  
CC to disease, especially colorectal, endometrial and ovarian carcinoma and  
CC leukemia; (ii) determining an increased mutation rate (frequency of base  
CC substitutions, insertions and/or deletions) in eukaryotic cells; (iii)  
CC predicting the progression, severity and survival time of patients with  
CC neoplastic disease; (iv) the development of therapeutic and 'life-style'  
CC drugs; (v) predicting individual differences in response to known  
CC chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);  
CC (vi) optimizing individual treatments and interventions against  
CC necrosis; (vii) controlling the mutation rate in eukaryotic cells, in

CC vitro or in vivo; (viii) constructing genes and vectors, particularly for  
CC development of pharmaceuticals; (ix) developing diagnostic kits and other  
CC systems for genotyping; and (x) developing in vivo and in vitro test  
CC systems for expressing individual forms of the MSH6 gene, e.g. for  
CC studying pathophysiology of disease or processes in which MSH6 is  
CC involved, and for drug development and testing.

XX SQ Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 22 AAAAAAAAAAAAAAAAAA 6

RESULT 522  
AAFL17413  
ID AAF17413 standard; DNA; 22 BP.  
XX AC AAF17413;  
XX DT 09-MAR-2001 (first entry)  
XX DE L1 cleavage site related sequence #3.  
XX KW Retrotransposon; genetic defect; cystic fibrosis; ds.  
XX OS Unidentified.  
XX PN US6150160-A.  
XX PD 21-NOV-2000.  
XX PF 28-APR-1997; 97US-0847844.  
XX PR 16-NOV-1995; 95US-0006831.  
XX PR 15-NOV-1996; 96US-0749805.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX PA (UYPE-) UNIV PENNSYLVANIA.  
XX PI Moran JV, Dombroski BA, Kazazian HH, Boeke JD;  
XX WPI; 2001-060015/07.  
XX DNAC comprising a promoter P and an L1 cassette sequence having a core  
XX retrotransposon element, useful for random insertion of a heterologous  
XX or homologous DNA sequence into a cell genome and for correcting  
XX genetic defects -  
XX PS Disclosure; Fig 14; 87pp; English.

CC The present invention relates to DNA for a promoter and an L1  
CC cassette sequence having a core retrotransposon element. The invention  
CC is useful for random insertion of a heterologous or homologous DNA  
CC sequence into a cell genome, and for correction of a genetic defect  
CC in the cell into which the insertion is made. Genetic defects which  
CC may be corrected includes cystic fibrosis, mutations in the  
CC dystrophin gene, genetic defects associated with blood clotting and  
CC other genetic defects.

XX SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 U; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 523  
AAQ30432/c  
ID AAQ30432 standard; DNA; 23 BP.  
XX AC AAQ30432;  
XX DT 25-MAR-2003 (updated)  
XX DT 07-DEC-1992 (first entry)  
XX DE Oligomer II6805 for forming triplex with HUMIL6 target duplex.  
XX KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;  
XX KW RSV; HPV; malignancy; hepatitis; inflammation; ss.  
XX OS Synthetic.

XX FH Key Location/Qualifiers  
XX FT modified\_base 1  
XX FT /\*tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "OTHER= N4 N4 ethanocytosine"  
XX FT modified\_base 23  
XX FT /\*tag= b  
XX FT /mod\_base= OTHER  
XX FT /note= "OTHER= N4 N4 ethanocytosine"  
XX FT misc\_feature 12..23  
XX FT /\*tag= c  
XX FT /label= inverted\_polarity\_region  
XX FT /note= "see comments"  
XX FT misc\_feature 11..12  
XX FT /\*tag= d  
XX FT /note= "o-xyloso dimer synthon linkage"

XX PN W09209705-A1.  
XX PD 11-JUN-1992.  
XX PF 25-NOV-1991; 91WO-US08811.  
XX PR 23-NOV-1990; 90US-0617907.  
XX PR 18-JAN-1991; 91US-0643382.  
XX PR 08-APR-1991; 91US-0683420.  
XX PR 17-APR-1991; 91US-0686544.  
XX PR 17-APR-1991; 91US-0686546.  
XX PR 17-APR-1991; 91US-0686547.  
XX PR 27-SEP-1991; 91US-0766733.  
XX (GILE-) GILEAD SCI INC.  
XX PF Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
XX WPI; 1992-217083/26.

XX New oligomers contg. modified bases - which form a triplex with  
XX G-C doublet in a DNA duplex, for treating and diagnosing HIV,  
XX hepatitis, herpes, malignancy and inflammation  
XX Claim 12; Page 71; 77pp; English.  
XX The synthetic oligomer is capable of forming a triplex at  
XX physiological pH with a purine rich target sequence by coupling  
XX into the major groove of the duplex. The specific target sequence  
XX of this oligomer is the human interleukin 6 gene untranslated  
XX sequence contg. a purine rich sequence concd. on one strand  
XX of the duplex. The oligomer, and others like it are useful in  
XX diagnosis and therapy of diseases characterised by specific DNA  
XX duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
XX tumours and inflammation. The triple helices form under mild conditions  
XX thus assays may be carried out without subjecting the test specimen to  
XX harsh conditions. The oligomer contains an inverted polarity region  
XX formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso

CC (nucleotides have the 3'positions of xylose sugars linked via the o-  
 CC xylene ring). Two nucleotides are coupled through a xylene residue  
 CC to form the dimer synthon. This additional modifications may render  
 CC the oligomer stable to nuclease activity. The oligomer is able to  
 CC inhibit gene expression, as verified by in vitro systems.  
 CC See also AAQ25452-25501 and AAQ30226-448.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 22 AAAAAAAAAAAAAAAAAA 6

RESULT 524

AAQ45360/C  
 ID AAQ45360 standard; DNA; 23 BP.

XX AC AAQ45360;

XX AC  
 DT 25-MAR-2003 (updated)  
 DT 09-OCT-1994 (first entry)

XX Human protein-tyrosine-phosphatase-ID cDNA primer.

DE Protein-tyrosine-phosphatase; enzyme; disease diagnosis;  
 XX DNA primer; ss.

KW Synthetic.

XX WO9408017-A1.

XX 14-APR-1994.

XX 06-OCT-1993; 93WO-EP02728.

XX 06-OCT-1992; 92US-0956315.

PR 16-FEB-1993; 93US-0018129.

XX (PLAC ) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.

XX Ullrich A, Vogel W;

DR WPI; 1994-135583/16.

XX New protein tyrosine phosphatase (PTP) protein, PTP-ID - are  
 PT useful for diagnosis and treatment of diseases associated with  
 PT abnormal PTP-ID levels

XX Disclosure; Page 48; 99pp; English.

CC This DNA primer is used in the PCR-based amplification of  
 CC protein-tyrosine-phosphatase-13 cDNA.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 525

AAQ75028

ID AAQ75028 standard; DNA; 23 BP.

XX AC AAQ75028;

XX 25-MAR-2003 (updated)

DT 03-AUG-1995 (first entry)

XX LCR oligo 2.

DE Synthetic oligo; solid phase immunoassay; ss.

XX Synthetic.

OS WO9426932-A1.

PN 24-NOV-1994.

XX 13-MAY-1994; 94WO-US05407.

PF 13-MAY-1993; 93US-0061694.

PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Fields HA, Khudyakov YE;

XX WPI; 1995-006819/01.

DR Solid phase immunoassay using oligo:nucleotide as label - also

XX new conjugates of oligo:nucleotide coupled to antigenic peptide,

PT partic. for diagnosing hepatitis C or E virus infection

XX Example; Page 13; 34pp; English.

PS AAQ62941 and AAQ62942 are examples of synthetic immunoreactive peptides.

CC They are used in a method for detecting an antigen in a subject. The

CC method involves binding the antigen to a solid support and then

CC reacting it with an immunoreactive ligand (L) bound to an oligo;

CC removing any unreacted L, and then detecting the presence of the

CC oligo. A similar method can be used to detect Ab, in which case the

CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as

CC the label allows Ag or Ab to be detected at very low levels. An

CC exemplary oligo is AAQ75024 which can be covalently attached by the 5'-

CC terminus to the N- or C-terminal of a synthetic peptide. For LCR

CC using oligo AAQ75024, oligos 1-4 (see AAQ75027-Q75030) can be used.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 23 BP; 19 A; 4 C; 0 G; 0 U; 0 other;

SQ Query Match 1.5%; Score 17; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100

|||||

Db 6 AAAAAAAAAAAAAAAAAA 22

RESULT 526

AAQ75029/C

ID AAQ75029 standard; RNA; 23 BP.

XX AC AAQ75029;

XX 25-MAR-2003 (updated)

DT 03-AUG-1995 (first entry)

XX LCR oligo 3.

DE Synthetic oligo; solid phase immunoassay; ss.

XX Synthetic.

OS WO9426932-A1.

XX



XX PD 24-NOV-1994.  
 XX PF 13-MAY-1994; 94WO-US05407.  
 XX PR 13-MAY-1993; 93US-0061694.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Fields HA, Khudyakov YE;  
 XX PS WPI; 1995-006819/01.  
 XX PT Solid phase immunoassay using oligo:nucleotide as label - also  
 XX FT new conjugates of oligo:nucleotide coupled to antigenic peptide,  
 XX FT partic. for diagnosing hepatitis C or E virus infection  
 XX PS Example; Page 13; 34pp; English.  
 XX CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
 XX CC They are used in a method for detecting an antigen in a subject. The  
 XX CC method involves binding the antigen to a solid support and then  
 XX CC reacting it with an immunoreactive ligand (L) bound to an oligo;  
 XX CC removing any unreacted L, and then detecting the presence of the  
 XX CC oligo. A similar method can be used to detect Abs, in which case the  
 XX CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as  
 XX CC the label allows Ag or Ab to be detected at very low levels. An  
 XX CC exemplary oligo is AAQ75024 which can be covalently attached by the 5'-  
 XX CC terminus to the N- or C-terminal of a synthetic peptide. For LCR  
 XX CC using oligo AAZ75024, oligos 1-4 (see AAQ75027-Q75030) can be used.  
 XX CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 527  
 AAT33701/C  
 ID AAT33701 standard; DNA; 23 BP.  
 XX AC AAT33701;  
 XX DT 19-MAY-1997 (first entry)  
 XX DE Primer #1 for tissue or cell derived RNA.  
 XX KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;  
 XX KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;  
 XX KW viral infection; hereditary disease; agricultural gene; ss.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT misc\_feature 1  
 XX FT /\*tag= a  
 XX FT /note= "hydroxylated"  
 XX PN EP735144-A1.  
 XX PD 02-OCT-1996.  
 XX PF 26-MAR-1996; 96EP-0104817.  
 XX PR 12-SEP-1995; 95JP-0234122.  
 XX PR 28-MAR-1995; 95JP-0069695.  
 XX PR 20-JUL-1995; 95JP-0184006.  
 PA (SUNR ) SUNTORY LTD.

XX PA (SHKJ ) RES DEV CORP JAPAN.  
 XX PI Kato K;  
 XX DR WPI; 1996-435619/44.  
 XX PT Molecular indexing of DNA - using restriction enzymes, PCR  
 XX PS amplification and electrophoresis to analyse DNA fragments  
 XX Claim 3; Page 14; 20pp; English.  
 XX CC AAT33701-T33703 represent amplification primers used in the reverse-  
 XX CC transcription of tissue or cell derived mRNA, in the method of the  
 XX CC invention. The method of the invention is a molecular indexing method,  
 XX CC and comprises digesting the cDNA amplified by these sequences with a  
 XX CC class IIS restriction enzyme. Each resultant cDNA fragment is then  
 XX CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors  
 XX CC cohesive to all possible overhangs), and digesting the products with two  
 XX CC further class IIS restriction enzymes. These steps are repeated (but  
 XX CC the enzyme used for the first step is different in each) to produce two  
 XX CC further cDNA samples. The ligation samples are then recovered using  
 XX CC streptavidin-coated paramagnetic beads, removing the strand  
 XX CC complementary to an adaptor-primer. The adaptor primer and an anchored  
 XX CC oligo-dr primer (such as this sequence) are then used to amplify the cDNA  
 XX CC samples. The amplified products are separated, and the sizes of the  
 XX CC fragments obtained is recorded. The method can be used for the analysis  
 XX CC search and isolation of the genes of physiologically active substances  
 XX CC that are potential pharmaceuticals, or causative genes of hereditary  
 XX CC diseases, as well as for the isolation of genes for improving  
 XX CC agricultural products. Using this method, it is possible to classify  
 XX CC (index) DNA into groups in a short period of time without duplication.  
 XX SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAAAAAAAAAAAAA 1099  
 Db 23 TAAAAAAAAAAAAAAAAA 7  
 RESULT 528  
 AAT33716/C  
 ID AAT33716 standard; DNA; 23 BP.  
 XX AC AAT33716;  
 XX DT 06-FEB-1997 (first entry)  
 XX DE RT-PCR Primer for aromatic acyl transferase sequence.  
 XX KW Aromatic acyl transferase; transformation; anthocyanin pigment;  
 XX KW plants; acylation; colour; tone; colouration; colour change;  
 XX KW Gentiana triflora; Petunia hybrida; Petilla ocimoides;  
 XX KW Scenecio cruentus; Lavandula angustifolia; ss.  
 XX OS Synthetic.  
 XX PN WO9625500-A1.  
 XX PD 22-AUG-1996.  
 XX PF 16-FEB-1996; 96WO-JP00348.  
 XX PR 30-JAN-1996; 96JP-0046534.  
 XX PR 17-FEB-1995; 95JP-0067159.  
 XX PR 29-JUN-1995; 95JP-0196915.  
 XX PA (SUNR ) SUNTORY LTD.

XX Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;  
 PI Nakao M, Tanaka Y, Yonekura K;  
 XX WPI; 1996-393401/39.  
 XX DNA coding for aromatic acyl transferase - for transforming plants  
 PT which produce anthocyanin pigments and thus altering colour tone,  
 PT e.g. of flowers  
 XX  
 XX Example 2; Page 21; 94pp; Japanese.  
 XX Vectors containing DNA fragments encoding proteins of plant origin  
 CC with aromatic acyl transferase activity may be used to transform  
 CC plants which produce anthocyanin pigments. The aromatic acyl  
 CC transferase acylates the pigments in the flower resulting in colour  
 CC tone changes and allowing new colourations to be produced. Six  
 CC specific DNA sequences encoding aromatic acyl transferase from  
 CC different plants are described in AAT37308-T37313. This  
 CC primer was used to reverse transcribe aromatic acyl transferase RNA  
 CC to produce a cDNA ready for cloning into expression vectors.  
 XX  
 XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 529  
 AAV61555/c  
 ID AAV61555 standard; DNA; 23 BP.  
 XX  
 AC AAV61555;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
 XX  
 KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
 KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;  
 KW gene expression; internal standard; calibration curve; ss.

XX Synthetic.  
 OS Mus sp.  
 XX  
 PN EP870842-A2.  
 XX  
 PD 14-OCT-1998.  
 XX  
 PF 07-APR-1998; 98EP-0302726.  
 XX  
 PR 07-APR-1997; 97JP-0088495.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Kato K;  
 XX  
 WPI; 1998-523164/45.  
 XX  
 PT Determination of gene expression levels - using combinations of  
 PT different cDNA samples tagged with different PCR adaptors  
 XX  
 XX Example 2; Page 9; 22pp; English.

The present sequence represents a primer which was used to synthesise  
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as  
 CC primers AAV61554 and AAV61555 were added to both mouse liver-derived and  
 CC mouse kidney-derived total RNA to generate single-stranded cDNA. These

CC primers were used in the method of the invention to determine the amount  
 CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a  
 CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using  
 CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene  
 CC expression to be quantitatively determined, and because internal  
 CC standards are not required to prepare a calibration curve, it is a  
 CC quicker and less laborious process.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1099  
 Db 23 TAAAAAAAAAAAAAAAAA 7

RESULT 530  
 AAV61556/c  
 ID AAV61556 standard; DNA; 23 BP.

XX  
 AC AAV61556;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
 XX  
 KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
 KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;  
 KW gene expression; internal standard; calibration curve; ss.

XX Synthetic.  
 OS Mus sp.

XX  
 PN EP870842-A2.  
 XX  
 PD 14-OCT-1998.  
 XX  
 PF 07-APR-1998; 98EP-0302726.  
 XX  
 PR 07-APR-1997; 97JP-0088495.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Kato K;

WPI; 1998-523164/45.

Determination of gene expression levels - using combinations of  
 PT different cDNA samples tagged with different PCR adaptors

XX Example 2; Page 9; 22pp; English.

The present sequence represents a primer which was used to synthesise  
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as  
 CC primers AAV61554 and AAV61555 were added to both mouse liver-derived and  
 CC mouse kidney-derived total RNA to generate single-stranded cDNA. These  
 CC primers were used in the method of the invention to determine the amount  
 CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a  
 CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using  
 CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene  
 CC expression to be quantitatively determined, and because internal  
 CC standards are not required to prepare a calibration curve, it is a  
 CC quicker and less laborious process.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1099  
 Db 23 TAAAAAAAAAAAAAAAAA 7

RESULT 531  
 AAV61554/C  
 ID AAV61554 standard; DNA; 23 BP.  
 XX  
 AC AAV61554;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
 XX  
 DE Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
 KW apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;  
 KW gene expression; internal standard; calibration curve; ss.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 PN EP870842-A2.  
 XX  
 PD 14-OCT-1998.  
 XX  
 PF 07-APR-1998; 98EP-0302726.  
 XX  
 PR 07-APR-1997; 97JP-0088495.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Kato K;  
 XX  
 PP WPI; 1998-523164/45.  
 XX  
 DR Determination of gene expression levels - using combinations of  
 PT different cDNA samples tagged with different PCR adaptors  
 XX  
 XX Example 2; Page 9; 22pp; English.  
 XX  
 CC The present sequence represents a primer which was used to synthesise  
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as  
 CC primers AAV61555 and AAV61556 were added to both mouse liver-derived and  
 CC mouse kidney-derived total RNA to generate single-stranded cDNA. These  
 CC primers were used in the method of the invention to determine the amount  
 CC ratio between a cDNA coding for mouse liver-derived Apolipoprotein and a  
 CC cDNA that codes for the mouse kidney-derived Apolipoprotein by using  
 CC Adaptor-tagged Competitive PCR (ATAC-PCR). This method allows gene  
 CC expression to be quantitatively determined, and because internal  
 CC standards are not required to prepare a calibration curve, it is a  
 CC quicker and less laborious process.  
 XX  
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1099  
 Db 23 TAAAAAAAAAAAAAAAAA 7

RESULT 532  
 AAC62450/C  
 ID AAC62450 standard; DNA; 23 BP.  
 XX  
 AC AAC62450;  
 XX  
 DT 07-FEB-2001 (first entry)  
 XX  
 DE Cleavage of nucleic acids from solid supports assay oligonucleotide #1.

XX Nucleic acid cleavage; solid support; DNA-RNA hybrid;  
 KW affinity chromatography; sequencing; mutagenesis; DNA preparation;  
 KW nucleic acid purification; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 23  
 FT misc\_RNA /\*tag= a  
 XX  
 PN WO200058329-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 28-MAR-2000; 2000WO-GB01190.  
 XX  
 PR 29-MAR-1999; 99GB-0007245.  
 XX  
 PA (GOLD/) GOLDBOROUGH A.  
 XX  
 XX WPI; 2000-664908/64.  
 DR Detaching nucleic acid molecule comprising unconventional nucleotide  
 XX incorporated at predetermined site from a solid support involves  
 PT cleaving the nucleic acid molecule at the site of unconventional  
 PT nucleotide -  
 XX  
 PS Disclosure; Page 16; 47pp; English.  
 XX  
 CC The present invention is concerned with the cleavage of nucleic acids  
 CC from solid supports. This is carried out by adding a non-conventional  
 CC nucleotide into the nucleic acid attached to the support, so that it is  
 CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
 CC released. This is useful in many molecular biological procedures such as  
 CC sequencing, in vitro amplifications, cDNA and template preparation,  
 CC DNA-based assays, mutagenesis procedures, nucleic acid purification and  
 CC affinity chromatography. The present sequence is an oligonucleotide used  
 CC in assays to demonstrate the methods of the invention.  
 XX  
 SQ Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 533  
 AAC62451/C  
 ID AAC62451 standard; RNA; 23 BP.  
 XX  
 AC AAC62451;  
 XX  
 DT 07-FEB-2001 (first entry)  
 XX  
 DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.  
 XX  
 KW Nucleic acid cleavage; solid support; affinity chromatography;  
 KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200058329-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 28-MAR-2000; 2000WO-GB01190.  
 XX  
 PR 29-MAR-1999; 99GB-0007245.

XX PA (GOLD/) GOLDSBOROUGH A.  
 XX DR WPI; 2000-664908/64.  
 XX PT Detaching nucleic acid molecule comprising unconventional nucleotide  
 XX PT incorporated at predetermined site from a solid support involves  
 XX PT cleaving the nucleic acid molecule at the site of unconventional  
 XX PT nucleotide -  
 XX PS Example 1; Page 32; 47pp; English.  
 XX CC The present invention is concerned with the cleavage of nucleic acids  
 XX CC from solid supports. This is carried out by adding a non-conventional  
 XX CC nucleotide into the nucleic acid attached to the support, so that it is  
 XX CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
 XX CC released. This is useful in many molecular biological procedures such as  
 XX CC sequencing, in vitro amplifications, cDNA and template preparation, and  
 XX CC DNA-based assays, mutagenesis procedures, nucleic acid purification and  
 XX CC affinity chromatography. The present sequence is an oligonucleotide used  
 XX CC in assays to demonstrate the methods of the invention.  
 XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 G; 23 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 23 AAAAAAAAAAAAAAAAAA 7  
 RESULT 534  
 AAA08407/C  
 ID AAA08407 standard; DNA; 23 BP.  
 XX AC AAA08407;  
 XX DT 13-JUL-2000 (first entry)  
 XX DE Oligonucleotide primer SEQ ID NO:1.  
 XX KW Detection; primer; adapter; probe; hybridisation; gene cluster;  
 XX KW fractionation; ss.  
 XX OS Synthetic.  
 XX PN JP2000055914-A.  
 XX PD 25-FEB-2000.  
 XX PF 13-AUG-1998; 98JP-0228944.  
 XX PR 13-AUG-1998; 98JP-0228944.  
 XX PA (TAIS ) TAISHO PHARM CO LTD.  
 XX PS WPI; 2000-368733/32.  
 XX DR Gene detection method involves hybridizing probe opposite to objective  
 XX PT gene out of fractional gene cluster -  
 XX PT Example 1; Page 9; 11pp; Japanese.  
 XX PS The present invention describes a gene detection method which comprises  
 XX CC fractionating using a probe opposite to the objective gene which is  
 XX CC hybridised out of fractioned gene cluster. The objective gene detected  
 XX CC belongs to the group of objective genes contained in the sample. The  
 XX CC method is used for gene detection by fractionation of cDNA by molecular  
 XX CC index method using specific primer. It provides high detection  
 XX CC sensitivity of objective gene. AAA08407 to AAA08414 represent  
 XX CC oligonucleotides used in the exemplification of the present invention.

XX SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAAAAAAAAAAAAA 1099  
 DB 23 TAAAAAAAAAAAAAAAAA 7  
 RESULT 535  
 AAF85497/C  
 ID AAF85497 standard; DNA; 23 BP.  
 XX AC AAF85497;  
 XX DT 23-JUL-2001 (first entry)  
 XX DE PCR primer for DNA encoding Kalata B1 polypeptide fragments.  
 XX KW Kalata B2; transgenic plant; cotton; calcium channel binding; pain;  
 XX KW stroke; C5a binding; antiinflammatory; PCR primer; ss.  
 XX OS Oldenlandia affinis.  
 XX PN WO200134829-A2.  
 XX PD 17-MAY-2001.  
 XX PF 03-NOV-2000; 2000WO-AU01352.  
 XX PR 05-NOV-1999; 99AU-0003884.  
 XX PR 25-NOV-1999; 99AU-0004235.  
 XX PA (UYQU ) UNIV QUEENSLAND.  
 XX PA (UYLA-) UNIV LATROBE.  
 XX PI Craik DJ, Anderson MA, Jennings CV;  
 XX PS WPI; 2001-343607/36.  
 XX DR Novel nucleic acid molecule encoding amino acid sequence capable of  
 XX PT forming cyclic structure, for generating transgenic plants capable of  
 XX PT producing cyclic knotted protein and resistant to pathogens such as  
 XX PT insects -  
 XX PS Example 10; Fig 1B; 112pp; English.  
 XX CC PCR primers AAF85495-97 were used to amplify a DNA fragment encoding  
 XX CC Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological  
 XX CC activities. The Kalata B1 polynucleotide represents a nucleic acid  
 XX CC molecule of the invention. The specification describes nucleic acid  
 XX CC molecules which encode an amino acid sequence which is capable of being  
 XX CC cyclised within a cell or a membrane of a cell to form a cyclic backbone.  
 XX CC The amino acid sequence comprises sufficient disulfide bonds to confer  
 XX CC a stabilized folded structure on the three-dimensional structure of the  
 XX CC backbone. The nucleic acid molecules of the invention are useful for  
 XX CC producing transgenic genetically modified food or non-food crop plants,  
 XX CC in particular cotton. The peptides or proteins can be manipulated to  
 XX CC introduce modulating activity, for modulating activity of calcium  
 XX CC channel binding is useful in treatment of pain or stroke and C5a binding  
 XX CC activity useful as an antiinflammatory agent. The nucleic acid molecules  
 XX CC are useful in the generation of molecules having animal or plant  
 XX CC therapeutic properties as well as in a range of diagnostic, industrial  
 XX CC and agricultural including horticultural applications and for  
 XX CC protecting plants such as crop plants from pest and/or pathogen  
 XX CC infestation.  
 XX SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 23;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1084 AAAAAAAAAAAAAA 1100
Db 23 AAAAAAAAAAAAAA 7

RESULT 536
AAF16627/c
ID AAF16627 standard; DNA; 23 BP.
XX
AC AAF16627;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
XX
KW Gastric acid disturbance; Gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU00498.
XX
PR 24-MAY-1999; 99AU-0000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
WPI; 2001-025093/03.
XX
Treating gastric acid disturbance by administering an oligonucleotide
PT production or secretion -
XX
Example 3; Page 152; 164pp; English.
XX
The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori.
XX
SQ Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
Db 23 AAAAAAAAAAAAAA 7

RESULT 537
AAD33503
ID AAD33503 standard; DNA; 23 BP.
XX
AC AAD33503;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS13-23-0001 probe for calibration of molecular array data.
```

```
XX Molecular array; probe; ss.
KW Unidentified.
OS
XX EP1186673-A2.
PN
XX 13-MAR-2002.
PD
XX 10-SEP-2001; 2001EP-0307665.
PF
XX 11-SEP-2000; 2000US-0659173.
PR
XX (AGIL-) AGILENT TECHNOLOGIES INC.
PA
XX Wobler PK, Delenstarr GC;
PI
XX WPI; 2002-282886/33.
DR
XX Calibration of molecular array data by employing calibration probes
XX that generate signals proportional to total concentrations of labeled
XX target molecules, and molecular arrays incorporating sets of
XX calibration probes -
XX
XX Disclosure; Page 14; 32pp; English.
XX
XX The invention relates to a method for calibrating data scanned from a
XX molecular array. The method involves employing calibrations probes that
XX generate signals proportional to the total concentrations of labeled
XX target molecules to which the molecular array probes are directed over
XX an entire range of sample solutions and molecular arrays incorporating
XX sets of calibration probes. Method is useful for calibrating different
XX types of signals scanned from a molecular array, or calibrating signals
XX scanned from different molecular arrays. The present sequence is poly
XX (A) normalisation probe used in calibration of molecular array data.
XX
XX Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100
Db 1 AAAAAAAAAAAAAA 17

RESULT 538
ABL95973/c
ID ABL95973 standard; DNA; 23 BP.
XX
AC ABL95973;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe #48 for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection;
KW disease diagnosis; microbial identification; ss.
XX
XX Unidentified.
OS
XX WO200208414-A1.
PN
XX 31-JAN-2002.
PD
XX 27-JUN-2001; 2001WO-IB01147.
PF
XX 27-JUN-2000; 2000JP-0193133.
PR 03-AUG-2000; 2000JP-0236115.
PR 26-SEP-2000; 2000JP-0292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
```

PA (KANK-) KANKYO ENG CO LTD.  
 XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
 PI Yokomaku T;  
 XX WPI; 2002-195876/25.  
 DR  
 XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids  
 XX and their polymorphism and mutation, particularly useful in science and  
 PT medicine for e.g. analytical applications, disease diagnosis and  
 PT microbial identification  
 XX Disclosure; Fig 3; 152pp; Japanese.  
 XX The present invention relates to nucleic acid probes, which are useful  
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
 CC which a single-stranded oligonucleotide is labelled with a fluorescent  
 CC substance and a quencher in a manner that the fluorescence intensity of  
 CC the hybridisation reaction system is increased after completion of the  
 CC hybridisation but no stem loop structure is formed. The probes are useful  
 CC for assaying nucleic acids and their polymorphism and mutation,  
 CC particularly useful for e.g. analytical applications, disease diagnosis  
 CC and microbial identification. The present sequence was used to illustrate  
 CC the invention.  
 XX Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 TAAAAAATAAAAA 1100  
 DB 17 TAAAAAATAAAAA 1  
 RESULT 539  
 ABA99682/C  
 ID ABA99682 standard; DNA; 23 BP.  
 XX  
 AC ABA99682;  
 DT 31-MAY-2002 (first entry)  
 XX Murine osteoporosis/arthritis-rheumatism associated gene PCR primer DAPAL.  
 DE Osteoporosis; murine; treatment; arthritis-rheumatism; PCR; primer; ss.  
 KW Mus musculus.  
 OS  
 XX JP2002051782-A.  
 FN  
 XX 19-FEB-2002.  
 PD  
 XX 09-AUG-2000; 2000JP-0241413.  
 PF  
 XX 09-AUG-2000; 2000JP-0241413.  
 PR  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX WPI; 2002-288360/33.  
 DR  
 XX Preventing or treating an agent for osteoporosis or arthritis-rheumatism  
 PT  
 XX Example 2; Page 38; 44pp; Japanese.  
 PS  
 XX This invention describes a novel method for testing the effect of a  
 CC substance as a preventive or treating agent for osteoporosis or  
 CC arthritis-rheumatism. This sequence represents a PCR primer used in the  
 CC amplification of a gene encoding a protein associated with osteoporosis  
 CC or arthritis-rheumatism which is described in the disclosure of the  
 CC invention.

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAA 1099  
 DB 23 TAAAAAATAAAAA 7  
 RESULT 540  
 ABA97431/C  
 ID ABA97431 standard; DNA; 23 BP.  
 XX  
 AC ABA97431;  
 DT 21-MAR-2002 (first entry)  
 XX Glycosyltransferase genes PCR primer #2.  
 DE Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.  
 KW Unidentified.  
 OS  
 XX WO200192509-A1.  
 FN  
 XX 06-DEC-2001.  
 PD  
 XX 01-JUN-2001; 2001WO-JP04675.  
 PF  
 XX 02-JUN-2000; 2000JP-0170436.  
 PR  
 XX (ITFL-) INT FLOWER DEV PTY LTD.  
 PA  
 XX Mizutani M, Sakakibara K, Tanaka Y, Kusumi T, Ono E;  
 PI WPI; 2002-114345/15.  
 DR  
 XX New gene encoding protein that transfers a sugar to the 3' position of  
 PT anthocyanin for changing flower color -  
 PT  
 XX Example 3; Page 13; 50pp; Japanese.  
 PS  
 XX The present invention provides the genes and proteins of  
 CC glycosyltransferases from Gentiana triflora, Senecio cruentus and  
 CC Clitoria ternatea. The protein transfers a sugar to the 3' position of  
 CC anthocyanin, and can be used for changing the colour of flowers. The  
 CC present sequence is a PCR primer used to isolate glycosyltransferase  
 CC coding sequences of the invention.  
 XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAATAAAAA 1100  
 DB 23 AAAAAAATAAAAA 7  
 RESULT 541  
 AAT68615/C  
 ID AAT68615 standard; DNA; 24 BP.  
 XX  
 AC AAT68615;  
 DT 20-FEB-1998 (first entry)  
 XX DNA probe used in fingerprinting technique.  
 DE  
 XX

KW probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.  
 XX Synthetic.  
 OS  
 PN EP778351-A2.  
 XX  
 XX PD 11-JUN-1997.  
 XX  
 XX PF 26-NOV-1996; 96EP-0118921.  
 XX  
 XX PR 30-NOV-1995; 95JP-0311949.  
 XX  
 XX PA (HITA ) HITACHI LTD.  
 XX  
 XX PI Kambara H, Okano K, Uematsu C;  
 XX  
 XX PS WPI; 1997-300347/28.  
 XX  
 XX DR Nucleic acid assay methods - based on restriction fragment length  
 XX PT determination  
 XX PT  
 XX PS Example 1; Page 7; 21pp; English.  
 XX  
 XX CC The present sequence is a DNA probe used in a novel method of analysis  
 XX CC or assay for nucleotides, which comprises: (i) digesting DNA with a  
 XX CC restriction enzyme; (ii) discriminating a difference in sequences of the  
 XX CC DNA fragments obtained around the 3' termini with a DNA probe and  
 XX CC extending the DNA probe by a complementary strand synthesis to  
 XX CC fractionate the DNA fragments into groups; and (iii) measuring lengths  
 XX CC of the DNA fragments which belong to the groups, or length of the  
 XX CC extended DNA probe, and using the lengths obtained for the fragments  
 XX CC around the 3' termini as fingerprints. Where polyA is present, the  
 XX CC presence of recognition sequence GCG is critical for clarifying the  
 XX CC terminal site, this is because the length of polyA cannot be controlled.  
 XX CC The method is useful for assaying a large number of cDNA molecules or  
 XX CC DNA fragments and for assaying long DNA sequences.  
 XX  
 XX SQ Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 2 other;

Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 542  
 AAH43079/c  
 ID AAH43079 standard; DNA; 24 BP.  
 XX  
 XX AC AAH43079;  
 XX  
 XX DT 15-OCT-2001 (first entry)  
 XX  
 XX DE Nucleotide sequence of a synthetic oligonucleotide.  
 XX  
 XX KW Nucleic acid immobilisation; ss.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN WO200155365-A1.  
 XX  
 XX PD 02-AUG-2001.  
 XX  
 XX PF 24-JAN-2001; 2001WO-JP00443.  
 XX  
 XX PR 27-JAN-2000; 2000JP-0019301.  
 XX  
 XX PA (TOJO ) TOYO KOHAN CO LTD.  
 XX  
 XX PI Tanga M, Okamura H, Takagi K, Takahashi K;

XX WPI; 2001-488794/53.  
 XX  
 XX PT Support for immobilizing nucleotides -  
 XX  
 XX PS Example 1; Page 8; 18pp; Japanese.  
 XX  
 XX CC The specification describes a support for immobilizing nucleotides  
 XX CC which contributes to the efficient clarification of DNA without damaging  
 XX CC the terminal parts of the DNA. The support is a chemically treated  
 XX CC modified substrate on which oligonucleotides with restriction enzyme  
 XX CC cleavage sites are immobilised. The support is useful for immobilizing  
 XX CC nucleic acids such as DNA. The present sequence represents a synthetic  
 XX CC oligonucleotide used in the course of the invention.  
 XX  
 XX SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 23 AAAAAAAAAAAAAAAAAA 7

RESULT 543  
 AAH24266/c  
 ID AAH24266 standard; DNA; 24 BP.  
 XX  
 XX AC AAH24266;  
 XX  
 XX DT 11-SEP-2001 (first entry)  
 XX  
 XX DE Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.

XX KW Phosphatase 79; human; BAC clone CTS-54D4-encoded protein homologue;  
 XX KW recombinant production; malignant tumour; cancer; blood disease;  
 XX KW HIV infection; human immunodeficiency virus; immune disorder;  
 XX KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;  
 XX KW immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO200138385-A1.  
 XX  
 XX PD 31-MAY-2001.  
 XX  
 XX PF 20-NOV-2000; 2000WO-CN00459.  
 XX  
 XX PR 22-NOV-1999; 99CN-0124059.  
 XX  
 XX PA (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.  
 XX  
 XX PI Mao Y, Xie Y;  
 XX  
 XX PS WPI; 2001-355903/37.

Human phosphatase 79 and encoded polynucleotide, applicable in  
 diagnosis and treatment of malignant tumor, hemopathy, HIV infection,  
 immunological diseases and various inflammation -  
 Example 3; Page 12; 38pp; Chinese.

The invention relates to human phosphatase 79 (AAB73700), nucleic acids  
 encoding it (AAH24266), and a method for the recombinant production of  
 human phosphatase 79. The present invention additionally discloses an  
 agonist of phosphatase 79 for therapeutic use, and an antibody which  
 specifically binds to human phosphatase 79. Human phosphatase 79, and  
 nucleotides which encode it may be used for treating a variety of  
 diseases, such as malignant tumours, blood diseases, HIV (human  
 immunodeficiency virus) infection, immune disorders and inflammatory  
 conditions. The protein may also be used to screen for modulators of its

CC activity or for peptide fingerprinting identification. The polynucleotide  
CC can be used as a primer for nucleic acid amplification reaction or as a  
CC probe for hybridisation reactions, or in producing gene chips or  
CC microarrays. Sequences AAH24265-AAH24266 represent reverse  
CC transcription-PCR (RT-PCR) primers used in an exemplification of the  
CC invention to isolate human phosphatase 79 cDNA.  
XX  
SQ Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 other;  
  
Query Match 1.5%; Score 17; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 24 AAAAAAAAAAAAAAAAAA 8  
  
RESULT 544  
ABQ79878/c  
ID ABQ79878 standard; DNA; 24 BP.  
XX  
AC ABQ79878;  
XX  
DT 23-DEC-2002 (first entry)  
DE Nucleotide sequence of a PCR primer #8.  
XX  
KW Polymerase chain reaction; thermal cycle; immobilisation;  
KW genetic engineering; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP2002191369-A.  
XX  
PD 09-JUL-2002.  
XX  
PF 27-DEC-2000; 2000JP-0399573.  
XX  
PR 27-DEC-2000; 2000JP-0399573.  
XX  
PA (TOJO ) TOYO KOHAN CO LTD.  
PA (TAKA) TAKAHASHI K.  
XX  
DR WPI; 2002-630904/68.  
XX  
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by  
PT using a substrate on which a DNA is immobilized used in medical,  
PT biochemical, molecular biological and gene engineering fields -  
XX  
PS Examples; Page 10; 13pp; Japanese.  
XX  
CC The invention relates to performing a thermal cycle of PCR by using a  
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
CC method is useful in the medical, biochemical, molecular biological and  
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
CC used in the method of the invention.  
XX  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 other;  
  
Query Match 1.5%; Score 17; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 23 AAAAAAAAAAAAAAAAAA 7  
  
RESULT 545  
ABK86172/c  
ID ABK86172 standard; DNA; 24 BP.  
XX

AC ABK86172;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Oligo dT primer #4 used in method to study gene expression.  
XX  
KW Oligo dT primer; gene expression analysis; primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO200236828-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 01-NOV-2001; 2001WO-US45401.  
XX  
PR 01-NOV-2000; 2000US-244933P.  
XX  
PA (GENO-) GENOMIC SOLUTIONS INC.  
XX  
PI Kane MD, Dombkowski AA, Nagel AC;  
XX  
DR WPI; 2002-508123/54.  
XX  
PT Identifying and characterizing gene expression in samples, for  
PT identifying mRNAs expressed at different levels, comprises employing an  
PT identifier having an oligo-dT primer of a specific sequence and a  
PT detectable marker at its 5' end -  
XX  
PS Example 1; Page 15; 45pp; English.  
XX  
CC The invention relates to systems for identification and characterisation  
CC of gene expression in one or more samples, comprising an identifier having  
CC a specific oligo-dT primer sequence, where the identifier comprises a  
CC detectable marker at its 5' end. The system is useful for identifying any  
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well  
CC as the relative differences in mRNA between 2 or more samples, where  
CC desired, for supporting discovery of new genes, and for identifying mRNAs  
CC that are expressed at different levels between 2 or more samples. The new  
CC system or method addresses limitations of prior methods by comprising  
CC compositions and systems that incorporate new strategies where molecular  
CC or biochemical assay compositions and systems are linked to DNA or RNA  
CC sequence databases for optimal resource efficiency in assaying gene  
CC expression. The system has the following advantages over existing  
CC methods: (a) prior sequence information or clone library construction is  
CC not needed to enable the assay; (b) provides immediate sequence  
CC information in addition to information concerning changes or differences  
CC in mRNA level, to determine mRNA expression level and mRNA identification  
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the  
CC sample for subsequent investigation by common molecular biology  
CC techniques; and (d) does not require prior knowledge of the sequence of  
CC the genome of the organism under investigation and can be employed in  
CC organisms lacking significant genomic sequence information. The present  
CC invention represents an oligo dT primer used in the method of the  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 4 other;  
  
Query Match 1.5%; Score 17; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 24 AAAAAAAAAAAAAAAAAA 8  
  
RESULT 546  
ABN85073/c  
ID ABN85073 standard; DNA; 24 BP.  
XX  
AC ABN85073;  
XX



DT 05-SEP-2002 (first entry)  
 XX Human S4 ribosomal protein 13.97 PCR primer #2.  
 DE  
 XX  
 XX Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;  
 KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;  
 KW PCR; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX CN1333268-A.  
 PN  
 XX  
 XX 30-JAN-2002.  
 PD  
 XX  
 XX 07-JUL-2000; 2000CN-0117077.  
 PF  
 XX  
 XX 07-JUL-2000; 2000CN-0117077.  
 PR  
 XX  
 XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
 PA  
 XX  
 XX Mao Y, Xie Y;  
 PI  
 XX  
 XX WPI; 2002-292916/34.  
 DR  
 XX  
 XX Human S4 ribosomal protein 13.97 polypeptide and encoding  
 PT polynucleotide, useful for treating malignant tumor, inflammation,  
 PT hemopathy, human immunodeficiency virus infection, immunological  
 PT disease and inflammation -  
 PT  
 XX  
 XX Example 2; Page 16 (Disclosure); 33pp; Chinese.  
 PS  
 XX  
 XX The present invention relates to human S4 ribosomal protein 13.97 (see  
 CC ABB83379). The ribosomal protein and its coding sequence are useful  
 CC for treating malignant tumours, haemopathy, HIV infection, immunological  
 CC diseases and various inflammations. The present sequence is a PCR primer,  
 CC which was used in an example from the invention.  
 CC  
 XX  
 XX Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 24 AAAAAAAAAAAAAA 8  
 RESULT 547  
 AAD33505  
 ID AAD33505 standard; DNA; 24 BP.  
 XX  
 XX AAD33505;  
 AC  
 XX  
 XX 01-JUL-2002 (first entry)  
 DT  
 XX  
 XX T7718Apad\_PS12-24-0001 probe for calibration of molecular array data.  
 DE  
 XX  
 XX Molecular array; probe; ss.  
 KW  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX EP1186673-A2.  
 PN  
 XX  
 XX 13-MAR-2002.  
 PD  
 XX  
 XX 10-SEP-2001; 2001EP-0307665.  
 PF  
 XX  
 XX 11-SEP-2000; 2000US-0659173.  
 PR  
 XX  
 XX (AGIL-) AGILENT TECHNOLOGIES INC.  
 PA  
 XX  
 XX Wobler PK, Delenstarr GC;  
 PI

XX WPI; 2002-282886/33.  
 DR  
 XX  
 XX Calibration of molecular array data by employing calibration probes  
 PT that generate signals proportional to total concentrations of labeled  
 PT target molecules, and molecular arrays incorporating sets of  
 PT calibration probes -  
 PT  
 XX  
 XX Disclosure; Page 14; 32pp; English.  
 PS  
 XX  
 XX The invention relates to a method for calibrating data scanned from a  
 CC molecular array. The method involves employing calibrations probes that  
 CC generate signals proportional to the total concentrations of labelled  
 CC target molecules to which the molecular array probes are directed over  
 CC an entire range of sample solutions and molecular arrays incorporating  
 CC sets of calibration probes. Method is useful for calibrating different  
 CC types of signals scanned from a molecular array, or calibrating signals  
 CC scanned from different molecular arrays. The present sequence is poly  
 CC (A) normalisation probe used in calibration of molecular array data.  
 CC  
 XX  
 XX Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 other;  
 SQ  
 Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 DB 1 AAAAAAAAAAAAAA 17  
 RESULT 548  
 ABL55130/C  
 ID ABL55130 standard; DNA; 24 BP.  
 XX  
 XX ABL55130;  
 AC  
 XX  
 XX 31-MAY-2002 (first entry)  
 DT  
 XX  
 XX Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.  
 DE  
 XX  
 XX Human; gonadotropin-releasing hormone 10; recombinant production;  
 KW cancer; HIV infection; human immunodeficiency virus; gene therapy;  
 KW cytostatic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.  
 KW  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX CN1325900-A.  
 FN  
 XX  
 XX 12-DEC-2001.  
 PD  
 XX  
 XX 31-MAY-2000; 2000CN-0116266.  
 PF  
 XX  
 XX 31-MAY-2000; 2000CN-0116266.  
 PR  
 XX  
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 PA  
 XX  
 XX Mao Y, Xie Y;  
 PI  
 XX  
 XX WPI; 2002-196660/26.  
 DR  
 XX  
 XX Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide  
 PT encoding it -  
 PT  
 XX  
 XX Example 2; Page 17 (Disclosure); 32pp; Chinese.  
 PS  
 XX  
 XX The invention relates to human gonadotropin-releasing hormone 10  
 CC (AAM49158) and to nucleic acids encoding it (ABL55128). The protein has  
 CC a molecular weight of 10 kD. The invention also relates to a method for  
 CC the recombinant production of the protein, an antagonist of the protein,  
 CC and the use of the protein, gene and antagonist in therapeutic  
 CC applications. Gonadotropin-releasing hormone 10 can be used in the  
 CC treatment of a variety of diseases such as cancer and HIV (human

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CC immunodeficiency virus) infection. Sequences ABL55129-ABL55130 represent  
 CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of  
 CC the invention to isolate human gonadotropin-releasing hormone 10 cDNA.  
 XX  
 SQ Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAA 1100  
 Db 19 AAAAAAAAAAAAAAAA 3  
 RESULT 549  
 ABX79809/C  
 ID ABX79809 standard; cDNA; 24 BP.  
 XX  
 AC ABX79809;  
 XX  
 DT 17-APR-2003 (first entry)  
 XX  
 DE EST polymorphic DNA repeat polynucleotide #134.  
 XX  
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6472154-B1.  
 XX  
 PD 29-OCT-2002.  
 XX  
 PF 31-DEC-1999; 99US-0475947.  
 XX  
 PR 31-DEC-1999; 99US-0475947.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Garner HR, Wren JD, Minna JD, Fondon JW;  
 XX  
 DR WPI; 2003-208818/20.  
 XX  
 PT Identifying a candidate polymorphic repeat within a coding sequence,  
 PT for understanding or treating genetic disease, comprises detecting  
 PT tandem repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability -  
 XX  
 PS Examples; Column 579; 588pp; English.  
 XX  
 CC The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs.  
 XX  
 SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAA 1100  
 Db 23 AAAAAAAAAAAAAAAA 7  
 RESULT 550  
 AAZ37719  
 ID AAZ37719 standard; DNA; 20 BP.  
 XX  
 AC AAZ37719;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #249.  
 XX  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;  
 KW cancer; antisense; modulation; oligonucleotide; expression;  
 KW inhibition; hyperproliferation; blood cancer; brain cancer;  
 KW breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;  
 KW atherosclerosis; restenosis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9949065-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US06702.  
 XX  
 PR 26-MAR-1998; 98US-0048810.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;  
 XX  
 DR WPI; 1999-610754/52.  
 XX  
 PT New antisense compounds used to treat eg. hyperproliferative conditions  
 PT -  
 XX  
 PS Example 9; Page 54; 157pp; English.  
 XX  
 CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.  
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the  
 CC exemplification of the present invention. The present invention  
 CC describes novel nucleotide antisense compounds, targeted to the 5',  
 CC untranslated, translation termination codon, or 3' untranslated region  
 CC of a nucleic acid encoding human mdm2, that modulates expression of  
 CC human mdm2. The oligonucleotides mediate their effect by antisense  
 CC inhibition of hyperproliferative gene expression. The antisense compound  
 CC is used to treat an animal having a disease or condition associated  
 CC with mdm2, particularly a hyperproliferative condition, more  
 CC particularly cancer, especially of the blood, brain, breast, lung or soft  
 CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.  
 XX  
 SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;  
 Query Match 1.5%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 996 AGCTGAGCGTGGAGATGG 1015  
 Db 1 AGGCTGAGCGAGGAGATGG 20  
 RESULT 551  
 AAS29488

AA29488 standard; DNA; 20 BP.  
AA29488;  
21-NOV-2001 (first entry)  
Human mdm2 antisense oligonucleotide 31623.  
Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
atherosclerosis; tumour; cytostatic; anti psoriatic;  
anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.  
Homo sapiens.  
Key Location/Qualifiers  
modified\_base 1..20  
/\*tag= a  
/mcd\_base= OTHER  
/note= "OTHER= All phosphorothioate linkages,  
additionally bases 1-6 and bases 15-20 are  
2'-O-methoxyethyl bases, and bases 7-14 are  
deoxynucleotides"  
US2001016575-A1.  
23-AUG-2001.  
02-JAN-2001; 2001US-0752983.  
26-MAR-1999; 99US-0280805.  
26-MAR-1998; 98US-0048810.  
(MIRA/) MIRAGLIA L J.  
(NERO/) NERO P.  
(GRAH/) GRAHAM M J.  
(MONI/) MONIA B P.  
(COWS/) COWSERT L M.  
Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;  
WPI; 2001-535565/59.  
An antisense compound, useful for treating e.g. cancer, comprises  
nucleobases targeted a region (e.g. translation termination codon  
region) of a nucleic acid encoding human mdm2 -  
Example 9; Page 18; 81pp; English.  
The present invention relates to antisense compounds, 8-30 nucleobases  
in length targeted to the 5' untranslated region, translation  
termination codon region, 3' untranslated region, coding region or  
translation start site of a nucleic acid encoding human mdm2, where  
the antisense compound modulates the expression of human mdm2. The  
antisense oligonucleotides of the invention are useful for encoding  
human mdm2 and for inhibiting the expression of human mdm2. They may be  
used for treating an animal having a disease or condition associated  
with amplification of mdm2 gene or overexpression of mdm2 e.g. a  
hyperproliferative disorder such as cancer (blood, brain, breast, lung,  
or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or  
restenosis, tumours, colorectal carcinoma and chronic myelogenous  
leukemia. The antisense compound may be administered with a  
chemotherapeutic agent to overcome drug resistance. The antisense  
compound reduces hyperproliferation of human cells. The method, which  
involves the use of the antisense compound, is also useful for detecting  
the role of mdm2 expression in various cell functions and physiological  
processes and useful in both clinical research and diagnostic tools.  
AA29242-AA29507 represent the human mdm2 antisense oligonucleotides  
of the present invention.  
Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;  
Query Match 1.5%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 996 AGTCTGAGGCTGGAGATGG 1015  
DB 1 AGGCTGAGGAGGAGATGG 20  
RESULT 552  
AAF83959/c  
ID AAF83959 standard; DNA; 20 BP.  
XX  
AC AAF83959;  
XX  
DT 06-AUG-2001 (first entry)  
XX  
DE BAP28 gene fragment amplifying primer BAP28polyTcourt.  
XX  
KW BAP28; prostate; tumour; cancer; diagnostic; genetic analysis;  
KW PCTA-1; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200100669-A2.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-IB01183.  
XX  
PR 25-JUN-1999; 99US-0141323.  
PR 18-JAN-2000; 2000US-0176880.  
XX  
PA (GEST ) GENSET.  
XX  
PI Barry C, Bougueleret L, Chumakov I, Cohen-Akenine A;  
XX WPI; 2001-367032/38.  
XX  
PT New BAP28 polynucleotides and polypeptides overexpressed in prostate  
PT cancer cells for diagnosing prostate tumors, e.g. by hybridization or  
PT polymerase chain reaction assays -  
XX  
PS Examples; Page 347; 349pp; English.  
XX  
CC The invention is directed to BAP28 polypeptides, BAP28 polynucleotide  
CC sequences and regulatory region located at the 3' and 5' ends of the  
CC BAP28 coding region. The BAP28 polypeptides can be expressed by standard  
CC recombinant methodology. BAP28 polynucleotides and polypeptides have been  
CC found to be over expressed in prostate tumour cells, therefore levels of  
CC BAP28 expression and/or activity may be assayed (e.g. by polymerase chain  
CC reaction (PCR)) to diagnose patient suffering from or susceptible to  
CC prostate cancer. Antibodies specific for the BAP28 polypeptides are  
CC useful as diagnostic reagents. Biallelic markers of the BAP28 gene are  
CC useful in genetic analysis. Sequences AAF83934-963 represent primers for  
CC the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on  
CC the opposite of the coding strand of BAP28).  
XX  
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;  
Query Match 1.5%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1080 TATTAAAAA 1099  
DB 20 TATACAAAAA 1  
RESULT 553  
AAF80873  
ID AAF80873 standard; DNA; 20 BP.  
XX  
AC AAF80873;  
XX

DT 02-MAY-2001 (first entry)  
 DE Human mdm2 phosphorothioate oligonucleotide #247.  
 DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
 KW Homo sapiens.  
 OS US6184212-B1.  
 XX 06-FEB-2001.  
 XX 26-MAR-1999; 99US-0280805.  
 XX 26-MAR-1998; 98US-0048810.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;  
 XX WPI; 2001-190948/19.  
 XX Novel antisense compound 8-30 nucleobases in length targeted to a  
 XX nucleic acid molecule encoding human mdm-2 useful for modulating the  
 XX expression of human mdm-2 and reducing hyperproliferation of human  
 XX cells -  
 XX Example 9; Column 31; 77pp; English.  
 XX The present invention relates to an antisense compound 8-30  
 XX nucleobases in length targeted to nucleobases 1-308 of the  
 XX 5' untranslated region, 1776-1806 of the translation termination  
 XX codon region or 1818-2370 of the 3' untranslated region of a  
 XX nucleic acid molecule encoding human mdm-2. The invention is  
 XX useful for reducing hyperproliferation of human cells,  
 XX modulating the expression of mdm2 in human cells or tissues  
 XX or in vitro. The hyperproliferative disorder includes cancer or  
 XX psoriasis.  
 XX Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 other;  
 XX  
 XX Query Match 1.5%; Score 16.8; DB 1; Length 20;  
 XX Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 996 AGTCTGAGCTGAGAAATGG 1015  
 DB 1 AGGCTGAGCGAGGAGAAATGG 20  
 XX  
 XX RESULT 554  
 XX AAS97833  
 XX ID AAS97833 standard; DNA; 20 BP.  
 XX AC AAS97833;  
 XX 12-MAR-2002 (first entry)  
 XX Murine SAC1 gene-specific oligonucleotide PCR primer #400.  
 XX Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;  
 XX obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;  
 XX blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;  
 XX protein replacement therapy.  
 XX Mus sp.  
 XX WO200183749-A2.  
 XX 08-NOV-2001.  
 XX 25-APR-2001; 2001WO-US13387.  
 XX 25-APR-2001; 2001WO-US13387.  
 XX 28-APR-2000; 2000US-200794P.  
 XX 28-JUL-2000; 2000US-221419P.

PR 28-APR-2000; 2000US-200794P.  
 PR 28-JUL-2000; 2000US-221419P.  
 PR 10-NOV-2000; 2000US-247443P.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX (MONE-) MONELL CHEM SENSES CENT.  
 XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;  
 XX Ohmen JD, Reed DR, Ross D, Tordoff MG;  
 XX WPI; 2002-075162/10.  
 XX Novel isolated polypeptide comprising variant form of mouse or human  
 XX SAC1 polypeptide, and is associated with altered preference for  
 XX carbohydrates or other sweeteners, useful for preventing obesity,  
 XX diabetes, alcoholism -  
 XX Claim 14; Page 89; 239pp; English.  
 XX The invention relates to an isolated polypeptide, comprising a variant  
 XX form of mouse or human SAC1 polypeptide. The variant form is associated  
 XX with altered preference for carbohydrates, other sweeteners or ethanol.  
 XX The polypeptide and its associated DNA sequence can be produced by  
 XX recombinant techniques and is useful for preventing obesity, diabetes or  
 XX alcoholism associated with SAC1 expression. The sequences are useful in  
 XX screening for drugs and sweeteners. Recombinant cell lines and transgenic  
 XX embryos may be used in screening for and identifying agents that induce  
 XX or repress function of SAC1. Predisposition to diabetes, obesity or  
 XX alcoholism can be ascertained by testing any fluid or tissue of a human  
 XX (such as blood, pancreas or tongue) for sequence variations of the SAC1  
 XX gene. A sequence variation of the SAC1 locus may indicate a  
 XX predisposition to diabetes, obesity and/or alcoholism and may provide a  
 XX diagnostic mark. The polynucleotide can be detected in a biological  
 XX sample by contacting the DNA with a probe to form a hybridisation complex  
 XX which is then detected. The sequences represent cDNA encoding human and  
 XX mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes.  
 XX Sequence 20 BP; 7 A; 0 C; 10 G; 3 T; 0 other;  
 XX  
 XX Query Match 1.5%; Score 16.8; DB 1; Length 20;  
 XX Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1000 TGAGGCTGGAGAAATGGGAG 1019  
 DB 1 TGAGGCTGGAGAAATGGGAG 20  
 XX  
 XX RESULT 555  
 XX AAS97860/C  
 XX ID AAS97860 standard; DNA; 20 BP.  
 XX AC AAS97860;  
 XX 12-MAR-2002 (first entry)  
 XX Murine SAC1 gene-specific oligonucleotide PCR primer #427.  
 XX Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;  
 XX obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;  
 XX blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;  
 XX protein replacement therapy.  
 XX Mus sp.  
 XX WO200183749-A2.  
 XX 08-NOV-2001.  
 XX 25-APR-2001; 2001WO-US13387.  
 XX 28-APR-2000; 2000US-200794P.  
 XX 28-JUL-2000; 2000US-221419P.

PR 10-NOV-2000; 2000US-247443P.  
XX (WARN ) WARNER LAMBERT CO.  
PA (MONE-) MONELL CHEM SENSES CENT.  
XX  
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;  
PI Ohmen JD, Reed DR, Ross D, Tordoff MG;  
XX WPI; 2002-075162/10.  
XX Novel isolated polypeptide comprising variant form of mouse or human  
PT SACL polypeptide, and is associated with altered preference for  
PT carbohydrates or other sweeteners, useful for preventing obesity,  
PT diabetes, alcoholism -  
XX Claim 14; Page 90; 239pp; English.  
XX The invention relates to an isolated polypeptide, comprising a variant  
CC form of mouse or human SACL polypeptide. The variant form is associated  
CC with altered preference for carbohydrates, other sweeteners or ethanol.  
CC The polypeptide and its associated DNA sequence can be produced by  
CC recombinant techniques and is useful for preventing obesity, diabetes or  
CC alcoholism associated with SACL expression. The sequences are useful in  
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic  
CC embryos may be used in screening for and identifying agents that induce  
CC or repress function of SACL. Predisposition to diabetes, obesity or  
CC alcoholism can be ascertained by testing any fluid or tissue of a human  
CC (such as blood, pancreas or tongue) for sequence variations of the SACL  
CC gene. A sequence variation of the SACL locus may indicate a  
CC predisposition to diabetes, obesity and/or alcoholism and may provide a  
CC diagnostic mark. The polynucleotide can be detected in a biological  
CC sample by contacting the DNA with a probe to form a hybridisation complex  
CC which is then detected. The sequences represent cDNA encoding human and  
CC mouse SACL polypeptides and PCR primers specific for the SACL genes.  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 0 G; 7 T; 0 other;  
Query Match 1.5%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1000 TGAGGCTGGAGATGGGAAG 1019  
Db 20 TGAGGCTGGAGATGGGAAG 1  
RESULT 556  
AAZ26500  
ID AAZ26500 standard; DNA; 21 BP.  
XX  
AC AAZ26500;  
XX  
DT 30-NOV-1999 (first entry)  
XX Human polymorphic region 689.  
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX cell viability; loss of heterozygosity; precancerous condition; ASI;  
XX allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO9841648-A2.  
XX  
XX 24-SEP-1998.  
XX  
XX 19-MAR-1998; 98WO-US05419.  
XX  
XX 20-MAR-1997; 97US-0041057.  
XX

PA (VARI-) VARIAGENICS INC.  
XX Housman D, Ledley FD, Stanton VP;  
XX WPI; 1998-521232/44.  
XX Identifying target genes for allele-specific drugs - used for  
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic  
PT plaque, dysplastic lesions, endometriosis or graft versus host disease  
XX Disclosure; Figure 7; 605pp; English.  
XX This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is  
CC active on a gene vital for cell growth or viability, and where the gene  
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to an allele of a first essential  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can  
CC be used in the diagnosis, prevention and treatment of LOH disorders,  
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or  
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney  
CC disease, and graft versus host disease. The method can also be used to  
CC remove malignant cells from bone marrow transplants. AA225812-226825  
CC represent human polymorphic sites described in the method of the  
CC invention.  
XX  
SQ Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 other;  
Query Match 1.5%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1078 ACTATTAAAAA 1097  
Db 2 ACITTCAAAAA 21  
RESULT 557  
AAH88803/c  
ID AAH88803 standard; DNA; 21 BP.  
XX  
AC AAH88803;  
XX  
DT 27-FEB-2002 (first entry)  
XX Human polymorphic oligonucleotide Y12855 fragment #5.  
XX Human; single nucleotide polymorphic; SNP; forensic science;  
XX paternity testing; phenotypic trait; genetic mapping; animal breeding;  
XX plant breeding; ds.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Variation replace(11,a)  
XX /\*tag= a  
XX /standard\_name= "single nucleotide polymorphism"  
XX  
XX WO200134840-A2.  
XX  
XX 17-MAY-2001.  
XX  
XX 10-NOV-2000; 2000WO-US30766.  
XX  
XX 10-NOV-1999; 99US-0164596.  
XX (GLAX ) GLAXO GROUP LTD.  
XX

PA (AFFY-) AFFYMETRIX INC.

XX Au K, Chen J, Patil N, Thomas D;

XX WPI; 2001-335945/35.

XX New polymorphic sites derived from the human genome are useful to  
PT determine sites correlating with phenotypic traits, particularly  
PT disease, and also in forensics and paternity testing.

XX Claim 27; Page 7; 43pp; English.

XX The present invention relates to human oligonucleotides comprising a  
CC single nucleotide polymorphic site (SNP: AAH897-AAH9219). The present  
CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
CC forensics, paternity testing, correlation of polymorphisms with  
CC phenotypic traits, genetic mapping of phenotypic traits and marker  
CC assisted breeding of animals and crop plants.

SQ Sequence 21 BP; 3 A; 9 C; 4 G; 5 T; 0 other;

Query Match 1.5%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 2.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 956 GCTGGGCGAGGTGGCAGT 975

DB 21 GCTGGGCGAGGTGGCAAAGT 2

RESULT 558

AAA64547/C

ID AAA64547 standard; DNA; 23 BP.

XX AC AAA64547;

XX 02-JAN-2001 (first entry)

XX Nucleotide sequence of a donor site of human FEZ1 gene.

XX Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein EF1-gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; ss.

XX Homo sapiens.

XX WO2000050565-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US04950.

XX 25-FEB-1999; 99US-0121537.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Croce CM, Ishii H;

XX WPI; 2000-558396/51.

XX New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer -

XX Example 1; Page 103; 255pp; English.

XX AAA64539-50 represent donor and acceptor sites of the human FEZ1 gene.  
CC FEZ1 is a tumour suppressor gene, located at chromosome location  
CC 8p22. Decreased or no expression of FEZ1 is detected in a variety  
CC of cancer cells. Expression of FEZ1 inhibits tumour growth and  
CC proliferation. FEZ1 also interacts with tubulin, with microtubules,

CC and with protein EF1-gamma. Post-translational phosphorylation and  
CC dephosphorylation modulates the effect of the FEZ1 protein.

CC Inhibitors of FEZ1 gene expression are useful for inducing cells to  
CC proliferate. Compounds which modulate FEZ1 association with tubulin  
CC are useful for alleviating tubulin hyper- or hypo-polymerisation  
CC disorders, such as those associated with aberrant initiation of  
CC mitosis, modulation of the initiation and rate of cell proliferation  
CC and cell growth, modulation of cell shape, cell rigidity, cell  
CC motility, rate and stage of cellular DNA replication, intracellular  
CC distribution of organelles, metastatic potential of cell and cellular  
CC transformation from a non-cancerous to cancerous phenotype. Compounds  
CC which modulate FEZ1 binding and phosphorylation are also useful for  
CC alleviating a disorder, such as tumorigenesis, tumour survival, growth  
CC and metastasis.

SQ Sequence 23 BP; 6 A; 4 C; 10 G; 3 T; 0 other;

Query Match 1.5%; Score 16.8; DB 1; Length 23;

Best Local Similarity 90.0%; Pred. No. 2.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 404 CCTGCTCAGCAGCTCTCC 423

DB 21 CCTGCTCAGCAGCTTCACC 2

RESULT 559

AAV06320/C

ID AAV06320 standard; DNA; 24 BP.

XX AC AAV06320;

XX 06-MAY-1998 (first entry)

XX Human prolyl 4-hydroxylase alpha subunit amplifying 3' primer.

XX Collagen; human; recombinant; post-translational enzyme; procollagen;  
KW prolyl 4-hydroxylase alpha subunit; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9738710-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-US07300.

XX 12-APR-1996; 96US-0631336.

XX (FIFI-) ACAD FINLAND.

XX (FIBR-) FIBROGEN INC.

XX Kivirikki KI, Pihlajaniemi T;

XX WPI; 1997-526203/48.

XX Recombinant production of (pro)collagen having correct folding -  
PT using vectors encoding collagen subunit and collagen  
PT post-translational enzyme respectively

XX Example 10; Page 57; 90pp; English.

XX This primer is used to mutate a plasmid pBS(SK-) by PCR by introducing a  
CC NotI site upstream of the initiation codon for human prolyl 4-hydroxylase  
CC alpha subunit. This is used in the construction of recombinant vectors  
CC containing collagen modifying enzymes. A novel method for producing a  
CC (pro)collagen polypeptide comprises culturing a host cell, where the host  
CC cell has been infected, transfected or transformed with a first  
CC expression vector comprising a polynucleotide molecule having a nucleic  
CC acid sequence which encodes a (pro)collagen subunit and a second  
CC expression vector comprising a polynucleotide molecule having a nucleic  
CC acid sequence which encodes at least one (pro)collagen post-translational

Query Match 1.5%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.4e+02;





KW hydrophobic protective group; deprotection; ds.  
 XX Synthetic.  
 OS JP2000342265-A.  
 XX  
 PN 12-DEC-2000.  
 XX  
 PD 02-JUN-1999; 99JP-0154374.  
 XX  
 PF 02-JUN-1999; 99JP-0154974.  
 XX  
 PR (TOAG ) TOA GOSEI CHEM IND LTD.  
 XX  
 PA WPI; 2001-268251/28.  
 XX  
 DR A process for purification of oligonucleotides using liquid  
 XX chromatography -  
 PT  
 PT Example 1; Page 4; 13pp; Japanese.  
 XX  
 PS The present sequence is an oligonucleotide provided in a specification  
 XX relating to the simplified purification of oligonucleotides by  
 CC liquid chromatography. The process comprises:  
 CC (a) pouring oligonucleotides protected with a hydrophobic group and  
 CC oligonucleotide with no protective group into a liquid chromatography  
 CC column packed with an acid and alkali resistant packing agent, such  
 CC as polystyrene resin;  
 CC (b) pouring a mixed developing solvent composed of a buffer made from a  
 CC volatile salt and a water soluble organic solvent at a suitable  
 CC concentration gradient into the column;  
 CC (c) pouring an acid, particularly 6-16 v/v% acetic acid, into the column  
 CC to deprotect the oligonucleotides protected with the hydrophobic group;  
 CC (d) pouring a mixed developing solvent composed of a buffer made from a  
 CC volatile salt, particularly 0.05-0.5 N aqueous ammonium  
 CC hydrogencarbonate solution adjusted at pH 8-10, and a water soluble  
 CC organic solvent at a suitable concentration gradient to elute the  
 CC deprotected oligonucleotides; and  
 CC (e) removal of the solvent and the salt from the eluted  
 CC oligonucleotides.  
 XX  
 SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 other;  
 XX  
 Query Match 1.5%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1083 TAAAAAAGAAAAA 1100  
 DB 1 TAAAAAAGAAAAA 18  
 RESULT 565  
 ABA05916/c  
 ID ABA05916 standard; DNA; 20 BP.  
 XX  
 AC ABA05916;  
 XX  
 DT 05-MAR-2002 (first entry)  
 XX  
 DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.  
 XX  
 KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;  
 XX PCR primer; ss.  
 OS Hepatitis B virus.  
 XX  
 PN EP1152063-A1.  
 XX  
 PD 07-NOV-2001.  
 XX  
 PF 03-MAY-2000; 2000EP-0109436.  
 XX

PR 03-MAY-2000; 2000EP-0109436.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Schroeder KH, Koike K;  
 XX  
 DR WPI; 2002-068256/10.  
 XX  
 PS Diagnosing hepatitis B virus (HBV) infection stages and determining the  
 XX risk for hepatocellular carcinoma, comprises identifying full length  
 PT HBV transcripts and truncated HBV transcripts in a serum sample -  
 PT  
 XX Example 1; Page 6; 25pp; English.  
 XX  
 PS The invention relates to diagnosis of hepatitis B virus (HBV) infection  
 CC stages comprising identification of full length HBV transcripts (I) and  
 CC truncated HBV transcripts (II) in a serum sample, where the ratio of  
 CC I:II is indicative of a particular infection stage. The method is useful  
 CC for diagnosing HBV infection stages and determining the risk for  
 CC developing hepatocellular carcinoma. The present sequence is that of a  
 CC HBV diagnostic PCR primer, useful for the invention.  
 XX  
 SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 other;  
 XX  
 Query Match 1.5%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2.7e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTAATAAATAAATAAATAA 1099  
 DB 18 TTAATAAATAAATAAATAA 1  
 RESULT 566  
 AAX23577/c  
 ID AAX23577 standard; DNA; 23 BP.  
 XX  
 AC AAX23577;  
 XX  
 DT 18-JUN-1999 (first entry)  
 XX  
 DE Deletion sequence oligonucleotide 30.  
 XX  
 KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;  
 XX probe; cellular adhesion modulator; cellular proliferation modulator;  
 XX human retrovirus; human immunodeficiency virus; non-human retrovirus;  
 XX HIV; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9911820-A1.  
 XX  
 PD 11-MAR-1999.  
 XX  
 PF 01-SEP-1998; 98WO-US18084.  
 XX  
 PR 02-SEP-1997; 97US-0923771.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Chen D, Srivatsa GS;  
 XX  
 DR WPI; 1999-205198/17.  
 XX  
 PS New compositions comprising sensor arrays made up of unique probe  
 PT oligonucleotides - useful for characterizing a sample of target  
 PT deletion oligonucleotides  
 XX  
 PS Example 9; Page 99; 163pp; English.  
 XX  
 CC This invention describes a novel composition comprising a number of  
 CC sensor arrays, where each array comprises a unique probe  
 CC oligonucleotide, which is the reverse complement of part of a unique

CC target oligonucleotide present in a mixture of target deletion sequence  
 CC oligonucleotides. The compositions form a method for characterizing a  
 CC sample of target deletion oligonucleotides which are labelled and  
 CC hybridize with the probe oligonucleotides of the sensor arrays. Such  
 CC oligonucleotides and their targets are represented in AAX23548-X23709.  
 CC Oligonucleotides characterized by the method form pharmaceutical  
 CC compositions that are useful for modulating cellular adhesion or  
 CC proliferation, and being active against a eukaryotic pathogen, a human  
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human  
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory  
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable  
 CC characterization of deletion sequence oligonucleotides having related,  
 CC but different nucleobase sequences, and quantification of different  
 CC species of deletion sequence ("target") oligonucleotides in a mixture.  
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence  
 CC for its reverse complement is not modified, the method may be performed  
 CC using oligodeoxynucleotides.

SQ Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;  
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAA 1099  
 |||||  
 DB 18 TTCAAAAAAAAAAAAAA 1

RESULT 567  
 AAA29753/c  
 ID AAA29753 standard; DNA; 23 BP.

XX AC AAA29753;

XX DT 15-AUG-2000 (first entry)

XX DE Synthetic oligonucleotide #1.

XX KW Primer; destabilise non-specific duplex formation; PCR; detection;  
 XX purification; sequencing; genetic marker; RACE; DNA synthesis; ss.  
 XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX modified\_base 8 /\*tag= a  
 FT /\*mod\_base= i  
 FT /\*note= "inosine"  
 FT modified\_base 18 /\*tag= b  
 FT /\*mod\_base= i  
 FT /\*note= "inosine"

XX WO200020630-A1.

XX PD 13-APR-2000.

XX PF 06-OCT-1999; 99WO-CA00933.

XX PR 07-OCT-1998; 98CA-2246623.

XX PA (UYMC-) UNIV MCGILL.

XX PI Pelletier J, Das M;

XX DR WPI; 2000-328943/28.

XX PT Novel method of stabilizing duplex formation, or destabilizing  
 XX non-specific duplex formation using primer containing modified  
 XX nucleotide analogs, useful for preventing mispriming during PCR, RACE,  
 XX DNA synthesis or sequencing -

PS Example 1; Page 25; 46pp; English.

XX The present invention describes a method for destabilising non-specific  
 CC duplex formation, between an oligonucleotide and a target nucleic acid  
 CC (NA), comprising incubating the target NA with a modified  
 CC oligonucleotide (I) comprising a homopolymeric sequence having a  
 CC modification which decreases or abrogates H-bonding between the  
 CC modified oligonucleotide and the non-specific target NA. The modified  
 CC oligonucleotide is used to improve discrimination between the targeted  
 CC homopolymeric sequence and a non-homopolymeric target sequence. It is  
 CC used to increase the proportion of full length cDNA clones for a library,  
 CC to reduce mispriming during sequencing, 5' or 3' RACE (rapid  
 CC amplification of cDNA ends) or DNA synthesis or to generate bona fide  
 CC genetic markers. The present sequence represents an oligonucleotide  
 CC which is used in the exemplification of the present invention.

SQ Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 2 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1081 ATTAATAAAAAAAAAAAAA 1100  
 |||||  
 DB 20 AAAAAAAAAAAAAA 1

RESULT 568  
 AAH30031/c  
 ID AAH30031 standard; DNA; 23 BP.

XX AC AAH30031;

XX DT 19-JUL-2001 (first entry)

XX DE Human interleukin 8 antigen sequencing primer C.

XX KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
 XX human antibody phage display library; immunisation; transgenic animal;  
 XX PCR primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200125492-A1.

XX PD 12-APR-2001.

XX PF 02-OCT-2000; 2000WO-US27237.

XX PR 02-OCT-1999; 99US-0157415.

XX PR 01-DEC-1999; 99US-0453234.

XX PA (BIOS-) BIOSITE DIAGNOSTICS INC.

XX PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.

XX PI Buechler J, Valkirs G, Gray J, Lonberg N;

XX WPI; 2001-335567/35.

XX Producing a human antibody phage display library comprises providing a  
 XX transgenic animal whose genome comprises human immunoglobulin genes and  
 XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
 XX Example 23; Page 102; 161pp; English.

XX The present invention describes a method (M1) for producing a human  
 XX antibody phage display library (I), comprising: (1) providing a nonhuman  
 XX transgenic animal (II) whose genome comprises human immunoglobulin genes;  
 XX (2) isolating nucleic acids encoding human antibody chains (III) from  
 XX lymphatic cells; and (3) forming a library of display packages whose  
 XX members comprise a nucleic acid encoding (III) which is displayed from  
 XX the package. The method is used for producing a human antibody display

CC library, e.g., a Fab phage display library. The display method may be  
CC used to screen nucleic acids encoding antibody chains obtained from  
CC immunised nonhuman transgenic animals, and from this a population of  
CC antibodies may be prepared. Production of a human monoclonal antibodies  
CC display library using this method means there is no need to immunise  
CC humans with antigens, and the difficulties faced with immortalising B  
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 997 GTCTGAGGCTTGAGAAATG 1014  
|||||  
Db 18 GTCTGAGGCTTGAGAAATG 1

RESULT 569  
AAH30035/c  
ID AAH30035 standard; DNA; 23 BP.

AC AAH30035;

DT 19-JUL-2001 (first entry)

XX Human myelin proteolipid protein (PLP) antigen sequencing primer C.

DE Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
KW human antibody phage display library; immunisation; transgenic animal;  
XW PCR primer; ss.

XX Homo sapiens.

OS Synthetic.

XX W0200125492-A1.

PN 12-APR-2001.

XX 02-OCT-2000; 2000WO-US7237.

XX 02-OCT-1999; 99US-0157415.

PR 01-DEC-1999; 99US-0453234.

XX (BIOS-) BIOSITE DIAGNOSTICS INC.

PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.

XX Buechler J, Valkirs G, Gray J, Lonberg N;

PI WPI; 2001-335567/35.

XX Producing a human antibody phage display library comprises providing a  
XX transgenic animal whose genome comprises human immunoglobulin genes and  
XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
XX Example 24; Page 103; 161pp; English.

XX The present invention describes a method (M1) for producing a human  
XX antibody phage display library (I), comprising: (1) providing a nonhuman  
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;  
XX (2) isolating nucleic acids encoding human antibody chains (III) from  
XX lymphatic cells; and (3) forming a library of display packages whose  
XX members comprise a nucleic acid encoding (III) which is displayed from  
XX the package. The method is used for producing a human antibody display  
XX library, e.g., a Fab phage display library. The display method may be  
XX used to screen nucleic acids encoding antibody chains obtained from  
XX immunised nonhuman transgenic animals, and from this a population of  
XX antibodies may be prepared. Production of a human monoclonal antibodies  
XX display library using this method means there is no need to immunise  
XX humans with antigens, and the difficulties faced with immortalising B  
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056

CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 other;

Query Match 1.5%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 997 GTCTGAGGCTTGAGAAATG 1014  
|||||  
Db 18 GTCTGAGGCTTGAGAAATG 1

RESULT 570  
AAH18389/c  
ID AAH18389 standard; DNA; 18 BP.

AC AAX18389;

DT 11-MAY-1999 (first entry)

XX RT-PCR primer of the invention SEQ ID 30.

DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.

XX JP11032765-A.

PN 09-FEB-1999.

XX 18-JUL-1997; 97JP-0208312.

XX 18-JUL-1997; 97JP-0208312.

XX (TAKI ) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in  
XX RT-PCR

XX Example 1; Page 12; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates  
XX to sequences of at least two nucleotides of formula:  
XX (X)MS'-(alpha)n-beta-N3'; or (X)MS'-(gamma)k-delta-N3'; where

XX X = a labelled compound and/or a nucleotide with voluntary sequence;  
XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition  
XX of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;  
XX N = adenine, guanine, cytosine or thymine; gamma = thymine;  
XX k = natural number of 3 or over indicating the repetition of gamma, in  
XX which thymine expressed by gamma is composed of 1/3 or less of adenine,  
XX guanine and/or cytosine. The new nucleotides are useful as primers for  
XX RT-PCR and determination of base sequences. The new sequences allow for  
XX reproductive and highly efficient analysis of gene sequences.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

Query Match 1.5%; Score 16.2; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.7e+02;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAA 1099  
:|||||  
Db 17 BAAAAAATAAAAAA 1

RESULT 571

AAZ26563

ID AAZ26563 standard; DNA; 21 BP.

XX AAZ26563;

XX DT 30-NOV-1999 (first entry)

XX DE Human polymorphic region 752.

XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.

XX OS Homo sapiens.

XX PN WO9841648-A2.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US05419.

XX PR 20-MAR-1997; 97US-0041057.

XX PA (VARI-) VARIAGENICS INC.

XX PI Housman D, Ledley FD, Stanton VP;

XX DR WPI; 1998-521232/44.

XX PT Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease

XX PS Disclosure; Figure 7; 605pp; English.

XX CC This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic form present in the normal somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z26825 represent human polymorphic sites described in the method of the invention.

XX SQ Sequence 21 BP; 19 A; 1 C; 1 G; 0 U; 0 other;

Query Match 1.5%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 3.1e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA 1097

DB 1 AACAAAGAAAAA 21

RESULT 572

AAF93028

ID AAF93028 standard; DNA; 22 BP.

XX AC AAF93028;

XX DT 17-MAY-2001 (first entry)

XX DE Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.

XX KW Secreted protein; fetal kidney; ds.

XX OS Homo sapiens.

XX PN WO9900405-A1.

XX PD 07-JAN-1999.

XX PF 29-JUN-1998; 98WO-US13530.

XX PR 30-JUN-1997; 97US-0885610.

DE Polymorphic sequence for ABC1 polymorphic site #38.

XX KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

XX OS Homo sapiens.

XX PN WO2000115676-A2.

XX PD 08-MAR-2001.

XX PF 01-SEP-2000; 2000WO-IB01492.

XX PR 01-SEP-1999; 99US-0151977.

XX PR 15-MAR-2000; 2000US-0526193.

XX PR 23-JUN-2000; 2000US-0213958.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PA (XENO-) XENON GENETICS INC.

XX PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX DR WPI; 2001-244356/25.

XX PT Treating a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR- or RXR-mediated transcriptional activity -

XX PS Disclosure; Fig 4; 317pp; English.

XX CC The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density lipoprotein-cholesterol (HDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treatment of a disease or condition selected a lower than normal HDL cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.

XX SQ Sequence 22 BP; 6 A; 2 C; 10 G; 3 T; 1 other;

Query Match 1.5%; Score 16.2; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 3.3e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 991 TTGGAAGTCTGAGGCTGGAGAA 1012

DB 1 TTGGGAGGCTNAGGAGGAGAA 22

RESULT 573

AAAX07568

ID AAAX07568 standard; cDNA; 16 BP.

XX AC AAAX07568;

XX DT 21-JUN-1999 (first entry)

XX DE Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.

XX KW Secreted protein; fetal kidney; ds.

XX OS Homo sapiens.

XX PN WO9900405-A1.

XX PD 07-JAN-1999.

XX PF 29-JUN-1998; 98WO-US13530.

XX PR 30-JUN-1997; 97US-0885610.

XX (GEMV ) GENETICS INST INC.  
 PA Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCooy JM;  
 PI Merberg D, Racie LA, Treacy M;  
 XX WPI; 1999-095671/08.  
 DR  
 XX New polynucleotides encoding secreted human proteins - are derived  
 PT from foetal kidney or adult retina cDNA libraries, used as, e.g.  
 PT potential vaccines  
 XX  
 XX Disclosure; Page 54; 76pp; English.  
 XX  
 CC The sequence is that of the 3' end of a sequence encoding  
 CC a secreted protein from a human fetal kidney clone AK296.  
 CC Such a sequence is predicted to have biological  
 CC activities which would make them suitable for treating, preventing or  
 CC ameliorating medical conditions in humans and animals, although no  
 CC supporting data is given. Suggested activities include nutritional  
 CC activity, cytokine and cell proliferation/differentiation activity,  
 CC immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. It is also stated to be useful for gene  
 CC therapy.  
 XX  
 XX Sequence 16 BP; 16 A; 0 C; 0 G; 0 U; 0 other;  
 SQ  
 Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1099  
 Db 1 AAAAAAAAAAAAAA 16  
 RESULT 574  
 AAC66068  
 ID AAC66068 standard; DNA; 16 BP.  
 AC AAC66068;  
 XX  
 DT 22-FEB-2001 (first entry)  
 XX  
 DE DNA chip primer #4.  
 XX  
 KW DNA chip; primer; nucleoside derivative; photolabile protecting group;  
 KW photolithographic nucleic acid chip; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200061594-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 07-APR-2000; 2000WO-DE01148.  
 XX  
 PR 08-APR-1999; 99DE-1015867.  
 PR 28-JAN-2000; 2000DE-1003631.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Beier M, Hoheisel J;  
 XX  
 DR WPI; 2000-679457/66.  
 XX  
 XX New nucleoside derivatives with photolabile protecting groups, useful  
 PT in oligonucleotide synthesis, particularly on solid phases, e.g. for  
 PT hybridization testing -

XX Disclosure; Fig 9; 48pp; German.  
 XX  
 CC This invention describes nucleoside derivatives (I) with photolabile  
 CC protecting groups. (I) are used to synthesize oligonucleotides using the  
 CC photolithographic nucleic acid chip method, particularly where these  
 CC are intended for performing enzymatic reactions initiated from a free  
 CC 3'-hydroxy (especially solid-phase polymerase reactions or ligase  
 CC reactions, but also reverse transcription, cDNA synthesis etc.), also  
 CC for hybridization testing, sequencing and in DNA computing. (I) are  
 CC produced with high selectivity by reaction with a mild acylating agent  
 CC that has high specificity for the 3'-position, without significant  
 CC side-reactions (cf. more reactive acylating agents such as  
 CC chloroformates).  
 XX  
 SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1099  
 Db 1 AAAAAAAAAAAAAA 16  
 RESULT 575  
 AAH42481/C  
 ID AAH42481 standard; DNA; 16 BP.  
 XX  
 AC AAH42481;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Oligonucleotide used to produce branched chain compounds.  
 XX  
 KW Branched chain compound; nucleic acid synthesis; primer extension;  
 KW reverse transcription; nucleic acid hybridization;  
 KW nucleic acid amplification; ss.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /note= "COOH attached"  
 FT modified\_base 2 /tag= b  
 FT /note= "COOH attached"  
 FT misc\_feature 2..3 /tag= c  
 FT /note= "branch present"  
 XX  
 PN EP1111068-A1.  
 XX  
 PD 27-JUN-2001.  
 XX  
 PF 21-DEC-1999; 99EP-0125484.  
 XX  
 PR 21-DEC-1999; 99EP-0125484.  
 XX  
 PA (LION-) LION BIOSCIENCE AG.  
 PA (VBOG-) VBC GENOMICS GMBH.  
 XX  
 PI Schmidt W, Hiller R, Huber M, Mueller M;  
 XX  
 DR WPI; 2001-466959/51.  
 XX  
 XX Branched compounds useful in e.g. nucleic acid synthesis reaction  
 PT comprises nucleic acid moieties optionally extended by a polymerase -  
 PS Example 1; Page 10; 31pp; English.  
 XX

CC The specification describes branched compounds containing nucleic  
 CC acid moieties optionally extended by a polymerase. The branched chain  
 CC compounds of the invention are used in nucleic acid synthesis reaction,  
 CC primer extension reaction, reverse transcription reaction of RNA into  
 CC DNA, nucleic acid hybridization experiment (for identifying sequence  
 CC of a nucleic acid), and nucleic acid amplification experiment (for  
 CC analysing the expression pattern of genes). The compounds are also used  
 CC in solid-phase enzymatic reactions. The present sequence was used  
 CC in the course of the invention to produce branched chain compounds.

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;  
 Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099  
 DB 16 AAAAAAAAAAAAAA 1

RESULT 576  
 AAF30880/c  
 ID AAF30880 standard; DNA; 16 BP.

XX AC AAF30880;

XX DT 09-JUL-2001 (first entry)

XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.

XX KW ODN-MGB-LF; oligonucleotide; minor groove binder;  
 XX latent fluorophore; hybridisation; detection; fluorescence; probe;  
 XX ss.

XX OS Synthetic.

XX PN WO200131063-A1.

XX PD 03-MAY-2001.

XX PF 26-OCT-2000; 2000WO-US29786.

XX PR 26-OCT-1999; 99US-0428236.

XX PA (EPOC-) EPOCH BIOSCIENCES INC.

XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;

XX DR WPI; 2001-328656/34.

XX PT Conjugate of oligonucleotide, minor groove binder and latent  
 XX fluorophore, useful for detecting specific nucleic acids, e.g. for  
 XX single-nucleotide mismatch discrimination -

XX PS Disclosure; Page 58; 105pp; English.

XX CC The present sequence is that of the oligonucleotide (ODN) component  
 CC of an ODN-MGB (minor groove binder)-LF (latent fluorophore)  
 CC conjugate of the invention. MGBs bind in a non-intercalating  
 CC manner to the minor groove of non-single-stranded DNA, RNA or their  
 CC hybrids, while a LF binds similarly but in an intercalating manner,  
 CC or lies in the minor groove, or is oriented in some other way to  
 CC the DNA molecule by MGB, such that it becomes fluorescent (or its  
 CC fluorescent properties change detectably). The conjugates are used  
 CC as hybridisation probes and amplification primers for fluorescent  
 CC detection of specifically hybridising sequences, for analysis or  
 CC diagnosis, especially (real-time) PCR, for single-nucleotide  
 CC mismatch discrimination, target or signal amplification,  
 CC array-based assays and sequencing, including detection of  
 CC double-stranded DNA by triplex formation. Many different targets  
 CC can be detected a single reaction vessel. The present ODN-MGB-LF  
 CC conjugate was used to demonstrate hybridisation-triggered

CC fluorescence. Upon hybridisation to the complementary target  
 CC sequence there was an increase in fluorescence yield, measured as  
 CC the ratio of the fluorescence emitted by the hybrid between the  
 CC ODN-MGB-LF conjugate and its target sequence to the fluorescence  
 CC emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, of 8.3.

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099  
 DB 16 AAAAAAAAAAAAAA 1

RESULT 577  
 AAF30895/c  
 ID AAF30895 standard; DNA; 16 BP.

XX AC AAF30895;

XX DT 09-JUL-2001 (first entry)

XX DE Oligonucleotide-minor groove binder complex.

XX KW ODN-MGB-LF; oligonucleotide; minor groove binder;  
 XX latent fluorophore; hybridisation; detection; fluorescence; probe;  
 XX ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified\_base 1

XX FT /\*tag= a

XX FT /note= "thymine modified by a minor groove binder  
 XX (2-dimethylaminonaphthalene-6-  
 XX sulfonamide"

XX PN WO200131063-A1.

XX XX 03-MAY-2001.

XX XX 26-OCT-2000; 2000WO-US29786.

XX XX 26-OCT-1999; 99US-0428236.

XX XX (EPOC-) EPOCH BIOSCIENCES INC.

XX XX Dempcy RO, Afonina IA, Vermeulen NMJ;

XX XX WPI; 2001-328656/34.

XX PT Conjugate of oligonucleotide, minor groove binder and latent  
 XX fluorophore, useful for detecting specific nucleic acids, e.g. for  
 XX single-nucleotide mismatch discrimination -

XX PS Disclosure; Page 101; 105pp; English.

XX CC The present sequence is that of an oligonucleotide (ODN)-minor  
 CC groove binder (MGB) complex. MGBs bind in a non-intercalating  
 CC manner to the minor groove of non-single-stranded DNA, RNA or their  
 CC hybrids. ODN-MGB-LF conjugates of the invention also comprise a  
 CC latent fluorophore (LF), which binds similarly to the MGB but in an  
 CC intercalating manner, or lies in the minor groove, or is oriented  
 CC in some other way to the DNA molecule by MGB, such that it becomes  
 CC fluorescent (or its fluorescent properties change detectably). The  
 CC conjugates are used as hybridisation probes and amplification  
 CC primers for fluorescent detection of specifically hybridising  
 CC sequences, for analysis or diagnosis, especially (real-time) PCR,  
 CC for single-nucleotide mismatch discrimination, target or signal  
 CC amplification, array-based assays and sequencing, including

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CC detection of double-stranded DNA by triplex formation.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

  Query Match      1.5%; Score 16; DB 1; Length 16;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 578
ABA04585/c
ID ABA04585 standard; DNA; 16 BP.
XX
AC ABA04585;
XX
DT 15-FEB-2002 (first entry)
XX
DE Oligonucleotide #5.
XX
KW Analytical support; genomic sequencing; mutation detection;
XX pharmaceutical development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT and PO is a phosphate group"
XX
FN FR2805348-A1.
PD 24-AUG-2001.
XX
PF 23-FEB-2000; 2000FR-0002236.
XX
PR 23-FEB-2000; 2000FR-0002236.
XX
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Curin M, Peltie P, Fontecave M, Decout JL, Dueymes C;
XX WPI; 2001-628265/73.
XX
DR Support for hybridization analysis of nucleic acids for sequencing
XX techniques, comprises an array of oligonucleotides having a label where
XX the fluorescence changes follow hybridization
XX
PS Example 1; Page 12; 33pp; French.
XX
CC The present invention relates to an analytical support, to which a number
CC of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC fluorescent compound, the fluorescence of which varies when the
CC oligonucleotide hybridises to its complement. The analytical support is
CC useful in hybridisation testing for identification of specific nucleic
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC development. The present oligonucleotide was used to illustrate the
CC invention.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

  Query Match      1.5%; Score 16; DB 1; Length 16;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 579
ABA97402/c
ID ABA97402 standard; DNA; 16 BP.
XX
AC ABA97402;
XX
DT 18-JUN-2002 (first entry)
XX
DE Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
KW Protein nucleic acid molecule; PNA; ds.
XX
OS Synthetic.
XX
FN WO200168673-A1.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US08111.
XX
PR 14-MAR-2000; 2000US-189190P.
XX
PR 30-NOV-2000; 2000US-250334P.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
XX Chakhmakchcheau O, Buryakova A, Choob M, Hondorp K;
XX WPI; 2002-041177/05.
XX
DR Oligonucleotides analogues useful in detection, separation and
XX purification of nucleic acid molecules, comprise monomers, dimers and
XX oligomers -
XX
PS Example 17; Page 118; 197pp; English.
XX
CC This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adapters and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase.
CC They are also used for enhancing or inhibiting the activity of an enzyme
CC or cellular activity. The compounds are stable to nucleases and
CC proteases, have high affinity, binding specificity and solubility. The
CC polyamide backbone of PNAs is resistant to both nucleases and proteases.
CC PNAs bind nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and
CC are used in a wide variety of applications. This sequence
CC represents a DNA oligomer which is used to represent the thermal
CC stability of the oligomers of the invention.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 other;

  Query Match      1.5%; Score 16; DB 1; Length 16;
  Best Local Similarity 100.0%; Pred. No. 2.5e+02;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 580
AAL54078/c
ID AAL54078 standard; DNA; 16 BP.
XX
AC AAL54078;
XX
DT 06-MAR-2003 (first entry)

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KW foetal liver kinase 1; ss.  
 XX Homo sapiens.  
 OS WO9715662-A2.  
 PN PD 01-MAY-1997.  
 XX 25-OCT-1996; 96WO-US17480.  
 XX 11-JAN-1996; 96US-0584040.  
 PR 26-OCT-1995; 95US-0005974.  
 XX (CHIR) CHIRON CORP.  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;  
 XX WPI; 1997-259017/23.  
 DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or  
 XX mRNA stability - useful for treating e.g. tumour angiogenesis,  
 PT psoriasis, rheumatoid arthritis, etc., in a human patient  
 XX Claim 4; Page 79; 218pp; English.  
 XX The present invention describes nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can  
 CC be treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention.  
 XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 U; 0 other;  
 SQ

Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1084 AAAAAAAAAAAAAA 1099  
 DB ||||||||||||  
 16 AAAAAAAAAAAAAA 1

RESULT 583  
 AAV49503/C  
 ID AAV49503 standard; cDNA to mRNA; 17 BP.  
 XX AAV49503;  
 XX 18-NOV-1998 (first entry)  
 DT Human eosinophil cell activator HVC002 primer #1.  
 DE  
 XX Bosinophil cell activator; treatment; diagnosis; malignant tumour;  
 KW parasitic infection; allergic inflammation; eosinophilic pneumonia;  
 KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 OS WO9824817-A1.  
 XX 11-JUN-1998.  
 PD 05-DEC-1997; 97WO-JP04470.  
 XX 05-DEC-1996; 96JP-0325762.  
 PR

(KYOW) KYOWA HAKKO KOGYO KK.  
 PA Koike M, Kuga T, Nakagawa S, Nishi T, Saito A;  
 PI Shinkai A, Yoshisue H;  
 XX WPI; 1998-333261/29.  
 DR DNA and encoded protein which activates eosinophil cells - for  
 XX treatment of cancer, parasite infection, autoimmune disease and  
 PT allergic inflammation  
 XX Example 1; Page 64; 92pp; Japanese.  
 PS AAV49503-V49507 are primers used in the isolation of a human eosinophil  
 CC cell activator. This protein and antibodies generated from the protein  
 CC can be used for treatment and diagnosis of malignant tumours, parasitic  
 CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset  
 CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis,  
 CC and the antisense DNA in gene therapy of these disorders. The protein  
 CC can be used for screening of potential agonists or antagonists of its  
 CC activity.  
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;  
 SQ

Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1083 TAAAAAAAAAAAAA 1098  
 DB ||||||||||||  
 17 TAAAAAAAAAAAAA 2

RESULT 584  
 AAX18371/C  
 ID AAX18371 standard; DNA; 17 BP.  
 XX AAX18371;  
 XX 11-MAY-1999 (first entry)  
 DT RT-PCR primer of the invention SEQ ID 12.  
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX Synthetic.  
 OS JPI1032765-A.  
 PN 09-FEB-1999.  
 PD 18-JUL-1997; 97JP-0208312.  
 PF 18-JUL-1997; 97JP-0208312.  
 XX (TAKI) TAKARA SHUZO CO LTD.  
 PA WPI; 1999-183822/16.  
 DR Peptides having at least two new nucleotides - useful as primers in  
 XX RT-PCR  
 XX Disclosure; Page 11; 19pp; Japanese.  
 PS This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula:  
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where  
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;  
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition  
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;  
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;  
 CC k = natural number of 3 or over indicating the repetition of gamma, in  
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

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QY      1083 TAAAAAAAAAAAAAAAAA 1098
        ||| ||| ||| ||| ||| |||
Db      17  TAAAAAAAAAAAAAAAAA 2

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RESULT 587
AAC64181/c
ID AAC64181 standard; DNA; 17 BP.
XX AC
XX AAC64181;
XX DT
XX 21-FEB-2001 (first entry)
XX DE
XX PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX KW
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
XX KW Fas-associated factor-1; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS
XX Synthetic.
XX FN
XX WO200065045-A1.
XX PD
XX 02-NOV-2000.
XX PF
XX 26-APR-2000; 2000WO-JP02729.
XX PR
XX 27-APR-1999; 99JP-0120490.
XX PA (GENO-) GENOX RES INC.
XX PI
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR
XX WPI; 2000-687338/67.
XX PT
XX Pollinosis-associated gene 419 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IGE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS
XX Example 6; Page 49; 77pp; Japanese.
XX CC
XX The invention relates to the human pollinosis-associated gene 419 which
XX CC exhibits reduced expression in the T-cells of individuals with high cedar
XX CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated
XX CC from T-cells from individuals allergic to cedar pollen using the
XX CC differential display method. Pollinosis-associated gene 419 has
XX CC homology with the gene encoding human Fas-associated factor-1 (FAF-1).
XX CC The invention also relates to the protein encoded by pollinosis gene
XX CC 419; expression constructs and host cells comprising pollinosis-
XX CC associated gene 419 nucleic acids; pollinosis-associated gene 419 primers
XX CC and probes; antibodies against the protein encoded by the gene; methods
XX CC of detection of pollinosis-associated gene 419 nucleic acids; and a
XX CC method of diagnosis of allergic diseases via the detection of pollinosis-
XX CC associated gene 419 nucleic acids. The invention additionally encompasses
XX CC methods of screening drug candidates for the treatment of allergic
XX CC disease by measuring the expression of pollinosis-associated gene 419 in
XX CC pollen antigen-stimulated T-cells in the presence of a test compound
XX CC relative to a control. Pollinosis-associated gene 419 is useful in the
XX CC diagnosis of allergic diseases and in the screening of drug candidates
XX CC for the treatment of such diseases. The present sequence represents
XX CC a PCR primer used in the isolation of human pollinosis-associated gene
XX CC 419 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAA 1098
DB 17 TAAAAAAAAAAAAA 2
RESULT 588
AAC64213/c
ID AAC64213 standard; DNA; 17 BP.
XX AC
XX AAC64213;
XX DT
XX 21-FEB-2001 (first entry)
XX DE
XX PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX KW
XX Human; pollinosis-associated gene 373; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS
XX Synthetic.
XX FN
XX WO200065046-A1.
XX PD
XX 02-NOV-2000.
XX PF
XX 26-APR-2000; 2000WO-JP02730.
XX PR
XX 27-APR-1999; 99JP-0120489.
XX PA (GENO-) GENOX RES INC.
XX PI
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR
XX WPI; 2000-687339/67.
XX PT
XX Pollinosis-associated gene 373 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific immunoglobulin-E levels,
XX PT useful in diagnosis of allergic diseases and screening drug candidates
XX PS
XX Example 6; Page 69; 80pp; Japanese.
XX CC
XX The invention relates to the human pollinosis-associated gene 373 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen
XX CC using the differential display method. The invention also relates also
XX CC relates to the protein encoded by pollinosis gene 373; expression
XX CC constructs and host cells comprising pollinosis-associated gene 373
XX CC nucleic acids; pollinosis-associated gene 373 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 373 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 373 nucleic acids. The invention additionally encompasses methods of
XX CC screening drug candidates for the treatment of allergic disease by
XX CC measuring the expression of pollinosis-associated gene 373 in pollen
XX CC antigen-stimulated T-cells in the presence of a test compound relative to
XX CC a control. Pollinosis-associated gene 373 is useful in the diagnosis of
XX CC allergic diseases and in the screening of drug candidates for the
XX CC treatment of such diseases. The present sequence represents a PCR primer
XX CC used in the isolation of human pollinosis-associated gene 373 cDNA.
XX SQ
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAA 1098
DB 17 TAAAAAAAAAAAAA 2
RESULT 589
AAC64213/c
ID AAC64213 standard; DNA; 17 BP.
XX AC
XX AAC64213;
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XX DT 21-FEB-2001 (first entry)
XX DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX KW Human, pollinosis-associated gene 627; IgE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection;
XX KW diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065051-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JF02735.
XX PR 27-APR-1999; 99JP-0120493.
XX PA (GENO-) GENOX RES INC.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR WPI; 2000-687344/67.
XX PT Pollinosis-associated gene 627 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IgE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS Example 6; Page 41; 51pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 627 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 627 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 627 nucleic acids; and a method of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 627
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 627 cDNA.
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 590
AAC64230/c
ID AAC64230 standard; DNA; 17 BP.
XX AC AAC64230;
XX DT 21-FEB-2001 (first entry)
XX DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX KW Human; pollinosis-associated gene 795; vimentin homologue;
XX KW IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
XX KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO9963085-A1.

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OS Synthetic.
XX PN WO200065050-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JF02734.
XX PR 27-APR-1999; 99JP-0120494.
XX PA (GENO-) GENOX RES INC.
XX PA (EISA) EISAI CO LTD.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX DR WPI; 2000-687343/67.
XX PT Pollinosis-associated gene 795 undergoing significantly low expression
XX PT in subjects with high cedar pollen-specific IgE levels, useful in
XX PT diagnosis of allergic diseases and screening drug candidates -
XX PS Page 45; Example 6; 73pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 795 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. Pollinosis-associated gene 795 has
XX CC homology with the human vimentin gene. The invention also relates also
XX CC relates to the protein encoded by pollinosis gene 795; to expression
XX CC constructs and host cells comprising pollinosis-associated gene 795
XX CC nucleic acids; pollinosis-associated gene 795 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 795 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 795 nucleic acids. The invention additionally encompasses methods of
XX CC screening drug candidates for the treatment of allergic disease by
XX CC measuring the expression of pollinosis-associated gene 795 in pollen
XX CC antigen-stimulated T-cells in the presence of a test compound relative to
XX CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
XX CC allergic diseases and in the screening of drug candidates for the
XX CC treatment of such diseases. The present sequence represents a PCR primer
XX CC used in the isolation of human pollinosis-associated gene 795 cDNA.
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 591
AAx82720/c
ID AAx82720 standard; DNA; 17 BP.
XX AC AAx82720;
XX DT 10-NOV-2000 (first entry)
XX DE Human IgA nephropathy-associated cDNA primer #51.
XX KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
XX KW human; primer; ss.
XX OS Homo sapiens.
XX PN WO9963085-A1.

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XX PD 09-DEC-1999.
XX PF 28-MAY-1999; 99WO-JP02855.
XX PR 02-JUN-1998; 98JP-0152603.
XX PA (KYOM) KYOMA HAKKO KOGYO KK.
XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
XX PI Sawada S, Takei M, Shibata K, Furuya A;
XX DR WPI; 2000-097328/08.
XX PT DNA sequences preferentially expressed in IgA nephropathy patients,
XX PT proteins encoded by them, and antibodies to those proteins -
XX PS Claim 3; Page 169; 180pp; Japanese.
XX CC This invention describes novel DNA sequences preferentially expressed in
XX CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
XX CC them. Independent claims cover diagnostic reagents for IgA nephropathy
XX CC incorporating the antisense sequences; the treatment of IgA nephropathy
XX CC using the antisense sequences for mRNA inhibition; proteins associated
XX CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
XX CC antibodies recognizing these proteins; the production of the proteins
XX CC by culture of host cells transformed with DNA encoding them; diagnostic
XX CC reagents for IgA nephropathy containing the antibodies; and compositions
XX CC for the treatment of IgA nephropathy which contain the antibodies. The
XX CC products of the invention can be used for the diagnosis and treatment of
XX CC IgA nephropathy. This sequence represents a primer used in the isolation
XX CC and identification of the human IgA nephropathy-associated proteins
XX CC described in the method of the invention.
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.58; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 592
AAA30179/c
ID AAA30179 standard; DNA; 17 BP.
AC AAA30179;
XX 16-AUG-2000 (first entry)
XX PCR primer GT15A used in pollenosis associated gene identification.
XX Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX Synthetic.
XX WO200020575-A1.
XX 13-APR-2000.
XX 06-OCT-1999; 99WO-JP05506.
XX 06-OCT-1998; 98JP-0284610.
XX (GENO-) GENOX RES INC.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Lu N, Ogawa K;

WPI; 2000-317712/27.
Gene highly expressed in patients with high cedar pollen-specific IgE
levels, useful for diagnosing pollenosis, and screening candidate
compounds for pollenosis treatment -
Example 6; Page 38; 44pp; Japanese.
This sequence represents a PCR primer used in the identification of a
human pollenosis associated gene. The gene is highly expressed in
individuals with high pollen-specific immunoglobulin E (IgE) levels. The
invention relates to the nucleotide sequence encoding the pollenosis
associated protein, diagnosing pollenosis and screening candidate
compounds for treating pollenosis. The gene can be used in diagnosing
pollenosis, particularly cedar pollenosis, and screening candidate
compounds for pollenosis treatment.
Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.58; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 593
AAA25449/c
ID AAA25449 standard; DNA; 17 BP.
AC AAA25449;
XX 19-JUL-2000 (first entry)
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX Oestrogen receptor; c-raf, k-ras, bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX WO9954459-A2.
XX 28-OCT-1999.
XX 19-APR-1999; 99WO-US08547.
XX 20-APR-1998; 98US-0082404.
XX 23-JUN-1998; 98US-0103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX Matulic-Adamic J;
XX WPI; 2000-013248/01.
XX New nucleic acids that interact, and optionally cleave, target
XX sequences, used to treat cancer -
XX Claim 77; Page 79; 148pp; English.
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any
XX catalytic nucleic acid (A') that modulates expression of the oestrogen
XX receptor gene, are used to treat cancer (particularly of breast or
XX endometrium), in vivo or by transforming cells ex vivo and implanting

```

CC treated cells, or for other conditions associated with levels of  
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)  
 CC can also be used to correlate inhibition of gene expression with  
 CC alterations in phenotype, particularly for identification of therapeutic  
 CC targets, and as research reagents (for RNA, in the same way that  
 CC restriction endonucleases are used with DNA). The combination of  
 CC modifications in (A) improves resistance to nucleases, binding affinity  
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor  
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their  
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen  
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent  
 CC their corresponding target sequences. AAA26219 to AAA26271 represent  
 CC other ribozyme sequences and antisense oligonucleotides used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;  
 Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1099  
 Db 17 AAAAAAAAAAAAAA 2  
 RESULT 594  
 AAA25451/C  
 ID AAA25451 standard; DNA; 17 BP.  
 XX  
 AC AAA25451;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.  
 XX  
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US08547.  
 XX  
 PR 20-APR-1998; 98US-0082404.  
 XX  
 PR 23-JUN-1998; 98US-0103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target  
 PT sequences, used to treat cancer -  
 XX  
 PS Claim 77; Page 79; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorothioate  
 CC link, having endonuclease activity. (A), and more generally any  
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen  
 CC receptor gene, are used to treat cancer (particularly of breast or  
 CC endometrium), in vivo or by transforming cells ex vivo and implanting  
 CC treated cells, or for other conditions associated with levels of  
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)

CC can also be used to correlate inhibition of gene expression with  
 CC alterations in phenotype, particularly for identification of therapeutic  
 CC targets, and as research reagents (for RNA, in the same way that  
 CC restriction endonucleases are used with DNA). The combination of  
 CC modifications in (A) improves resistance to nucleases, binding affinity  
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor  
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their  
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen  
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent  
 CC their corresponding target sequences. AAA26219 to AAA26271 represent  
 CC other ribozyme sequences and antisense oligonucleotides used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;  
 Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1099  
 Db 16 AAAAAAAAAAAAAA 1  
 RESULT 595  
 AAZ36739/C  
 ID AAZ36739 standard; DNA; 17 BP.  
 XX  
 AC AAZ36739;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Anchored oligo(dT) primer AT15A used for modified differential display.  
 XX  
 KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;  
 KW differentially expressed nucleic acid; disease state; cancer;  
 KW autoimmune disease; infectious disease; aging; developmental disorder;  
 KW proliferative disorder; neurological disorder; toxicity; primer;  
 KW treatment resistance; differential expression; drug discovery;  
 KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9955913-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 27-APR-1999; 99WO-US09119.  
 XX  
 PR 27-APR-1998; 98US-0083331.  
 XX  
 PR 27-AUG-1998; 98US-0098070.  
 XX  
 PR 04-FEB-1999; 99US-0118624.  
 XX  
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.  
 XX  
 PI McClelland M, Welsh J, Trenkle T;  
 XX  
 DR WPI; 2000-086388/07.  
 XX  
 PT Measuring expression of low abundance reduced complexity target nucleic  
 PT acid molecules -  
 XX  
 PS Example 3; Page 91; 187pp; English.  
 XX  
 CC AAZ36739-41 represent oligo(dT) primers used for modified differential  
 CC display, in the method of the invention. The specification describes a  
 CC method for measuring the level of two or more nucleic acid molecules in  
 CC a target. The method comprises contacting a probe with an arbitrarily or  
 CC statistically sampled target and detecting the amount of specific  
 CC binding of the target to the probe. The methods can be used to identify  
 CC differentially expressed nucleic acid molecules associated with disease  
 CC states, such as cancer, autoimmune disease, infectious disease, aging,  
 CC developmental disorder, proliferative disorder or neurological disorder.

CC Alternatively the methods can be used to assess the efficacy or toxicity  
CC of or a resistance to a treatment. Also the methods can be used to  
CC determine differential expression of nucleic acid molecules in response  
CC to a stimulus, e.g. a chemical, drug or growth factor (especially  
CC epidermal growth factor), radiation, stress or a pathogen. The methods  
CC can also be used to determine co-regulated genes that can be potential  
CC targets for drug discovery.

XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098

DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 596

AAC82874/C

ID AAC82874 standard; DNA; 17 BP.

XX AC AAC82874;

XX 20-MAR-2001 (first entry)

XX Human pollinosis-associated gene 441 primer #1.

XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;

XX pollen scattering; antigen; primer; ss.

XX Homo sapiens.

XX WO2000073435-A1.

XX 07-DEC-2000.

XX 18-MAY-2000; 2000WO-JP03190.

XX 27-MAY-1999; 99JP-0148783.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX WPI; 2001-061526/07.

XX Pollinosis-associated gene 441 which undergoes lower expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus

PS Example 6; Page 35; 42pp; Japanese.

XX This invention describes a novel nucleic acid molecule comprising a  
CC sequence (I) which undergoes significantly low expression in subjects  
CC after pollen scattering, and is useful in diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098

DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 597  
AAC91719/C

ID AAC91719 standard; DNA; 17 BP.

XX AC AAC91719;

XX 27-MAR-2001 (first entry)

XX PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.

XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;

XX reduced expression; detection; diagnosis; drug screening;

XX allergic disease; PCR primer; ss.

XX Synthetic.

XX WO2000073440-A1.

XX 07-DEC-2000.

XX 18-MAY-2000; 2000WO-JP03192.

XX 27-MAY-1999; 99JP-0148785.

XX (GENO-) GENOX RES INC.

XX (EISA) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
XX Yokoi A;

XX WPI; 2001-032159/04.

XX Pollinosis-associated gene 787 undergoing significantly low expression  
PT in subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus

XX Example 6; Page 40; 54pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 787 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC after the pollen-scattering season, relative to expression levels in  
CC T-cells before the pollen-scattering season. The gene was isolated from  
CC T-cells from individuals allergic to pollen using the differential  
CC display method. The invention also relates to pollinosis-associated gene  
CC 787 primers and probes; methods of detection of pollinosis-associated  
CC gene 787 nucleic acids; and a method of diagnosis of allergic diseases  
CC via the detection of pollinosis-associated gene 787 nucleic acids. The  
CC invention additionally encompasses a method of screening drug candidates  
CC for the treatment of allergic disease by measuring the expression of  
CC pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in  
CC the presence of a test compound relative to a control. Pollinosis-  
CC associated gene 787 is useful in the diagnosis of allergic diseases and  
CC in the screening of drug candidates for the treatment of such diseases.  
CC The present sequence represents a PCR primer used in the isolation of  
CC human pollinosis-associated gene 787 cDNA.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098

DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 598

AAC92292/C

ID AAC92292 standard; DNA; 17 BP.

XX







```

PD 25-APR-2002.
XX
XX
XX 28-SEP-2001; 2001WO-JP08574.
XX
XX 13-OCT-2000; 2000JP-0314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI; 2002-372311/40.
XX
XX Method for examining allergic diseases by differential display of
XX seventeen genes showing different expression particularly significant
XX increase in eosinophils in patients with mild atopic dermatitis, also
XX applicable in screening compounds -
XX
XX Example 1; Page 109; 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX which involves determining the expression level of a gene, having one of
XX the 17 nucleotide sequences shown in ABN9812-ABN99828, in the
XX eosinophils in a patient and comparing the expression level with that in
XX the eosinophils of a healthy individual. The method can be used to
XX examine allergic diseases, particularly atopic dermatitis, and its early
XX diagnosis, which is also applicable in screening candidate compounds for
XX remedies. The present sequence is a PCR primer described in the
XX exemplification of the invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match      1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 604
ABK49634/c
ID ABK49634 standard; DNA; 17 BP.
XX
XX AC ABK49634;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
XX Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX differential display; eosinophil; antiallergic; atopic dermatitis;
XX GT15A.
XX
XX OS Homo sapiens.
XX
XX PN WO200224903-A1.
XX
XX 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-JP08246.
XX
XX 25-SEP-2000; 2000JP-0291318.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA) EISAI CO LTD.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX Takahashi E;
XX WPI; 2002-315738/35.
XX

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```

XX
XX Examining allergic diseases by differential display of gene showing
XX different expression particularly increased expression in remission
XX stage in eosinophils of patients, also applicable in screening
XX candidate compounds for remedies -
XX
XX Example 1; Page 56; 72pp; Japanese.
XX
XX The invention relates to a method for examining allergic diseases
XX comprising determining the expression level of a gene containing,
XX the human cDNA appearing as ABK49633 which has homology with
XX acetyltransferases in the eosinophils of a patient and comparing the
XX expression level with that in the eosinophils of a healthy individual
XX (i.e. differential display). Also included are methods of screening
XX for candidate compounds which affect the expression level of the gene or
XX the activity of the protein encoded by the gene (including related
XX proteins and mutants), the use of probes based on the gene sequence
XX in the examination of allergic diseases, the use of reporter
XX constructs in the screening of candidate compounds, a vector containing a
XX the transcription-controlling region of the gene, cells transformed a
XX with the vector, an antibody against the protein and a model animal for
XX allergic diseases which is a transgenic non-human vertebrate with
XX lowering of expression intensity of the gene in eosinophils.
XX The method is examining intensity of the gene in eosinophils.
XX dermatitis which is also applicable in screening candidate
XX compounds for remedies. Such method can be performed in high throughput,
XX at low cost. The present sequence is a differential display PCR primer
XX for the cDNA encoding the human acetyltransferase-like protein 20-90-05.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

Query Match      1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1098
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 605
ABK49756/c
ID ABK49756 standard; DNA; 17 BP.
XX
XX AC ABK49756;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human atopic dermatitis cDNA related PCR primer GT15a.
XX
XX Atopic dermatitis; ss; differential display; primer; PCR;
XX eosinophil; allergic disease; antiallergic; dermatological; GT15a.
XX
XX OS Synthetic.
XX
XX PN WO200226962-A1.
XX
XX 04-APR-2002.
XX
XX 21-SEP-2001; 2001WO-JP08247.
XX
XX 26-SEP-2000; 2000JP-0293021.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients -
XX

```

XX PS Example 1; Page 54; 74pp; Japanese.

XX CC This invention relates to gene sequences that are differentially

CC expressed in eosinophils from patients with atopic dermatitis in the

CC increment stage as compared with those in the remission stage. These

CC sequences are used in a novel method for examining allergic diseases

CC comprising determining the expression levels of these genes and

CC comparing the expression level with that in the eosinophils of a

CC healthy individual. The method of the invention may have anti-allergic

CC or dermatological activities. The method can be used to diagnose

CC allergic diseases particularly atopic dermatitis, and may also

CC be used to screen candidate compounds for remedies. The method of the

CC invention can be performed in high throughput, at low cost. The

CC present sequence represents the G715a PCR primer used to amplify

CC the differentially amplified atopic dermatitis related cDNA sequences

CC of the invention.

XX CC Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;

SQ Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1098

DB 17 TAAAAAATAAAAAA 2

RESULT 606

ABK13941/C

ID ABK13941 standard; DNA; 17 BP.

XX AC ABK13941;

XX DT 21-MAY-2002 (first entry)

XX DE 5'-PCR primer used to produce single pattern characteristic by FokI.

XX KW Identification of transcribed gene; mRNA profile; gene expression;

KW cellular process; fingerprinting; susceptibility to external factor;

KW development; disease; PCR; primer; ss.

XX OS Synthetic.

XX PN WO200208461-A2.

XX PD 31-JAN-2002.

XX PF 23-JUL-2001; 2001WO-IB01539.

XX PR 21-JUL-2000; 2000GB-0018016.

XX PR 21-JUL-2000; 2000US-219925P.

XX PA (GLOB-) GLOBAL GENOMICS AB.

XX PI Linnarsson S, Ernfors P, Bauren G;

XX DR WPI; 2002-217065/27.

XX PT Providing mRNA profile, by generating two independent patterns

PT characteristic of sample mRNA population, analysing patterns, comparing

PT gene expression by cell types under varied conditions, and identifying

PT genes -

XX PS Disclosure; Fig 2; 67pp; English.

XX CC The present invention relates to a method for providing a profile of

CC mRNA molecules present in a sample. The method comprises generating

CC two independent patterns characteristic of the population of mRNA

CC molecules expressed in the sample and analysing the patterns using a

CC combinatorial algorithm, comparing gene expression by different or

CC same cell types under different conditions, and identifying genes

CC having a role in various cellular processes. The method is useful

CC for the analysis and identification of transcribed genes, and

CC fingerprinting. The method can be used to identify genes which play a

CC role in determining various cellular processes, including susceptibility

CC to external factors, development, and disease. The present sequence for

CC a PCR primer is used in the production of a single pattern

CC characteristic of a sample, employing a Type IIS restriction enzyme

CC (i.e. FokI) in the methods of the present invention.

XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAAA 1099

DB 16 AAAAAAATAAAAAA 1

RESULT 607

ABZ70578/C

ID ABZ70578 standard; DNA; 17 BP.

XX AC ABZ70578;

XX DT 23-MAY-2003 (first entry)

XX DE Primer.

XX KW Aspergillus phenolics; oxalate decarboxylase; APOXD;

KW transgenic plant; crop protection; primer; ss.

XX OS Synthetic.

XX PN CA2350328-A1.

XX PD 26-DEC-2002.

XX PF 26-JUN-2001; 2001CA-2350328.

XX PR 26-JUN-2001; 2001CA-2350328.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Scelonge C, Bidney D;

XX DR WPI; 2003-240188/25.

XX PT New isolated nucleic acid encoding oxalate decarboxylase from

PT Aspergillus phenolics, for degrading oxalic acid, identifying

XX transformed plant cells, and preventing pathogenic disease in plants -

PS Disclosure; Page 50; 60pp; English.

XX CC The present sequence is that of a primer used in the invention.

CC The invention relates to a novel nucleic acid (see ABZ70560)

CC encoding Aspergillus phenolics oxalate decarboxylase (APOXD)

CC (see ABZ72475). The gene and its encoded protein are useful in

CC degrading oxalate, in diagnostic assays, for protecting plants

CC against disease, and as a selectable marker.

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAATAAAAAA 1099

DB 17 AAAAAAATAAAAAA 2

```

RESULT 608
AAV54167/c
ID AAV54167 standard; DNA; 18 BP.
XX
AC AAV54167;
XX
DT 05-APR-1992 (first entry)
XX
DE Sequence derived from the L1 region of the bovine papillomavirus (bpv)
DE type 1a genome.
XX
KW Diagnostic reagent; vaccine; medicine; wart; tumour; ss.
XX
OS Bovine papillomavirus.
XX
FH Key Location/Qualifiers
CDS 1..18
FT /*tag= a
XX
XX EP2456-A.
XX
XX 26-OCT-1983.
XX
XX 01-APR-1983; 83EP-0901081.
XX
XX 05-APR-1982; 82FR-0005887.
XX
XX (INSP ) INST PASTEUR.
XX
XX (DANO/) DANOS O.
XX
XX Danos O, Katinka M, Yaniv M;
XX
XX WPI; 1983-802979/44.
XX
XX P-PSDB; AAP30313.
XX
DNA fragment coding for Papillomavirus antigenic proteins - and
PT derived immunogen, vaccine and antibody
XX
XX Claim 6; Page 16; 25pp; French.
XX
The inventors claim DNA fragments capable of expressing, in a host,
CC a prod. contg. at least one antigenic determinant of papillomavirus
CC (PV), (see AAN30173-N30173). Also claimed are immunogens consisting
CC of at least one peptide sequence coded for by the DNA fragments (see
CC AAP3010-P3013), vaccines contg. the immunogens and antibodies raised
CC from them. The vaccines are useful in human and veterinary medicine
CC and the antibodies are useful as diagnostic reagents. The DNA
CC fragments are most esp. derived from the L1 region of human PV type
CC 1a.
XX
XX Sequence 18 BP; 16 A; 1 C; 1 G; 0 U; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 3 AAAAAAAAAAAAAA 18

RESULT 609
AAV54167/c
ID AAV54167 standard; cDNA; 18 BP.
XX
AC AAV54167;
XX
XX 21-DEC-1998 (first entry)
XX
XX Nucleotide sequence PCR primer 4.
XX
PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.

```

```

XX Synthetic.
OS
XX WO9839437-A1.
FN
XX 11-SEP-1998.
PD
XX
XX 05-MAR-1998; 98WO-JP00905.
PF
XX 05-MAR-1997; 97JP-0050302.
PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
DR
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis
XX
XX Example 1; Page 48; 70pp; Japanese.
PS
XX
XX This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 other;
XX
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAA 1098
Db 17 TAAAAAAAAAAAAA 2

RESULT 610
AAV54170/c
ID AAV54170 standard; cDNA; 18 BP.
XX
AC AAV54170;
XX
XX 21-DEC-1998 (first entry)
DT
XX
XX Nucleotide sequence PCR primer 7.
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
XX Synthetic.
OS
XX WO9839437-A1.
FN
XX 11-SEP-1998.
PD
XX
XX 05-MAR-1998; 98WO-JP00905.
PF
XX 05-MAR-1997; 97JP-0050302.
PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
DR
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis
XX
XX Example 1; Page 49; 70pp; Japanese.
PS

```

XX This is the nucleotide sequence of a PCR primer used in the method  
 CC of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for  
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1083 TAAAAAATAAAAAA 1098  
 DB 17 TAAAAAATAAAAAA 2

RESULT 611  
 AAV54173/c  
 ID AAV54173 standard; cDNA; 18 BP.

XX AC AAV54173;  
 XX  
 DT 21-DEC-1998 (first entry)  
 XX  
 DE Nucleotide sequence PCR primer 10.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 KW immunohistological staining.

XX Synthetic.  
 XX WO9839437-A1.  
 XX  
 PD 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP00905.  
 XX  
 PR 05-MAR-1997; 97JP-0050302.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Sakaki Y;

XX WPI; 1998-495844/42.  
 XX  
 DR Novel apoptosis-related DNAs and proteins - for diagnosis,  
 XX preventing or treating diseases associated with apoptosis

XX Example 1; Page 50; 70pp; Japanese.  
 XX  
 CC This is the nucleotide sequence of a PCR primer used in the method  
 CC of the invention, involving the use of novel apoptosis-related DNAs  
 CC and proteins. The inventions can be used as diagnostic reagents for  
 CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent  
 CC in immunohistological staining, as apoptosis inhibitors. It can also  
 CC be used for treatment of apoptosis-related diseases.

XX  
 SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;  
 Query Match 1.5%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1083 TAAAAAATAAAAAA 1098  
 DB 17 TAAAAAATAAAAAA 2

RESULT 612  
 AAZ90640/c

ID AAZ90640 standard; DNA; 18 BP.  
 XX  
 AC AAZ90640;  
 XX  
 DT 13-JUN-2000 (first entry)  
 XX  
 DE Human adipose tissue gene amplifying primer #1.  
 XX  
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
 OS Homo sapiens.  
 XX  
 PN JP2000037190-A.  
 XX  
 PD 08-FEB-2000.  
 XX  
 PF 23-JUL-1998; 98JP-0225228.  
 XX  
 PR 23-JUL-1998; 98JP-0225228.  
 XX  
 PA (NISE ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal  
 PT tissue -  
 XX  
 PS Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension,  
 CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes  
 CC (AAZ90631-633) and the proteins (AAZ90631-633) are used in the genetic  
 CC diagnosis, prevention and treatment of adipose tissue related diseases.  
 CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose  
 CC tissue genes.  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1083 TAAAAAATAAAAAA 1098  
 DB 17 TAAAAAATAAAAAA 2

RESULT 613  
 AAZ90643/c  
 ID AAZ90643 standard; DNA; 18 BP.

XX AC AAZ90643;  
 XX  
 DT 13-JUN-2000 (first entry)  
 XX  
 DE Human adipose tissue gene amplifying primer #4.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
 OS Homo sapiens.  
 XX  
 PN JP2000037190-A.  
 XX  
 PD 08-FEB-2000.  
 XX  
 PF 23-JUL-1998; 98JP-0225228.  
 XX  
 PR 23-JUL-1998; 98JP-0225228.

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PA (NISB ) JAPAN TOBACCO INC.
XX
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal
XX tissue -
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension,
XX arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic
XX diagnosis, prevention and treatment of adipose tissue related diseases.
XX Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX tissue genes.
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAAAAAAAAA 1098
XX |||||
XX DB 17 TAAAAAAAAAAAAA 2
XX
XX RESULT 614
XX AAZ90649/C
XX ID AAZ90649 standard; DNA; 18 BP.
XX
XX AC AAZ90649;
XX
XX DT 13-JUN-2000 (first entry)
XX
XX DE Human adipose tissue gene amplifying primer #10.
XX
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX XN JP2000037190-A.
XX
XX PD 08-FEB-2000.
XX
XX PF 23-JUL-1998; 98JP-0225228.
XX
XX PR 23-JUL-1998; 98JP-0225228.
XX
XX PA (NISB ) JAPAN TOBACCO INC.
XX
XX PS WPI; 2000-306578/27.
XX
XX PT A physiologically active protein specifically derived from mammal
XX PT tissue -
XX
XX PS Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension,
XX arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes
XX (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic
XX diagnosis, prevention and treatment of adipose tissue related diseases.
XX Sequences AAZ90640-51 represent PCR primers amplifying the human adipose
XX tissue genes.
XX
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1099
XX |||||
XX DB 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 616
XX AAF75597/C
XX ID AAF75597 standard; DNA; 18 BP.
XX
XX AC AAF75597;
XX
XX DT 10-MAY-2001 (first entry)
XX
XX DE Binary encoded sequence tag method anchored primer #2.
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1083 TAAAAAAAAAAAAA 1098
XX |||||
XX DB 17 TAAAAAAAAAAAAA 2
XX
XX RESULT 615
XX AAF75596/C
XX ID AAF75596 standard; DNA; 18 BP.
XX
XX AC AAF75596;
XX
XX DT 10-MAY-2001 (first entry)
XX
XX DE Binary encoded sequence tag method anchored primer #1.
XX
XX KW Binary encoded sequence tag; BEST; nucleic acid analysis;
XX KW gene expression; adaptor; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX XN WO200112855-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 11-AUG-2000; 2000WO-US22164.
XX
XX PR 13-AUG-1999; 99US-0148870.
XX
XX PR 06-APR-2000; 2000US-0544713.
XX
XX PA (UYVA ) UNIV YALE.
XX
XX PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX
XX WPI; 2001-202878/20.
XX
XX PT Producing binary sequence tags, useful for analyzing nucleic acid
XX PT sequence tags, gene expression or gene-expression patterns, involves
XX PT generating nucleic acid fragments, which are mixed with offset adaptors
XX PT and adaptor-indexers -
XX
XX PS Disclosure; Page 100; 101pp; English.
XX
XX CC The present invention describes a method of producing binary sequence
XX CC tags from nucleic acid fragments in a sample, involving incubating the
XX CC sample with cleaving reagents, mixing offset adaptors with the sample,
XX CC incubating with more cleaving reagents and mixing the sample with
XX CC adaptor-indexers where the adaptors are coupled to binary sequence tags.
XX CC The method is useful in sequence analysis, including analysis and
XX CC comparison of gene expression, nucleic acid samples and genomes.
XX
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 other;
XX
XX Query Match 1.5%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAA 1099
XX |||||
XX DB 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 616
XX AAF75597/C
XX ID AAF75597 standard; DNA; 18 BP.
XX
XX AC AAF75597;
XX
XX DT 10-MAY-2001 (first entry)
XX
XX DE Binary encoded sequence tag method anchored primer #2.
```

```

XX KW Binary encoded sequence tag; BEST; nucleic acid analysis;
XX KW gene expression; adaptor; PCR primer; ss.
XX OS Synthetic.
XX PN WO200112855-A2.
XX PD 22-FEB-2001.
XX PF 11-AUG-2000; 2000WO-US22164.
XX PR 13-AUG-1999; 99US-0148870.
XX PR 06-APR-2000; 2000US-0544713.
XX PA (UYUA ) UNIV YALE.
XX PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX PT Producing binary sequence tags, useful for analyzing nucleic acid
XX PT sequence tags, gene expression or gene-expression patterns, involves
XX PT generating nucleic acid fragments, which are mixed with offset adaptors
XX PT and adaptor-indexers -
XX PS Disclosure; Page 100; 101pp; English.
XX CC The present invention describes a method of producing binary sequence
XX CC tags from nucleic acid fragments in a sample, involving incubating the
XX CC sample with cleaving reagents, mixing offset adaptors with the sample,
XX CC incubating with more cleaving reagents and mixing the sample with
XX CC adaptor-indexers where the adaptors are coupled to binary sequence tags.
XX CC The method is useful in sequence analysis, including analysis and
XX CC comparison of gene expression, nucleic acid samples and genomes.
XX SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 617
ABK51158/c
ID ABK51158 standard; DNA; 18 BP.
AC ABK51158;
XX 30-JUL-2002 (first entry)
XX Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
XX cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
XX reverse transcriptase PCR; RT-PCR; primer; ss.
XX Human cytomegalovirus.
XX OS
XX Key Location/Qualifiers
XX misc_difference 17
XX /tag= a
XX /label= n
XX /note= "n= dATP, dCTP or dGTP"
XX EP1201765-A2.
XX 02-MAY-2002.
XX

Binary encoded sequence tag; BEST; nucleic acid analysis;
gene expression; adaptor; PCR primer; ss.
Synthetic.
WO200112855-A2.
22-FEB-2001.
11-AUG-2000; 2000WO-US22164.
13-AUG-1999; 99US-0148870.
06-APR-2000; 2000US-0544713.
(UYUA ) UNIV YALE.
Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
WPI; 2001-202878/20.
Producing binary sequence tags, useful for analyzing nucleic acid
sequence tags, gene expression or gene-expression patterns, involves
generating nucleic acid fragments, which are mixed with offset adaptors
and adaptor-indexers -
Disclosure; Page 100; 101pp; English.
The present invention describes a method of producing binary sequence
tags from nucleic acid fragments in a sample, involving incubating the
sample with cleaving reagents, mixing offset adaptors with the sample,
incubating with more cleaving reagents and mixing the sample with
adaptor-indexers where the adaptors are coupled to binary sequence tags.
The method is useful in sequence analysis, including analysis and
comparison of gene expression, nucleic acid samples and genomes.
Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 618
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
AC ABK13935;
XX 21-MAY-2002 (first entry)
XX 5'-PCR primer used to produce single pattern characteristic by Haerl.
XX Identification of transcribed gene; mRNA profile; gene expression;
XX cellular process; fingerprinting; susceptibility to external factor;
XX development; disease; PCR; primer; ss.
XX Synthetic.
XX WO200208461-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-IB01539.
XX 21-JUL-2000; 2000GB-0018016.
XX 21-JUL-2000; 2000US-219925P.
XX (GLOB-) GLOBAL GENOMICS AB.
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.
XX

Providing mRNA profile, by generating two independent patterns
characteristic of sample mRNA population, analysing patterns, comparing
gene expression by cell types under varied conditions, and identifying

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```

PT genes -
XX
PS Disclosure; Fig 1; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of
CC mRNA molecules present in a sample. The method comprises generating
CC two independent patterns characteristic of the population of mRNA
CC molecules expressed in the sample and analysing the patterns using a
CC combinatorial algorithm, comparing gene expression by different or
CC same cell types under different conditions, and identifying genes
CC having a role in various cellular processes. The method is useful
CC for the analysis and identification of transcribed genes, and
CC fingerprinting. The method can be used to identify genes which play a
CC role in determining various cellular processes, including susceptibility
CC to external factors, development, and disease. The present sequence for
CC a PCR primer is used in the production of a single pattern
CC characteristic of a sample, employing a Type II restriction enzyme
CC (i.e. HaeII) in the methods of the present invention.
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 619
AADS2799/c
ID AADS2799 standard; DNA; 18 BP.
XX
AC AADS2799;
XX
DT 14-MAY-2003 (first entry)
XX
DE Primer used to prepare radioactively labelled cDNA probes from RNA.
XX
KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW TSE; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;
KW fatal familial insomnia; FFI; Kuru and Alpers syndrome, especially BSE, CJD,
KW Alzheimer's disease; primer; ss.
XX
OS Homo sapiens.
XX
FN WO200293164-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-EP05420.
XX
PR 16-MAY-2001; 2001EP-0111858.
XX
PR 29-MAY-2001; 2001US-293528P.
XX
PR 13-JUL-2001; 2001EP-0117113.
XX
PR 18-JUL-2001; 2001US-305898P.
XX
FA (AXXI-) AXXIMA PHARM AG.
XX
FI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;
XX
DR WPI; 2003-120714/11.
XX
XX New pyridylpyrimidine derivatives useful in the treatment or prevention
XX of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease
XX (CJD) -
XX
XX Example; Page 38; 96pp; English.
XX

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CC The invention relates to novel pyridylpyrimidine derivatives and methods
CC of detecting prion infections and/or prion disease in an individual or in
CC cells, cell cultures and/or cell lysates. The method involves adding at
CC least one monoclonal antibody, oligonucleotide or pyridyl-
CC pyrimidine derivative to the sample or in cells, cell cultures and/or
CC cell lysates and detecting the activity of at least one human cellular
CC protein kinases (e.g., GGF-R1 (also known as fig, Fl-1, Flt-2, b-FGFR),
CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
CC known as c-abl), ctki, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
CC known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL
CC (also known as MCP83) and PTP-zeta, the cellular signal transduction
CC molecules HSP90 and GPCR-1. The invention is useful for regulating the
CC production of prions in cells and in the manufacture of pharmaceutical
CC composition for prophylaxis and/or treatment of infectious disease (e.g.
CC Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
CC (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
CC (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal
CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
CC vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
CC or ruminants. The present DNA sequence is a primer used to prepare
CC radioactively labelled cDNA probes from RNA. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 2 other;

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1099
Db 16 AAAAAAAAAAAAAA 1

RESULT 620
AAS05714
ID AAS05714 standard; DNA; 20 BP.
XX
AC AAS05714;
XX
DT 07-SEP-2001 (first entry)
XX
DE Aminopurine substituted region of an RP-TFO.
XX
KW reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*label= "OTHER"
FT /*note= "A is aminopurine substituted"
FT modified_base 3 /*tag= b
FT /*label= "OTHER"
FT /*note= "A is aminopurine substituted"
FT modified_base 5 /*tag= c
FT /*label= "OTHER"
FT /*note= "A is aminopurine substituted"
FT modified_base 7 /*tag= d
FT /*label= "OTHER"
FT /*note= "A is aminopurine substituted"
FT modified_base 9 /*tag= f
FT /*label= "OTHER"
FT /*note= "A is aminopurine substituted"
FT modified_base 11 /*tag= g
FT

```





XX OS Unidentified.  
 XX PN BP1186673-A2.  
 XX PD 13-MAR-2002.  
 XX PF 10-SEP-2001; 2001EP-0307665.  
 XX PR 11-SEP-2000; 2000US-0659173.  
 XX PA (AGIL-) AGILENT TECHNOLOGIES INC.  
 XX PI Wobler PK, Delenstarr GC;  
 XX DR WPI; 2002-282886/33.  
 XX PT Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes -  
 XX PS Disclosure; Page 14; 32pp; English.  
 XX CC The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibrations probes that generate signals proportional to the total concentrations of labeled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data.  
 XX SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 other;  
 Query Match 1-5%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1099  
 Db 1 AAAAAAAAAAAAAA 16  
 RESULT 623  
 ABA05917/c  
 ID ABA05917 standard; DNA; 20 BP.  
 AC ABA05917;  
 DT 05-MAR-2002 (first entry)  
 DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.  
 KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis; PCR primer; ss.  
 OS Hepatitis B virus.  
 XX EP1152063-A1.  
 XX PD 07-NOV-2001.  
 XX PF 03-MAY-2000; 2000EP-0109436.  
 XX PR 03-MAY-2000; 2000EP-0109436.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Schroeder KH, Koike K;  
 XX DR WPI; 2002-068256/10.

XX PT Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample -  
 XX PS Example 1; Page 6; 25pp; English.  
 XX CC The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:II is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention.  
 XX SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 other;  
 Query Match 1-5%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAAAAAAAAA 1098  
 Db 16 TAAAAAAAAAAAAA 1  
 RESULT 624  
 AAZ09196/c  
 ID AAZ09196 standard; DNA; 21 BP.  
 XX AC AAZ09196;  
 XX DT 19-OCT-1999 (first entry)  
 XX DE Oligonucleotide 8 for DNA analysis.  
 XX KW Primer; DNA analysis; amplification; hybridisation; ss.  
 XX OS Synthetic.  
 XX PN JP11196874-A.  
 XX PD 27-JUL-1999.  
 XX PF 14-JAN-1998; 98JP-0005399.  
 XX PR 14-JAN-1998; 98JP-0005399.  
 XX PA (HITA) HITACHI LTD.  
 XX DR WPI; 1999-496652/42.  
 XX PT Analysis of DNA fragment - comprises addition of known common oligonucleotide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA  
 XX PS Example 1; Page 12; 17pp; Japanese.  
 XX CC This invention describes a novel method for the analysis of a DNA fragment which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment, (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence to the above mentioned known common oligonucleotide sequence, a second common primer containing a complementary nucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the gene having known sequence, to give amplified DNA, (iii) analysis of the amplified DNA to find the information of the DNA fragment, in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation.



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PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
XX WPI; 1996-259862/26.
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
XX Example 10; Page 119; 433pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Radi/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are
CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus and simian immunodeficiency virus. The
CC human tyrosinase gene (both wild type and mutant gene fragments) was
CC used as a test sequence for the method. Three primers (AAT29080-82)
CC were used alongside other primers (AAT27699-90) and in combination, to
CC amplify fragments of wild type and mutant tyrosinase genes.
XX
XX Sequence 19 BP; 3 A; 2 C; 7 G; 7 T; 0 other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 GCACGTTTGGCATTTGGGA 528
Db 1 GCACGTTTGGCATTTGGGA 19

RESULT 628
AAV01125/c
ID AAV01125 standard; DNA; 19 BP.
XX
XX AAV01125;
AC AAV01125;
XX
XX 23-MAR-1998 (first entry)
DE Elastin PCR primer for universal mammalian STS's.
XX
XX PCR primer; polymerase chain reaction; amplification; UM-STS;
KW universal mammalian sequence tagged site; genomic map; clone; ss.
XX
XX Synthetic.
XX
XX WO9731012-A1.
XX
PD 28-AUG-1997.
XX

```

```

PF 18-FEB-1997; 97WO-US02403.
XX
XX 22-FEB-1996; 96US-0012061.
XX
XX (UNMI ) UNIV MICHIGAN.
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
DR WPI; 1997-435083/40.
XX
XX New oligonucleotide primers amplifying gene regions conserved among
PT mammals - useful for developing genomic maps, isolating clones and
PT making cross-species comparisons
XX
XX Claim 1; Page 9; 26pp; English.
XX
XX The present sequence represents a specifically claimed oligonucleotide
CC PCR primer. The oligonucleotide can be used for polymerase chain
CC reaction (PCR) amplification of DNA, specifically regions of specific
CC genes that are conserved among mammalian species, i.e. pairs of
CC oligonucleotides from the present specification represent universal
CC mammalian sequence-tagged site (UM-STs) primers. The primers are used
CC to develop genomic maps, to isolate clones from libraries, to make
CC cross-species comparisons and to develop additional genetic markers.
CC UM-STs allow genomic comparisons to be made between more species.
XX
XX Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
SQ
Query Match 1.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 CTGCTTTGGGGCTGCAGC 154
Db 19 CTGCTTTGGGGCTGCAGC 1

RESULT 629
ABT13587/c
ID ABT13587 standard; DNA; 19 BP.
XX
XX ABT13587;
AC ABT13587;
XX
XX 07-FEB-2003 (first entry)
DE Liver regeneration-related gene panel PCR primer #115.
XX
XX PCR; primer; ss; liver regeneration; gene panel; expression profile;
KW drug screening; drug development; hepatitis; liver transplantation.
XX
XX Unidentified.
XX
XX WO200277222-A1.
XX
XX 03-OCT-2002.
XX
XX 13-MAR-2002; 2002WO-JP02372.
XX
XX 13-MAR-2001; 2001JP-0070940.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;
PI Sonaka I;
XX
XX WPI; 2003-018922/01.
XX
XX Gene panel participating in liver regeneration, applicable in providing
PT expression data, diagnosis and development of drugs for promoting liver
PT regeneration e.g. after transplantation or removal of liver during
PT cancer
XX

```



KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.  
 XX Synthetic.  
 OS WO200132929-A1.  
 PN 10-MAY-2001.  
 PD 03-NOV-2000; 2000WO-US30534.  
 PF 03-NOV-1999; 99US-0163356.  
 XX 03-NOV-1999; 99US-0163416.  
 PR 21-DEC-1999; 99US-0171348.  
 PR 07-JUL-2000; 2000US-0216579.  
 XX (CYGE-) CYGENE INC.  
 PA (OSTE/) OSTE C C.  
 PA Oste CC, Ramberg ER;  
 XX WPI; 2001-343488/36.  
 DR Analysing target nucleic acid sequences, useful for population  
 PT genetics, drug development and diagnosing cancer, comprises hybridizing  
 PT triple forming oligonucleotide and probe to target sequence -  
 XX Example 2; Page 66; 141pp; English.  
 PS The sequence is a polypyrimidine oligonucleotide for binding a second  
 CC reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to  
 CC the target SNP used to analyse Factor V Leiden SNP using the  
 CC method of the invention. The invention relates to analysing target  
 CC nucleic acid sequences comprising restricting isolated DNA, hybridising  
 CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',  
 CC exonuclease to form a protected nucleic acid sequence (PNAs) tail  
 CC structure, hybridising the captured structure with a single nucleotide  
 CC polymorphisms (SNP) identification probe and determining the SNP score.  
 CC The methods can be used for analysing target nucleic acid sequences,  
 CC especially genomic DNA sequences, to determine if they contain SNPs or  
 CC short tandem repeats (STRs). The methods can be used to detect SNPs for  
 CC use in population genetics, drug development, forensics, cancer, genetic  
 CC disease research, genomic analysis, diagnostics and therapeutics in  
 CC humans, plants and animals.  
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;  
 SQ Query Match 1.4%; Score 15.8; DB 1; Length 20;  
 Best Local Similarity 89.5%; Pred. No. 3.5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1081 ATTAAAAA 1099  
 DB 19 AATAAGAAAAA 1  
 RESULT 633  
 AAT48469/C  
 ID AAT48469 standard; DNA; 21 BP.  
 XX AAT48469;  
 AC AAT48469;  
 DT 12-APR-1997 (first entry)  
 DE Third-strand oligonucleotide pyrimidine/parallel motif for TDR.  
 XX Haemoglobinopathy; sickle cell anaemia; haemoglobin; beta-globin;  
 KW HbS; HbA; gene therapy; triple helix; triplex; psoralen; mutagen;  
 KW targeted DNA replacement; TDR; homologous recombination; ss.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 XX Key difference 2  
 FT

FT  
 FT  
 XX  
 PN  
 XX  
 PD  
 XX  
 PF  
 XX  
 PR  
 XX  
 PA  
 XX  
 PI  
 XX  
 DR  
 XX  
 PT  
 PT  
 PT  
 PT  
 XX  
 PS  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 CC  
 SQ  
 Query Match 1.4%; Score 15.8; DB 1; Length 21;  
 Best Local Similarity 89.5%; Pred. No. 3.6e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 114 AGAAACGGGAGAAAGGA 132  
 DB 19 AGAAACGGGAGAAAGGA 1  
 RESULT 634  
 AAZ26632  
 ID AAZ26632 standard; DNA; 21 BP.  
 XX AAZ26632;  
 AC AAZ26632;  
 DT 30-NOV-1999 (first entry)  
 XX Human polymorphic region 821.  
 DE Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
 KW graft versus host disease; malignant cell removal; bone marrow; ss.  
 XX Homo sapiens.  
 OS WO9841648-A2.  
 PN 24-SEP-1998.  
 PD 19-MAR-1998; 98WO-US05419.  
 PF 20-MAR-1997; 97US-0041057.  
 PR (VARI-) VARIAGENICS INC.  
 PA

/\*tag= a  
 /note= "psoralen attachment site"

XX  
PI Houseman D, Ledley FD, Stanton VP;  
XX WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for  
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic  
PT plaque, dysplastic lesions, endometriosis or graft versus host disease  
XX  
PS Disclosure; Figure 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is  
CC active on a gene vital for cell growth or viability, and where the gene  
CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can  
CC be used in the diagnosis, prevention and treatment of LOH disorders,  
CC e.g. cancers, atherosclerotic plaques, premalignant metaplastic or  
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney  
CC disease, and graft versus host disease. The method can also be used to  
CC remove malignant cells from bone marrow transplants. AAZ25812-226825  
CC represent human polymorphic sites described in the method of the  
CC invention.  
XX  
SQ Sequence 21 BP; 15 A; 2 C; 1 G; 3 T; 0 other;  
Query Match 1.4%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 3.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1081 ATTAAAAA 1099  
DB 3 ATTAAC 1099  
RESULT 635  
AAZ14729/c  
ID AAZ14729 standard; DNA; 21 BP.  
XX  
AC AAZ14729;  
XX  
XX 24-MAR-1999 (first entry)  
XX  
DE Triple helix third strand of Beta-globin gene nucleotides 742-762.  
XX  
KW Triple helix formation; DNA detection; triple helix; identification;  
KW bacteria; oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX US5861244-A.  
XX  
XX 19-JAN-1999.  
XX  
XX 22-DEC-1993; 93US-0173489.  
XX  
XX 22-DEC-1993; 93US-0173489.  
XX  
XX 29-OCT-1992; 92US-0968436.  
XX  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
XX Hepburn AG, Wang C;  
XX  
XX WPI; 1999-130384/11.  
XX

PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria  
XX  
PS Disclosure; Columns 17-18; 168pp; English.  
XX  
CC The present sequence represents a polynucleotide that is able to  
CC form a triple helix with a double stranded sequence. Cytosine bases  
CC in the present can be replaced with 5-methylcytosine for increased  
CC triplex stability. The present sequence is used in the assay of the  
CC invention, where it can be part of the anchor DNA or reporter DNA  
CC sequence. The assay comprises adding a sample containing double-stranded  
CC DNA test sequences to an aqueous medium containing at least one complex  
CC of anchor DNA, attached to a solid support, and reporter DNA, where  
CC either a part of the anchor DNA or reporter DNA is designed to form  
CC a triple-strand structure with part of the test sequence. Triplex  
CC formation results in displacement of the reporter DNA which is  
CC detected as an indication of the presence of the DNA test sequence.  
CC The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.  
XX  
SQ Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 other;  
Query Match 1.4%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 3.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 114 AAGAAACGGGAAGGA 132  
DB 19 AAGAAACGGGAAGGA 132  
RESULT 636  
AAZ27844/c  
ID AAZ27844 standard; DNA; 22 BP.  
XX  
AC AAZ27844;  
XX  
XX 23-DEC-1999 (first entry)  
XX  
DE PCR primer for human DNA marker clone S103.  
XX  
KW Tandem repeat sequence; DNA isolation; intermediate tandem repeat;  
KW IIR sequence; pentanucleotide tandem repeat; stutter artifact;  
KW DNA typing; DNA profiling; linkage analysis; criminal justice;  
KW paternity testing; animal lineage analysis; microsatellite loci;  
KW polymorphism detection; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9940194-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 04-FEB-1999; 99WO-US02345.  
XX  
XX 04-FEB-1999; 98US-0018584.  
XX  
XX (PROM-) PROMEGA CORP.  
XX  
XX Schumm JW, Bacher JW;  
XX  
XX WPI; 1999-590696/50.  
XX  
XX Isolating DNA containing intermediate tandem repeat sequences, useful  
XX in DNA profiling  
XX  
XX Claim 30; Page 22; 111pp; English.  
XX  
XX This sequence is a PCR primer for a human DNA marker clone used in the

method of the invention. The method is for isolating a fragment of DNA containing an intermediate tandem repeat (ITR) sequence using hybridization selection, and comprises: (a) providing several DNA fragments, at least one of which contains an ITR sequence, a region of the DNA fragment which contains at least one repeat unit consisting of a sequence of five, six or seven bases repeated in tandem at least two times; (b) providing a stationary support having at least one oligonucleotide associated with it, where the oligonucleotide includes a sequence of nucleotides which is complementary to a portion of the ITR sequence; and (c) combining the DNA fragments with the support under conditions where the DNA fragments including the DNA fragment containing the ITR sequence hybridize to the support. The method is particularly used to isolate DNA containing pentanucleotide tandem repeat sequences as well as to detect target ITR DNA sequences having a low incidence of stutter artifacts (no more than 2.4%). The method is useful in DNA profiling for linkage analysis, criminal justice, paternity testing and other forensic and medical uses. DNA typing is also useful for confirming the lineage of horses, dogs and other prize animals. The invention overcomes problems related to the use of microsatellite loci in DNA profiling. The method can detect polymorphisms with a low incidence of stutter artifacts, which has previously been a problem in interpreting allelic content of loci. The development of markers based on larger repeat units, enables easier separation of the fragments on larger electrophoretic gels. This allows the simultaneous analysis of more loci.

XX Sequence 22 BP; 2 A; 12 C; 2 G; 6 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1001 GAGGCTGGAGATGGGAAG 1019

DB 20 GAGGCTGGGGAATGGCAG 2

RESULT 637

AA563416  
ID AA563416 standard; DNA; 22 BP.

XX AC AA563416;

XX DT 29-JAN-2002 (first entry)

XX DE Oligonucleotide-nanoparticle probe #40.

XX KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;  
XX KW nucleic acid detection; nanostructure; biochip; biofilter;  
XX KW drug delivery; ss.

XX OS Synthetic.

XX PN WO200173123-A2.

XX PD 04-OCT-2001.

XX PF 28-MAR-2001; 2001WO-US10071.

XX PR 28-MAR-2000; 2000US-192699P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-213906P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 08-DEC-2000; 2000US-254392P.

XX PR 11-DEC-2000; 2000US-255235P.

XX PR 12-JAN-2001; 2001US-0760500.

XX PR 28-MAR-2001; 2001US-0820279.

XX PA (NANO-) NANOSPHERE INC.

XX MI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA, Park S, Li Z;

XX DR WPI; 2001-656926/75.

XX

PT Detecting and separating nucleic acid, useful e.g. for diagnosis,  
PT comprises reaction with nanoparticles that carry oligonucleotides  
PT complementary to parts of the target

XX Example 16; Page 139; 404pp; English.

XX The invention relates to a method for detection of nucleic acid (I)  
XX having at least 2 portions, comprising treatment with nanoparticles that  
XX carry oligonucleotides complementary to at least 2 parts of (I), where  
XX detectable change caused by hybridisation of the oligonucleotide to (I)  
XX is observed. The method is used to detect (or to separate) specific (I),  
XX e.g. for diagnosing a wide variety of diseases, sequencing, in forensic  
XX analysis etc., and generally to detect analytes other than (I). The  
XX oligonucleotide-derivatised nanoparticles are also useful for preparing  
XX nanostructures useful, for example, as biochips, biofilters, mechanical  
XX devices, separation membranes, chemical sensors, in computers, and for  
XX drug delivery. Very stable nanoparticle-oligonucleotide conjugates  
XX can be produced, allowing their direct use (as probes) in polymerase  
XX chain reaction, i.e. they survive multiple heating/cooling cycles so do  
XX not need to be added after amplification. (I) are detected by simple  
XX colour change, without the need for special equipment, making possible  
XX rapid field testing for e.g. pathogens. AA563374-AA563448 represent  
XX oligonucleotide-nanoparticle probes, and related sequences, used in the  
XX method of the invention.

XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAAAA 1094

DB 4 CAACCTCGTAAAAAAA 22

RESULT 638

AA563419

ID AA563419 standard; DNA; 22 BP.

XX AC AA563419;

XX DT 29-JAN-2002 (first entry)

XX DE Oligonucleotide-nanoparticle probe #43.

XX KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;  
XX KW nucleic acid detection; nanostructure; biochip; biofilter;  
XX KW drug delivery; ss.

XX OS Synthetic.

XX PN WO200173123-A2.

XX PD 04-OCT-2001.

XX PF 28-MAR-2001; 2001WO-US10071.

XX PR 28-MAR-2000; 2000US-192699P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-213906P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 08-DEC-2000; 2000US-254392P.

XX PR 11-DEC-2000; 2000US-255235P.

XX PR 12-JAN-2001; 2001US-0760500.

XX PR 28-MAR-2001; 2001US-0820279.

XX PA (NANO-) NANOSPHERE INC.

XX MI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA, Park S, Li Z;



```

DR WPI; 2001-656926/75.
XX
XX Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
XX complementary to parts of the target
XX
XX Example 17; Figure 26B; 404pp; English.
XX
XX The invention relates to a method for detection of nucleic acid (I)
XX having at least 2 portions, comprising treatment with nanoparticles that
XX carry oligonucleotides complementary to at least 2 parts of (I), where
XX detectable change caused by hybridisation of the oligonucleotide to (I)
XX is observed. The method is used to detect (or to separate) specific (I),
XX e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
XX analysis etc., and generally to detect analytes other than (I). The
XX oligonucleotide-derived nanoparticles are also useful for preparing
XX nanostructures useful, for example, as biochips, biofilters, mechanical
XX devices, separation membranes, chemical sensors, in computers, and for
XX drug delivery. Very stable nanoparticle-oligonucleotide conjugates
XX can be produced, allowing their direct use (as probes) in polymerase
XX chain reaction, i.e. they survive multiple heating/cooling cycles so do
XX not need to be added after amplification. (I) are detected by simple
XX colour change, without the need for special equipment, making possible
XX rapid field testing for e.g. pathogens. AAS63374-AAS63448 represent
XX oligonucleotide-nanoparticle probes, and related sequences, used in the
XX method of the invention.
XX
XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CAACTATTAAAAA 1094
XX ||||| ||||| ||||| |||||
XX 4 CAACTCGTAAAAA 22
XX
XX Db
XX
XX RESULT 639
XX AAS10359
XX ID AAS10359 standard; DNA; 22 BP.
XX
XX AC AAS10359;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Oligonucleotide-gold conjugate, capture oligonucleotide.
XX
XX KW Nanoparticle; oligonucleotide; DNA detection; DNA isolation;
XX genetic disease; bacterial disease; viral disease; forensic science;
XX paternity testing; gene therapy; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 11..22
XX FT /*tag= a
XX FT /bound_moiety= "Nucleotides 12-1 of the sequence
XX FT appearing as AAS010360"
XX FT misc_feature 22
XX FT /*tag= b
XX FT /note= "C is covalently linked to a colloidal gold
XX FT particle via a HS(CH2)3 moiety"
XX
XX PN WO200151665-A2.
XX
XX PD 19-JUL-2001.
XX
XX PF 12-JAN-2001; 2001WO-US011190.
XX
XX PR 13-JAN-2000; 2000US-0176409.
XX
XX PR 26-APR-2000; 2000US-0200161.
XX
XX PR 26-JUN-2000; 2000US-0603830.

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PR 12-JAN-2001; 2001US-0760500.
XX
XX PA (NANO-) NANOSPHERE INC.
XX
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JU, Elghanian R;
XX Taton TA, Li Z;
XX
XX DR WPI; 2001-451868/48.
XX
XX PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial
XX or viral diseases, by contacting the nucleic acid with oligonucleotides
XX attached to nanoparticles and having sequences complementary a portion
XX of the nucleic acid
XX
XX Example 16; Page 110; 323pp; English.
XX
XX CC The sequence represents an oligonucleotide which is linked by its 3' end
XX to a nanoparticle. The sequence is complementary to a target
XX oligonucleotide. The nanoparticle may be linked to several
XX oligonucleotides. The sequence is used to demonstrate the method of the
XX invention. The invention relates to isolating or detecting a nucleic acid
XX of interest, in a mixture of nucleic acids, by binding it to 2 or more
XX complementary nucleotides which have a nanoparticle attached to their 5'
XX ends. The nanoparticles (e.g. colloidal gold) are used to both isolate
XX and detect (e.g. by linking the particle to a fluorescent probe) the
XX resultant complex. The methods are useful for detecting nucleic acids, be
XX natural or synthetic, and modified or unmodified. The methods may also be
XX applied in the diagnosis of genetic, bacterial and viral diseases, in
XX forensics, in DNA sequencing, for paternity testing, for cell line
XX authentication, and for monitoring gene therapy. The methods are
XX further useful in research and analytical laboratories in DNA
XX sequencing, in the field to detect the presence of specific pathogens,
XX for quick identification of an infection to assist in drug
XX prescription, and in homes and health centres for inexpensive
XX first-line screening. The methods, which are based on observing
XX colour change with the naked eye, are cheap, fast, simple, robust
XX (reagents are stable), do not require specialised or expensive equipment,
XX and little or no instrumentation is required.
XX
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CAACTATTAAAAA 1094
XX ||||| ||||| ||||| |||||
XX 4 CAACTCGTAAAAA 22
XX
XX Db
XX
XX RESULT 640
XX AAS10362
XX ID AAS10362 standard; DNA; 22 BP.
XX
XX AC AAS10362;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Oligonucleotide-gold conjugate, capture oligonucleotide #2.
XX
XX KW Nanoparticle; oligonucleotide; DNA detection; DNA isolation;
XX genetic disease; bacterial disease; viral disease; forensic science;
XX paternity testing; gene therapy; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 11..22
XX FT /*tag= a
XX FT /bound_moiety= "Nucleotides 12-1 of the sequence
XX FT appearing as AAS010364"
XX FT misc_feature 22
XX FT /*tag= b

```

FT /note= "A is covalently linked to a colloidal gold  
 XX particle"  
 PN WO200151665-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 XX 12-JAN-2001; 2001WO-US01190.  
 PF  
 XX 13-JAN-2000; 2000US-0176409.  
 PR  
 XX 26-APR-2000; 2000US-0200161.  
 PR  
 XX 26-JUN-2000; 2000US-0603830.  
 PR  
 XX 12-JAN-2001; 2001US-0760500.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Li Z;  
 XX  
 XX WPI; 2001-4518668/48.  
 DR  
 XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial  
 PT or viral diseases, by contacting the nucleic acid with oligonucleotides  
 PT attached to nanoparticles and having sequences complementary a portion  
 PT of the nucleic acid -  
 XX  
 XX Example 17; Fig 23; 323pp; English.  
 PS  
 XX The sequence represents an oligonucleotide which is linked by its 3' end  
 CC to a nanoparticle. The sequence is complementary to a target  
 CC oligonucleotide. The nanoparticle may be linked to several  
 CC oligonucleotides. The sequence is used to demonstrate the method of the  
 CC invention. The invention relates to isolating or detecting a nucleic acid  
 CC of interest, in a mixture of nucleic acids, by binding it to 2 or more  
 CC complementary nucleotides which have a nanoparticle attached to their 5'  
 CC ends. The nanoparticles (e.g. colloidal gold) are used to both isolate  
 CC and detect (e.g. by linking the particle to a fluorescent probe) the  
 CC resultant complex. The methods are useful for detecting nucleic acids,  
 CC natural or synthetic, and modified or unmodified. The methods may also be  
 CC applied in the diagnosis of genetic, bacterial and viral diseases, in  
 CC forensics, in DNA sequencing, for paternity testing, for cell line  
 CC authentication, and for monitoring gene therapy. The methods are  
 CC further useful in research and analytical laboratories in DNA  
 CC sequencing, in the field to detect the presence of specific pathogens,  
 CC for quick identification of an infection to assist in drug  
 CC prescription, and in homes and health centres for inexpensive  
 CC first-line screening. The methods, which are based on observing  
 CC colour change with the naked eye, are cheap, fast, simple, robust  
 CC (reagents are stable), do not require specialised or expensive equipment,  
 CC and little or no instrumentation is required.  
 XX  
 XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;  
 SQ  
 Query Match 1.4%; Score 15.8; DB 1; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1076 CAACCTATTAAAAA 1094  
 |||||  
 Db 4 CAACCTCGTAAAAA 22  
 RESULT 641  
 AAF28471  
 ID AAF28471 standard; DNA; 22 BP.  
 XX  
 XX AAF28471;  
 AC  
 XX  
 XX 03-APR-2001 (first entry)  
 DT  
 XX Random oligonucleotide, SEQ ID NO: 43.  
 DE  
 XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
 KW

KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;  
 KW cell line authentication; gene therapy; ss.  
 XX Synthetic.  
 OS  
 XX WO200100876-A1.  
 PN  
 XX PD 04-JAN-2001.  
 XX  
 XX 26-JUN-2000; 2000WO-US17507.  
 PF  
 XX 25-JUN-1999; 99US-0344667.  
 PR  
 XX 26-APR-2000; 2000US-0200161.  
 PR  
 XX (MIRK/) MIRKIN C A.  
 PA (LETS/) LETSINGER R L.  
 PA (MUCI/) MUCIC R C.  
 PA (STOR/) STORHOFF J J.  
 PA (ELGH/) ELGHANIAN R.  
 PA (TATO/) TATON T A.  
 XX  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA;  
 XX  
 XX WPI; 2001-061976/07.  
 DR  
 XX Detecting nucleic acid, useful for e.g. diagnosis of diseases,  
 PT forensics and DNA sequencing, comprises observing detectable change  
 PT brought about by hybridization of nucleic acid with substrate or  
 PT particle bound oligonucleotides -  
 XX  
 XX Example 16; Page 85; 205pp; English.  
 PS  
 XX The present sequence is an oligonucleotide used in a method for detecting  
 CC a nucleic acid having at least 2 portions. The method comprises  
 CC hybridising the nucleic acid with oligonucleotides, such as the present  
 CC sequence, attached to a substrate and/or particle and detecting a change  
 CC in colour, conductivity or optical density. The method is useful for the  
 CC diagnosis and/or monitoring of diseases in forensics, in DNA sequencing,  
 CC for paternity testing, for cell line authentication and for monitoring  
 CC gene therapy. Detecting nucleic acids based upon observing a colour  
 CC change is cheap, fast, simple, and does not require specialised or  
 CC expensive equipment. The nanoparticle oligonucleotide conjugates remain  
 CC stable for at least 6 months. A single base mismatch and as little as 20  
 CC femtomoles (fm) of target can be detected using the conjugates.  
 XX  
 XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;  
 SQ  
 Query Match 1.4%; Score 15.8; DB 1; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1076 CAACCTATTAAAAA 1094  
 |||||  
 Db 4 CAACCTCGTAAAAA 22  
 RESULT 642  
 AAF28474  
 ID AAF28474 standard; DNA; 22 BP.  
 XX  
 XX AAF28474;  
 AC  
 XX  
 XX 03-APR-2001 (first entry)  
 DT  
 XX Random oligonucleotide, SEQ ID NO: 46.  
 DE  
 XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
 KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;  
 KW cell line authentication; gene therapy; ss.  
 XX Synthetic.  
 OS

```

PN WO200100876-A1.
XX
PD 04-JAN-2001.
XX
XX 26-JUN-2000; 2000WO-US17507.
XX
XX 25-JUN-1999; 99US-0344667.
XX
XX 26-APR-2000; 2000US-0200161.
XX
XX (MIRK/) MIRKIN C A.
XX (LETS/) LETSINGER R L.
XX (MUCI/) MUCIC R C.
XX (STOR/) STORHOFF J J.
XX (ELGH/) ELGHANIAN R.
XX (TATO/) TATON T A.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA;
XX WPI; 2001-061976/07.
XX
XX Detecting nucleic acid, useful for e.g. diagnosis of diseases,
XX forensics and DNA sequencing, comprises observing detectable change
XX brought about by hybridization of nucleic acid with substrate or
XX particle bound oligonucleotides -
XX
XX Example 17; Fig 26; 205pp; English.
XX
XX The present sequence is an oligonucleotide used in a method for detecting
XX a nucleic acid having at least 2 portions. The method comprises
XX hybridising the nucleic acid with oligonucleotides, such as the present
XX sequence, attached to a substrate and/or particle and detecting a change
XX in colour, conductivity or optical density. The method is useful for the
XX diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
XX for paternity testing, for cell line authentication and for monitoring
XX gene therapy. Detecting nucleic acids based upon observing a colour
XX change is cheap, fast, simple, and does not require specialised or
XX expensive equipment. The nanoparticle oligonucleotide conjugates remain
XX stable for at least 6 months. A single base mismatch and as little as 20
XX femtomoles (fM) of target can be detected using the conjugates.
XX
XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CAACTATTAAAAA 1094
XX ||||| ||||| ||||| |||||
XX 4 CAACTCGTAAAAA 22
XX
XX RESULT 643
XX ABS54436
XX ID ABS54436 standard; DNA; 22 BP.
XX
XX AC ABS54436;
XX
XX DT 28-NOV-2002 (first entry)
XX
XX DE Silver staining method capture oligonucleotide.
XX
XX KW Silver staining; capture oligonucleotide; ss; DNA detection chip;
XX gold nanoparticle; cyanide etching; ultrasound wave; sonication; probe;
XX three component sandwich assay; glass substrate; signal; detection;
XX target-complementary DNA; tree; re-cycled; re-used.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX misc_binding 1..12
XX /*tag= a
XX /bound_moiety= "Target oligonucleotide bases 12-1"
XX
XX FT
XX

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FT /note= "Forms a double-stranded region with bases 12-1 of
FT sequence ABS54437"
FT modified_base 22
FT /*tag= b
FT /mod_base= "OTHER"
FT /note= "3' labelled with HS(CH2)3"
XX
XX PN WO200246483-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 30-NOV-2001; 2001WO-US45039.
XX
XX PR 06-DEC-2000; 2000US-251715P.
XX
XX (NOUN ) UNIV NORTHWESTERN.
XX
XX Mirkin CA, Park S, Jin R;
XX WPI; 2002-698435/75.
XX
XX Removing silver from used DNA detection chips using cyanide etching
XX solutions and ultrasound, allows chips to be re-cycled -
XX
XX Example 1; Page 5; 10pp; English.
XX
XX The invention discloses methods for removing silver from a silver stained
XX DNA detection chip having bound gold nanoparticles, which comprises using
XX a cyanide etching solution or ultrasound waves. The chip based DNA
XX detection method employs gold nanoparticle probes, modified with
XX oligonucleotides, to indicate the presence of a particular DNA sequence
XX hybridised on a transparent substrate in a three component sandwich assay
XX format. Initially the capture oligonucleotide is immobilised onto a glass
XX substrate. The target oligonucleotide is then hybridised to the capture
XX oligonucleotide and then rinsed in a solution containing gold
XX nanoparticle probes functionalised with target-complementary DNA. The
XX signal can be enhanced, creating trees of nanoparticles, which can be
XX visualised with the naked eye. The silver staining method is preferred to
XX fluorescent methods as it is more simplified, selective and sensitive,
XX but the re-use of the chips depended on the complete removal of the stain
XX without damaging the chip. The advantage of these removal methods is that
XX the DNA detection chips from which the silver has been removed may be
XX re-cycled and re-used. The sequence presented is the capture
XX oligonucleotide.
XX
XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CAACTATTAAAAA 1094
XX ||||| ||||| ||||| |||||
XX 4 CAACTCGTAAAAA 22
XX
XX Db
XX
XX RESULT 644
XX ABS64661
XX ID ABS64661 standard; DNA; 22 BP.
XX
XX AC ABS64661;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Nucleic acid detection method associated polynucleotide #43.
XX
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX nanoparticle; viral RNA detection; bacterial DNA detection;
XX fungal DNA detection; nanoprobe conjugate; ss.
XX
XX OS Synthetic.
XX
XX PN WO200246472-A2.

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XX PD 13-JUN-2002.
XX XX
XX PF 07-DEC-2001; 2001WO-US46418.
XX XX
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 08-DEC-2000; 2000US-254418P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR 09-APR-2001; 2001US-282640P.
XX PR 10-AUG-2001; 2001US-0927777.
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-608256/65.
XX XX
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change
XX PT
XX PS Example 16; Page 151; 442pp; English.
XX CC The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridization of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db 4 CAACTCGTAAAAA 22

RESULT 645
ABS64664
ID ABS64664 standard; DNA; 22 BP.
XX AC ABS64664;
XX AC ABS64664;
XX DT 15-NOV-2002 (first entry)
XX DE Nucleic acid detection method associated polynucleotide #46.
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX KW nanoparticle; viral RNA detection; bacterial DNA detection;
XX KW fungal DNA detection; nanoprobe conjugate; ss.

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OS Synthetic.
XX WO200246472-A2.
XX PN
XX PD 13-JUN-2002.
XX XX
XX PF 07-DEC-2001; 2001WO-US46418.
XX XX
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 08-DEC-2000; 2000US-254418P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 11-DEC-2000; 2000US-255233P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR 09-APR-2001; 2001US-282640P.
XX PR 10-AUG-2001; 2001US-0927777.
XX XX
XX PA (NANO-) NANOSPHERE INC.
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX DR WPI; 2002-608256/65.
XX XX
XX PT Detecting nucleic acid having two portions, by providing nanoparticles
XX PT having oligonucleotides attached to it, contacting nucleic acid and
XX PT nanoparticles to allow hybridization, and observing detectable change
XX PT
XX PS Example 17; Fig 26B; 442pp; English.
XX CC The invention describes a method of detecting (M1) a nucleic acid having
XX CC two portions, involving providing nanoparticles having oligonucleotides
XX CC attached to it, which has a sequence complementary to sequence of two
XX CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX CC allow hybridization of oligonucleotides with two or more portions of
XX CC nucleic acid, and observing a detectable change brought about by
XX CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX CC conjugates (II) and the aggregate probe are useful for detecting two or
XX CC more nucleic acids (from a biological source) having at least two
XX CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX CC with a disease, synthetic, or structurally-modified natural or synthetic
XX CC RNA or DNA, or a product of a polymerase chain reaction amplification.
XX CC (II) is useful for preparing a nanoprobe conjugate for detecting an
XX CC analyte, and for detecting a nucleic acid bound to an electrode surface.
XX CC nucleic acid having two portions from other nucleic acids. (I), (II) and
XX CC the aggregate probe are useful for detecting an analyte (especially
XX CC polyvalent analyte) in a sample. This sequence represents a
XX CC polynucleotide used to demonstrate the method of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACTATTAAAAA 1094
Db 4 CAACTCGTAAAAA 22

RESULT 646
ABS64691
ID ABS64691 standard; DNA; 22 BP.
XX AC ABS64691;
XX AC ABS64691;
XX DT 15-NOV-2002 (first entry)
XX DE Nucleic acid detection method associated polynucleotide #73.
XX KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

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KW nanoparticle; viral RNA detection; bacterial DNA detection;
XX fungal DNA detection; nanoprobe conjugate; ss.
XX Synthetic.
OS WO200246472-A2.
XX 13-JUN-2002.
XX 07-DEC-2001; 2001WO-US46418.
XX 08-DEC-2000; 2000US-254392P.
XX 08-DEC-2000; 2000US-254418P.
XX 11-DEC-2000; 2000US-255235P.
XX 11-DEC-2000; 2000US-255236P.
XX 12-JAN-2001; 2001US-0760500.
XX 28-MAR-2001; 2001US-0820279.
XX 09-APR-2001; 2001US-282640P.
XX 10-AUG-2001; 2001US-0927777.
XX (NANO-) NANOSPHERE INC.
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-608256/65.
XX Detecting nucleic acid having two portions, by providing nanoparticles
XX having oligonucleotides attached to it, contacting nucleic acid and
XX nanoparticles to allow hybridization, and observing detectable change
XX
XX Example 26; Fig 52B; 442pp; English.
XX
XX The invention describes a method of detecting (M1) a nucleic acid having
XX two portions, involving providing nanoparticles having oligonucleotides
XX attached to it, which has a sequence complementary to sequence of two
XX portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX allow hybridisation of oligonucleotides with two or more portions of
XX nucleic acid, and observing a detectable change brought about by
XX hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX conjugates (II) and the aggregate probe are useful for detecting two or
XX more nucleic acids (from a biological source) having at least two
XX portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX with a disease, synthetic, or structurally-modified natural or synthetic
XX RNA or DNA, or a product of a polymerase chain reaction amplification.
XX (II) is useful for preparing a nanoprobe conjugate for detecting an
XX analyte, and for detecting a nucleic acid bound to an electrode surface.
XX (I) and (II) are useful for fabrication, and for separating a selected
XX nucleic acid having two portions from other nucleic acids. (I), (II) and
XX the aggregate probe are useful for detecting an analyte (especially
XX polyvalent analyte) in a sample. This sequence represents a
XX polynucleotide used to demonstrate the method of the invention.
XX
XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CCACTATTAAAAAAA 1094
XX ||||| ||||| ||||| ||||| |||||
XX 4 CCACTCGTAAAAAAA 22
XX
XX RESULT 647
XX ABK65023
XX ID ABK65023 standard; DNA; 22 BP.
XX AC ABK65023;
XX XX
XX DT 02-JUL-2002 (first entry)
XX

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DE Nanoparticle-oligonucleotide #43.
XX
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX KW nucleic acid detection; ss.
XX OS Synthetic.
XX PN WO200218643-A2.
XX 07-MAR-2002.
XX 10-AUG-2001; 2001WO-US25237.
XX 11-AUG-2000; 2000US-224631P.
XX 08-DEC-2000; 2000US-254392P.
XX 11-DEC-2000; 2000US-255235P.
XX 12-JAN-2001; 2001US-0760500.
XX 28-MAR-2001; 2001US-0820279.
XX (NANO-) NANOSPHERE INC.
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-259024/30.
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX bacterial diseases, comprises hybridising nanoparticles with attached
XX oligonucleotides to nucleic acid and detecting change brought about by
XX hybridisation -
XX
XX Example 16; Page 407; 412pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid (NA) having
XX at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX attached oligonucleotides (OGN), where OGN has a sequence complementary
XX to the sequence of NA; (b) contacting NA and NP under conditions
XX effective to allow hybridisation of OGN with NA; and (c) observing a
XX detectable change brought about by hybridisation of OGN with NA.
XX The method is useful for detecting a nucleic acid, separating a
XX selected nucleic acid from others and methods of nanofabrication.
XX Detecting analytes such as nucleic acids and proteins are useful for the
XX diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX assays. In particular assays using OGN-NP conjugates prepared using
XX linkers comprising a steroid residue attached to a cyclic disulphide have
XX been found to be approximately 10 times more sensitive than assays
XX employing conjugates prepared using alkanethiols or acyclic disulphides
XX as the linker. The OGN-NP conjugates are stable allowing them to be used
XX directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX target to be PCR amplified can be carried through the 30 or 40 heating
XX cooling cycles of the PCR and are still able to detect the amplicons
XX without opening the tubes and causing contamination. ABK64981-ABK65055
XX represent nanoparticle-oligonucleotides of the invention.
XX
XX Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
XX
XX Query Match 1.4%; Score 15.8; DB 1; Length 22;
XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1076 CCACTATTAAAAAAA 1094
XX ||||| ||||| ||||| ||||| |||||
XX 4 CCACTCGTAAAAAAA 22
XX
XX RESULT 648
XX ABK65026
XX ID ABK65026 standard; DNA; 22 BP.
XX AC ABK65026;
XX XX
XX DT 02-JUL-2002 (first entry)
XX

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XX DE Nanoparticle-oligonucleotide #46.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX KW nucleic acid detection; ss.
XX OS Synthetic.
XX FN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR (NANO-) NANOSPHERE INC.
XX PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX PI WPI; 2002-258024/30.
XX DR Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 17; Figure 26B; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analytes such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABK64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACATTATTAATAAAAAA 1094
||||| |||||||
Db 4 CAACCTGTAATAAAAAA 22
RESULT 649
ABK65053
ID ABK65053 standard; DNA; 22 BP.
XX AC ABK65053;
XX AC ABK92165;

```

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DT XX 02-JUL-2002 (first entry)
DE XX Nanoparticle-oligonucleotide #73.
XX KW Nanoparticle-oligonucleotide; nanofabrication;
XX KW nucleic acid detection; ss.
XX OS Synthetic.
XX FN WO200218643-A2.
XX PD 07-MAR-2002.
XX PF 10-AUG-2001; 2001WO-US25237.
XX PR 11-AUG-2000; 2000US-224631P.
XX PR 08-DEC-2000; 2000US-254392P.
XX PR 11-DEC-2000; 2000US-255235P.
XX PR 12-JAN-2001; 2001US-0760500.
XX PR 28-MAR-2001; 2001US-0820279.
XX PR (NANO-) NANOSPHERE INC.
XX PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX PI Taton TA, Garimella V, Li Z, Park S;
XX PI WPI; 2002-258024/30.
XX DR Detecting nucleic acid, useful for diagnosis of genetic, viral or
XX PT bacterial disease, comprises hybridising nanoparticles with attached
XX PT oligonucleotides to nucleic acid and detecting change brought about by
XX PT hybridisation -
XX PS Example 28; Figure 52; 412pp; English.
XX CC The invention relates to a method of detecting a nucleic acid (NA) having
XX CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
XX CC attached oligonucleotides (OGN), where OGN has a sequence complementary
XX CC to the sequence of NA; (b) contacting NA and NP under conditions
XX CC effective to allow hybridisation of OGN with NA; and (c) observing a
XX CC detectable change brought about by hybridisation of OGN with NA.
XX CC The method is useful for detecting a nucleic acid, separating a
XX CC selected nucleic acid from others and methods of nanofabrication.
XX CC Detecting analytes such as nucleic acids and proteins are useful for the
XX CC diagnosis of genetic, bacterial and viral diseases. The OGN-NP conjugates
XX CC that use cyclic disulphide linkers improve the sensitivity of diagnostic
XX CC assays. In particular assays using OGN-NP conjugates prepared using
XX CC linkers comprising a steroid residue attached to a cyclic disulphide have
XX CC been found to be approximately 10 times more sensitive than assays
XX CC employing conjugates prepared using alkanethiols or acyclic disulphides
XX CC as the linker. The OGN-NP conjugates are stable allowing them to be used
XX CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
XX CC target to be PCR amplified can be carried through the 30 or 40 heating
XX CC cooling cycles of the PCR and are still able to detect the amplicons
XX CC without opening the tubes and causing contamination. ABK64981-ABK65055
XX CC represent nanoparticle-oligonucleotides of the invention.
XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1076 CAACATTATTAATAAAAAA 1094
||||| |||||||
Db 4 CAACCTGTAATAAAAAA 22
RESULT 650
ABX92165
ID ABX92165 standard; DNA; 22 BP.
XX AC ABX92165;

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XX DB 12-MAY-2003 (first entry)

XX DE Nanoparticle-associated oligonucleotide SEQ ID 43.

XX KW Nonparticle; nucleic acid detection; hybridisation; diagnosis;

XX KW sequencing; viral infection; human immunodeficiency virus; HIV;

XX KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

XX KW bacterial infection; sexually transmitted disease; inherited disorder;

XX KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX OS Synthetic.

XX PN US2002155458-A1.

XX PD 24-OCT-2002.

XX PF 28-SEP-2001; 2001US-0967409.

XX PR 29-JUL-1996; 96US-031809P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 21-JUL-1997; 97WO-US12783.

XX PR 29-JAN-1999; 99US-0240755.

XX PR 25-JUN-1999; 99US-0344667.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2003-182627/18.

XX PT Detecting nucleic acids having at least two portions involves use of

XX PT nanoparticles which have oligonucleotides attached to them that are

XX PT complementary to portions of the nucleic acid sequence -

XX PS Example 16; Page 57; 130pp; English.

XX CC This invention describes a novel method of detecting nucleic acid having

XX CC at least two portions. The method involves providing nanoparticles

XX CC attached to oligonucleotides, where the oligonucleotide on each

XX CC nanoparticle have a sequence complementary to a sequence of at least two

XX CC portions of nucleic acid, contacting nucleic acid and nanoparticle to

XX CC allow hybridisation of the oligonucleotide on the nanoparticle with two

XX CC or more portions of nucleic acid and observing a detectable change

XX CC brought about by hybridisation of the oligonucleotide nanoparticle with

XX CC nucleic acid. The method is useful for separating a selected nucleic

XX CC acid having at least two portions, from other nucleic acids and for

XX CC detecting nucleic acids having at least two portions. The method is

XX CC useful for detecting any type of nucleic acids which may be used for

XX CC diagnosis of disease and in sequencing of nucleic acids. Preferably, the

XX CC method is useful for detecting nucleic acids for diagnosis and/or

XX CC monitoring of viral infections (human immunodeficiency virus (HIV),

XX CC hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus),

XX CC bacterial diseases, sexually transmitted diseases, inherited disorders,

XX CC in forensics, in DNA sequencing, for paternity testing, for cell line

XX CC authentication, and for monitoring gene therapy. The method is useful in

XX CC research and analytical laboratories in DNA sequencing, in the field to

XX CC detect the presence of specific pathogens. Detecting nucleic acids based

XX CC on observing a colour change with the naked eye is cheap, fast, simple

XX CC and robust and does not require specialised expensive equipment.

XX CC ABX92123-ABX92186 and ABQ7356 represent oligonucleotides used to

XX CC illustrate the method of the invention.

XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;

XX Query Match 1.4%; Score 15.8; DB 1; Length 22;

XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;

XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 1076 CAACTATTAAAAAAA 1094

XX ||||| |||||||||

DB 4 CAACTCGTAAAAAAA 22

RESULT 651

ABX92168

ID ABX92168 standard; DNA; 22 BP.

XX AC ABX92168;

XX DT 12-MAY-2003 (first entry)

XX DE Nanoparticle-associated oligonucleotide SEQ ID 46.

XX KW Nonparticle; nucleic acid detection; hybridisation; diagnosis;

XX KW sequencing; viral infection; human immunodeficiency virus; HIV;

XX KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

XX KW bacterial infection; sexually transmitted disease; inherited disorder;

XX KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX OS Synthetic.

XX PN US2002155458-A1.

XX PD 24-OCT-2002.

XX PF 28-SEP-2001; 2001US-0967409.

XX PR 29-JUL-1996; 96US-031809P.

XX PR 26-APR-2000; 2000US-200161P.

XX PR 26-JUN-2000; 2000US-0603830.

XX PR 21-JUL-1997; 97WO-US12783.

XX PR 29-JAN-1999; 99US-0240755.

XX PR 25-JUN-1999; 99US-0344667.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2003-182627/18.

XX PT Detecting nucleic acids having at least two portions involves use of

XX PT nanoparticles which have oligonucleotides attached to them that are

XX PT complementary to portions of the nucleic acid sequence -

XX PS Example 17; Figure 26; 130pp; English.

XX CC This invention describes a novel method of detecting nucleic acid having

XX CC at least two portions. The method involves providing nanoparticles

XX CC attached to oligonucleotides, where the oligonucleotide on each

XX CC nanoparticle have a sequence complementary to a sequence of at least two

XX CC portions of nucleic acid, contacting nucleic acid and nanoparticle to

XX CC allow hybridisation of the oligonucleotide on the nanoparticle with two

XX CC or more portions of nucleic acid and observing a detectable change

XX CC brought about by hybridisation of the oligonucleotide nanoparticle with

XX CC nucleic acid. The method is useful for separating a selected nucleic

XX CC acid having at least two portions, from other nucleic acids and for

XX CC detecting nucleic acids having at least two portions. The method is

XX CC useful for detecting any type of nucleic acids which may be used for

XX CC diagnosis of disease and in sequencing of nucleic acids. Preferably, the

XX CC method is useful for detecting nucleic acids for diagnosis and/or

XX CC monitoring of viral infections (human immunodeficiency virus (HIV),

XX CC hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus),

XX CC bacterial diseases, sexually transmitted diseases, inherited disorders,

XX CC in forensics, in DNA sequencing, for paternity testing, for cell line

XX CC authentication, and for monitoring gene therapy. The method is useful in

XX CC research and analytical laboratories in DNA sequencing, in the field to

XX CC detect the presence of specific pathogens. Detecting nucleic acids based

XX CC on observing a colour change with the naked eye is cheap, fast, simple

XX CC and robust and does not require specialised expensive equipment.

XX CC ABX92123-ABX92186 and ABQ7356 represent oligonucleotides used to

XX CC illustrate the method of the invention.

```
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CCACTATTAAAAAAA 1094
||||| |||||||
4 CCACTCGTAAAAAAA 22

Db
RESULT 652
ABX98146
ID ABX98146 standard; DNA; 22 BP.
XX
AC ABX98146;
XX
DT 16-MAY-2003 (first entry)
XX
DE Nucleic acid detection method associated oligonucleotide #42.
XX
KW Nucleic acid detection; nanoparticle; HIV; bacterial disease;
KW inherited disease; cystic fibrosis; cancer; sequencing;
KW forensic; paternity testing; cell line authentication; gene therapy;
KW ss.
XX
OS Synthetic.
XX
PN US6495324-B1.
XX
PD 17-DEC-2002.
XX
PF 20-OCT-2000; 2000US-0693005.
XX
PR 29-JUL-1996; 96US-031809P.
PR 25-JUN-1999; 99US-0344667.
PR 21-JUL-1997; 97WO-US12783.
PR 29-JAN-1999; 99US-0240755.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX WPI; 2003-237646/23.
XX
PT Detecting a nucleic acid using oligonucleotides attached to
PT nanoparticles, where each oligonucleotide has a sequence complementary
PT to at least two portions of the nucleic acid being detected, useful in
PT diagnosis of a diseases (e.g. HIV) -
XX
PS Example 16; Column 60; 79pp; English.
XX
CC The invention describes a method of detecting a nucleic acid using
CC oligonucleotides (OG) attached to nanoparticles. The OG on each
CC nanoparticle have a sequence complementary to the sequences of at least
CC two portions of the nucleic acid being detected. Contacting between the
CC nanoparticle conjugated OG and nucleic acids takes place under
CC hybridisation conditions, where binding is detected via a colour change.
CC The method has applications in diagnosis of a diseases (e.g. diagnosing
CC and monitoring viral diseases such as HIV, bacterial diseases, inherited
CC diseases such as cystic fibrosis, cancers, etc.), in sequencing of
CC nucleic acids, in forensics for paternity testing, for cell line
CC authentication and for monitoring gene therapy. This sequence
CC represents a DNA associated with the nucleic acid detection method of
CC the invention.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CCACTATTAAAAAAA 1094
||||| |||||||
4 CCACTCGTAAAAAAA 22

Db
RESULT 654
ABX79169
ID ABX79169 standard; DNA; 22 BP.
```

```
Db
||||| |||||||
4 CCACTCGTAAAAAAA 22

RESULT 653
ABX98149
ID ABX98149 standard; DNA; 22 BP.
XX
AC ABX98149;
XX
DT 16-MAY-2003 (first entry)
XX
DE Nucleic acid detection method associated oligonucleotide #45.
XX
KW Nucleic acid detection; nanoparticle; HIV; bacterial disease;
KW inherited disease; cystic fibrosis; cancer; sequencing;
KW forensic; paternity testing; cell line authentication; gene therapy;
KW ss.
XX
OS Synthetic.
XX
PN US6495324-B1.
XX
PD 17-DEC-2002.
XX
PF 20-OCT-2000; 2000US-0693005.
XX
PR 29-JUL-1996; 96US-031809P.
PR 25-JUN-1999; 99US-0344667.
PR 21-JUL-1997; 97WO-US12783.
PR 29-JAN-1999; 99US-0240755.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX WPI; 2003-237646/23.
XX
PT Detecting a nucleic acid using oligonucleotides attached to
PT nanoparticles, where each oligonucleotide has a sequence complementary
PT to at least two portions of the nucleic acid being detected, useful in
PT diagnosis of a diseases (e.g. HIV) -
XX
PS Example 17; Fig 26B; 79pp; English.
XX
CC The invention describes a method of detecting a nucleic acid using
CC oligonucleotides (OG) attached to nanoparticles. The OG on each
CC nanoparticle have a sequence complementary to the sequences of at least
CC two portions of the nucleic acid being detected. Contacting between the
CC nanoparticle conjugated OG and nucleic acids takes place under
CC hybridisation conditions, where binding is detected via a colour change.
CC The method has applications in diagnosis of a diseases (e.g. diagnosing
CC and monitoring viral diseases such as HIV, bacterial diseases, inherited
CC diseases such as cystic fibrosis, cancers, etc.), in sequencing of
CC nucleic acids, in forensics for paternity testing, for cell line
CC authentication and for monitoring gene therapy. This sequence
CC represents a DNA associated with the nucleic acid detection method of
CC the invention.
XX
SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;
Query Match 1.4%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CCACTATTAAAAAAA 1094
||||| |||||||
4 CCACTCGTAAAAAAA 22

Db
RESULT 654
ABX79169
ID ABX79169 standard; DNA; 22 BP.
```



XX AC ABX79169;  
 XX DT 15-APR-2003 (first entry)  
 XX DE Immobilised capture probe for assay involving silver staining.  
 XX KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;  
 XX KW human immunodeficiency virus infection; hepatitis virus infection;  
 XX KW herpes virus infection; cytomegalovirus infection; forensic science;  
 XX KW Epstein-Barr virus infection; bacterial disease; gene therapy;  
 XX KW sexually transmitted disease; inherited disorder; DNA sequencing;  
 XX KW paternity testing; cell line authentication.  
 XX OS Synthetic.  
 XX PN US2002155462-A1.  
 XX PD 24-OCT-2002.  
 XX PF 12-OCT-2001; 2001US-0976577.  
 XX PR 29-JUL-1996; 96US-031809P.  
 XX PR 26-APR-2000; 2000US-200161P.  
 XX PR 26-JUN-2000; 2000US-0603830.  
 XX PR 21-JUL-1997; 97WO-US12783.  
 XX PR 29-JAN-1999; 99US-0240755.  
 XX PR 25-JUN-1999; 99US-0344667.  
 XX PA (NANO-) NANOSPHERE INC.  
 XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 XX PI Taton TA;  
 XX DR WPI; 2003-198491/19.  
 XX PT Detecting nucleic acids having at least 2 portions comprises use of  
 XX PT nanoparticles which have oligonucleotides attached to them that are  
 XX PT complementary to portions of the nucleic acid sequence -  
 XX PS Example 16; Page 37; 130pp; English.  
 XX CC The invention relates to detecting a nucleic acid (NA) having at least  
 XX CC 2 portions, comprises providing a type of nanoparticles (NP) having  
 XX CC attached to oligonucleotides (O) ((O) on each NP has a sequence  
 XX CC complementary to sequence of at least 2 portions of NA), contacting NA  
 XX CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,  
 XX CC and observing a detectable change brought about by hybridisation of (O)  
 XX CC on NP with NA. The nanoparticle is useful for separating a selected  
 XX CC nucleic acid having at least 2 portions, from other nucleic acids, and  
 XX CC for detecting nucleic acids having at least 2 portions. The method of  
 XX CC using NP is useful for detecting any type of nucleic acids which may be  
 XX CC used for diagnosis of disease and in sequencing of nucleic acids.  
 XX CC Preferably, the method is useful for detecting nucleic acids for  
 XX CC diagnosis and/or monitoring of viral diseases (human immunodeficiency  
 XX CC virus), bacterial diseases, sexually transmitted diseases, inherited  
 XX CC disorders, in forensics, in DNA sequencing, for paternity testing, for  
 XX CC cell line authentication and for monitoring gene therapy. The method is  
 XX CC useful in research and analytical laboratories in DNA sequencing and in  
 XX CC the field to detect the presence of specific pathogens. Detecting nucleic  
 XX CC acids based on observing a colour change with the naked eye is cheap,  
 XX CC fast, simple and robust, and do not require specialised expensive  
 XX CC equipment. The present sequence is a nanoparticle (e.g. gold  
 XX CC particles) labelled probe used to demonstrate the method of the  
 XX CC invention.  
 XX SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;  
 XX Query Match 1.4%; Score 15.8; DB 1; Length 22;  
 XX Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1076 CAACCTATTAAAAA 1094  
 DB 4 CAACTCGTAAAAA 22  
 RESULT 655  
 ABX79172  
 ID ABX79172 standard; DNA; 22 BP.  
 XX AC ABX79172;  
 XX DT 15-APR-2003 (first entry)  
 XX DE CdSe/ZnS core/shell quantum dots oligonucleotide #1.  
 XX KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;  
 XX KW human immunodeficiency virus infection; hepatitis virus infection;  
 XX KW herpes virus infection; cytomegalovirus infection; forensic science;  
 XX KW Epstein-Barr virus infection; bacterial disease; gene therapy;  
 XX KW sexually transmitted disease; inherited disorder; DNA sequencing;  
 XX KW paternity testing; cell line authentication; quantum dot;  
 XX KW semiconductor.  
 XX OS Synthetic.  
 XX PN US2002155462-A1.  
 XX PD 24-OCT-2002.  
 XX PF 12-OCT-2001; 2001US-0976577.  
 XX PR 29-JUL-1996; 96US-031809P.  
 XX PR 26-APR-2000; 2000US-200161P.  
 XX PR 26-JUN-2000; 2000US-0603830.  
 XX PR 21-JUL-1997; 97WO-US12783.  
 XX PR 29-JAN-1999; 99US-0240755.  
 XX PR 25-JUN-1999; 99US-0344667.  
 XX PA (NANO-) NANOSPHERE INC.  
 XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 XX PI Taton TA;  
 XX DR WPI; 2003-198491/19.  
 XX PT Detecting nucleic acids having at least 2 portions comprises use of  
 XX PT nanoparticles which have oligonucleotides attached to them that are  
 XX PT complementary to portions of the nucleic acid sequence -  
 XX PS Example 17; Fig 26; 130pp; English.  
 XX CC The invention relates to detecting a nucleic acid (NA) having at least  
 XX CC 2 portions, comprises providing a type of nanoparticles (NP) having  
 XX CC attached to oligonucleotides (O) ((O) on each NP has a sequence  
 XX CC complementary to sequence of at least 2 portions of NA), contacting NA  
 XX CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,  
 XX CC and observing a detectable change brought about by hybridisation of (O)  
 XX CC on NP with NA. The nanoparticle is useful for separating a selected  
 XX CC nucleic acid having at least 2 portions, from other nucleic acids, and  
 XX CC for detecting nucleic acids having at least 2 portions. The method of  
 XX CC using NP is useful for detecting any type of nucleic acids which may be  
 XX CC used for diagnosis of disease and in sequencing of nucleic acids.  
 XX CC Preferably, the method is useful for detecting nucleic acids for  
 XX CC diagnosis and/or monitoring of viral diseases (human immunodeficiency  
 XX CC virus), hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr  
 XX CC virus), bacterial diseases, sexually transmitted diseases, inherited  
 XX CC disorders, in forensics, in DNA sequencing, for paternity testing, for  
 XX CC cell line authentication and for monitoring gene therapy. The method is  
 XX CC useful in research and analytical laboratories in DNA sequencing and in  
 XX CC the field to detect the presence of specific pathogens. Detecting nucleic  
 XX CC acids based on observing a colour change with the naked eye is cheap,  
 XX CC fast, simple and robust, and do not require specialised expensive  
 XX CC equipment. The present sequence is a nanoparticle (e.g. gold  
 XX CC particles) labelled probe used to demonstrate the method of the  
 XX CC invention.

CC particles) labelled probe used to demonstrate the method of the  
 CC invention. In this case the oligonucleotides are immobilised onto  
 CC semiconductor nanoparticle quantum dots.  
 XX  
 SQ Sequence 22 BP; 13 A; 4 C; 1 G; 4 T; 0 other;  
 Query Match 1.4%; Score 15.8; DB 1; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1076 CAACTATTAAAAA 1094  
 Db 4 CAACTGTAATAAAAAA 22  
 RESULT 656  
 ABV74140/c  
 ID ABV74140 standard; DNA; 22 BP.  
 XX  
 AC ABV74140;  
 XX  
 DT 23-JAN-2003 (first entry)  
 XX  
 DE Oligonucleotide used in cDNA library array.  
 XX  
 KW G-protein coupled receptor; odourant; receptor; olfaction; array;  
 KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer;  
 KW ss.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1.  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "5, polylinker"  
 XX  
 PN WO200277200-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US09559.  
 XX  
 PR 27-MAR-2001; 2001US-279168P.  
 PR 31-JAN-2002; 2002US-353392P.  
 XX  
 PA (INSC-) INSCENT INC.  
 XX  
 PI Woods D, Dimitratos S;  
 XX  
 DR WPI; 2003-029930/02.  
 XX  
 PT Identifying nucleic acid encoding novel sex-linked-tissue-linked  
 PT receptors, useful for isolating odourant binding proteins or pesticide  
 PT alternatives, by analyzing sequences from a male- and female-specific  
 PT nucleic acid library  
 XX  
 PS Disclosure; Fig 5; 83pp; English.  
 XX  
 CC The present sequence is that of an oligonucleotide used in a method  
 CC designed to rapidly array and normalize a complex cDNA library  
 CC obtained from a target species. Clones are arrayed into multi-well  
 CC plates. Each well contains 16 oligonucleotides with a 5' polylinker,  
 CC a poly-T run capable of binding cDNAs by their poly-A tail and a  
 CC unique 3' sequence, which allows an anchored oligonucleotide in each  
 CC well to selectively hybridise only to those cDNA clones with a  
 CC complementary 5' end. The unique 3' key sequences are designed to  
 CC give a comprehensive level of degeneracy since they are diverse and  
 CC numerous enough to ensure that every possible cDNA sequence can be  
 CC bound by an individual, specific oligonucleotide in a single well.  
 CC The cDNA library is heated to denature the clones into single  
 CC stranded DNA, and an aliquot is added to every well. The anchored  
 CC oligonucleotide serves as the 3' primer in PCR, and the common 5'

CC region present in every cDNA clone serves as the 5' priming site.  
 CC Denaturing and washing leave anchored cDNA in each well. The library  
 CC is now arrayed and normalised. The method was used to identify and  
 CC isolate clones encoding G-protein coupled receptors, especially  
 CC odourant receptors, and active effectors involved in the olfactory  
 CC pathway of invertebrates and vertebrates, e.g. odourant binding  
 CC proteins, or other olfactory or neuronal proteins. The identified  
 CC receptors and proteins are useful for identifying compounds that  
 CC reduce a target animal's sensitivity to odours, for manufacturing  
 CC compounds or devices that mask odours, or trapping invertebrates with  
 CC odourants. Semiochemicals (e.g. aromatics or pheromone mimetics) can  
 CC be developed with desirable effects on specific species, for the  
 CC development of pest monitoring systems or non-toxic, species-specific  
 CC pesticide alternatives, for controlling insect feeding and breeding  
 CC behaviour, detecting the presence of small air-borne molecules, etc.  
 XX  
 SQ Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 other;

Query Match 1.4%; Score 15.8; DB 1; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1098  
 Db 19 TGTCAAAAAA 1

RESULT 657  
 AAZ89372/c  
 ID AAZ89372 standard; DNA; 17 BP.  
 XX  
 AC AAZ89372;  
 XX  
 DT 15-JUN-2000 (first entry)  
 XX  
 DE RNA detecting primer #2.  
 XX  
 KW Amplification; detection; gene expression; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN DE19840731-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 07-SEP-1998; 98DE-1040731.  
 XX  
 PR 07-SEP-1998; 98DE-1040731.  
 XX  
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.  
 XX  
 DR WPI; 2000-257789/23.  
 XX  
 PT Analysis of RNA samples, useful for detection of differential gene  
 PT expression uses two differently labeled primers  
 XX  
 PS Disclosure; Page 10; 10pp; German.  
 XX

CC This invention describes a novel method for analysis of an RNA sample  
 CC which comprises amplifying cDNA with first and second differently  
 CC labeled primers and analysis of the amplified labeled cDNA. The method  
 CC is useful for analyzing differential gene expression, for identifying  
 CC and/or characterizing pharmacological activities or for identifying  
 CC target genes. The use of different primer combinations allow more cDNAs  
 CC to be amplified. The method also provides a more detailed analysis than  
 CC prior art methods. This sequence represents a primer used to illustrate  
 CC the method of the invention.

Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 2 other;

Query Match 1.4%; Score 15.6; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1098  
 Db 16 KAAAAA...AAAAA 1

RESULT 658  
 AAQ82104/C  
 ID AAQ82104 standard; DNA; 22 BP.  
 XX  
 AC AAQ82104;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 31-AUG-1995 (first entry)  
 XX  
 DE Chromosome 11 (locus D11S1037) STS primer CSRL-2c7-tz.  
 XX  
 KW sequence sampled mapping; genomic analysis; complex genome mapping;  
 KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN W09429486-A1.  
 XX  
 PD 22-DEC-1994.  
 XX  
 XX 15-JUN-1994; 94WO-US06810.  
 XX  
 PR 15-JUN-1993; 93US-0078471.  
 PR 07-SEP-1993; 93US-0117952.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Evans GA, Smith MW;  
 XX  
 DR WPI; 1995-036508/05.  
 XX  
 XX Sequencing complex genomes, present as fragments in a cosmid  
 PT library - by sequencing end-specific nucleotides of each clone  
 PT then correlating with spatial relationship of cosmid, esp. for  
 PT mammalian chromosomes.  
 XX  
 PS Example 4; Page 66; 128pp; English.  
 XX  
 CC Sequences were determined from the ends of chromosome 11-specific  
 CC cosmids by automated sequencing without intermediate subcloning.  
 CC A sample of 371 DNA sequence fragments were determined and of  
 CC these, 277 were suitable for STS primer prediction and of  
 CC analysis (using the "Primer" program available from E.Lander, MIT).  
 CC The STSs and cosmids were mapped by in situ hybridization, somatic  
 CC cell hybrid analysis or both. Using this method, 370 STSs specific  
 CC for human chromosome 11 were generated and most of them were  
 CC regionally mapped. This procedure illustrates a novel method for  
 CC sequencing complex genomes, designated "sequence sampled mapping".  
 CC The sequence sampled mapping method is useful for the completion of  
 CC high density sequence-based maps, and ultimately, for the complete  
 CC sequencing of genomic DNA directly from cosmid clones.  
 CC See AAQ82001-Q82706 for STS primers.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 other;  
 XX

Query Match 1.4%; Score 15.6; DB 1; Length 22;  
 Best Local Similarity 81.8%; Pred. No. 4.1e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 548 CTCTGTAGCCCAACAGCAGGGA 569  
 Db 22 CTTTGTAGACAAAGCAGGTA 1

RESULT 659  
 AAC69375

ID AAC69375 standard; DNA; 22 BP.  
 XX  
 AC AAC69375;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200055318-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-IB00532.  
 XX  
 PR 15-MAR-1999; 99US-0124702.  
 PR 08-JUN-1999; 99US-0138048.  
 PR 17-JUN-1999; 99US-0139600.  
 PR 01-SEP-1999; 99US-0151977.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON BIORESEARCH INC.  
 XX  
 PI Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 DR WPI; 2000-587528/55.  
 XX  
 XX New ABC1 polypeptide is useful for treating diseases associated with  
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 PT disease and cancer -  
 XX  
 PS Examples; Fig 11; 229pp; English.  
 XX

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHD). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.

CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1.  
 CC The present sequence represents a polymorphic site of the human ABC1  
 CC gene.  
 XX

SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;  
 Query Match 1.4%; Score 15.6; DB 1; Length 22;  
 Best Local Similarity 81.8%; Pred. No. 4.1e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 991 TTGGAGGCTTAAGCAGGAGAA 1012  
 DB 1 TTGGAGGCTTAAGCAGGAGAA 22

RESULT 660  
 AAA57767/C  
 ID AAA57767 standard; DNA; 22 BP.  
 XX  
 AC AAA57767;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Nucleotide sequence which is bound by 22 domain of RIP60 polypeptide.  
 XX  
 KW Human; RIP60; zinc finger protein; nucleic acid delivery complex;  
 KW nucleic acid binding domain; nucleic acid condensation domain; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200040723-A2.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 04-JAN-2000; 2000WO-US00212.  
 XX  
 PR 04-JAN-1999; 99US-0114743.  
 PR 04-JAN-1999; 99US-0114745.  
 XX  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 XX  
 PI Heintz NH, Houchens CR;  
 XX  
 DR WPI; 2000-465985/40.  
 XX

PT Non-viral nucleic acid delivery complex for delivering a nucleic acid  
 PT molecule into a cell comprises a modular polypeptide -  
 XX  
 PS Example 17; Page 74; 115pp; English.  
 XX  
 CC The present sequence is bound by the 22 domain of the human RIP60  
 CC polypeptide. RIP60 is a zinc finger protein. The nucleic acid  
 CC binding domain of the RIP60 polypeptide is used to construct a  
 CC non-viral nucleic acid delivery complex comprising a modular  
 CC polypeptide. The complex comprises a modular peptide containing  
 CC a nucleic acid binding domain and a nucleic acid condensation domain  
 CC that bind with and condense a nucleic acid molecule of more than  
 CC 50 kilobases in length. The complex also comprises one or more  
 CC polypeptides selected from a cell recognition domain, a protein  
 CC transduction domain, a protein degradation domain, an intracellular  
 CC targeting domain, a protein interaction domain, an epitope domain and  
 CC a protein purification domain. The complexes are used to deliver a  
 CC nucleic acid to a cell. The nucleic acids delivered are of various  
 CC sizes and preferably greater than 50 kilobases, especially more than  
 CC 100 or more than 200 kilobases in length.  
 XX

SQ Sequence 22 BP; 5 A; 0 C; 1 G; 16 T; 0 other;  
 Query Match 1.4%; Score 15.6; DB 1; Length 22;  
 Best Local Similarity 81.8%; Pred. No. 4.1e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1078 ACTATTAAAAA 1099  
 DB 22 ACTAATAATAATAAAAAA 1

RESULT 661  
 ABQ93623/C  
 ID ABQ93623 standard; DNA; 22 BP.  
 XX  
 AC ABQ93623;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE Human DISC1/DISC2 PCR primer disc25 f2.  
 XX

KW Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy;  
 KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;  
 KW unipolar affective disorder; adolescent conduct disorder;  
 KW schizophrenia; PCR; primer; ss.  
 XX

OS Homo sapiens.

PN WO200258637-A2.

PD 01-AUG-2002.

PF 23-JAN-2002; 2002WO-US02186.

PR 24-JAN-2001; 2001US-0770107.

PA (MILL-) MILLENIUM PHARM INC.

PI Meyer JM, Barrington-martin R, Parker A, Barnes GT;

DR WPI; 2002-590791/63.

PT New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes  
 PT containing single nucleotide polymorphisms, useful for preventing or  
 PT treating neuropsychiatric disorders e.g. schizophrenia -  
 XX  
 PS Claim 17; Figure 4; 169pp; English.

CC The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1  
 CC allelic variant polynucleotide. The polypeptides of the invention have  
 CC neuroleptic activity. The polynucleotides may have a use in gene therapy.  
 CC DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or  
 CC treating a subject having a disease or disorder associated with specific  
 CC DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g.  
 CC neuropsychiatric disorder such as schizoaffective, bipolar, unipolar  
 CC affective or adolescent conduct disorder or schizophrenia. Similarly,  
 CC the compound that inhibits DISC1 protein activity may be used in the  
 CC method for treating such neuropsychiatric disorders. The sequences shown  
 CC in ABQ93575-ABQ93658 represent the PCR primers used in the invention to  
 CC amplify the sequences of DISC2 and DISC2.  
 XX

SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 other;

Query Match 1.4%; Score 15.6; DB 1; Length 22;  
 Best Local Similarity 81.8%; Pred. No. 4.1e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1030 GCCTGGCTTTCATAGTGAGGCT 1051  
 DB 22 GCCTAGACTTCACAGTGAGGCT 1

RESULT 662  
 AAD31453  
 ID AAD31453 standard; DNA; 22 BP.  
 XX  
 AC AAD31453;  
 XX

```

DT 31-MAY-2002 (first entry)
XX Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt1p.
DE Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
XX autosomal recessive disorder; chromosome 17; chromosome 17q21;
KW bone dysplasia; 92Kb gene fragment; PCR primer; ss.
XX Homo sapiens.
OS WO200210455-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US23968.
XX
XX 28-JUL-2000; 2000US-221855P.
XX
XX 06-JUL-2001; 2001US-303386P.
XX
XX (CELL-) CELLTECH R & D INC.
XX (STRA/) STRAEHLING HAMPTON K.
XX
XX Brunkow ME, Proll S, Paepers B;
XX WPI; 2002-227089/28.
XX
XX Methods for identifying subjects who are afflicted with or carriers of
XX diseases associated with genomic deletion(s), e.g. Van Buchem's
XX disease, by determining the presence of a deletion in the 92 kb region
XX of human chromosome 17 at 17q21 -
XX
XX Example 3; Page 26; 109pp; English.
XX
XX The present invention relates to methods for distinguishing between
XX individuals homozygous for and therefore afflicted with Van Buchem's
XX disease, individuals heterozygous for and therefore carriers of Van
XX Buchem's disease and individuals who are not afflicted with Van Buchem's
XX disease comprise identifying a large genomic deletion in chromosome 17 at
XX 17q21. The method is useful for identifying individuals who are afflicted
XX with or carriers of diseases associated with one or more genomic
XX deletion, particularly Van Buchem's disease, which is a rare autosomal
XX recessive disorder that results in a bone dysplasia referred to as
XX craniotubular hypertosis. The present sequence is a PCR primer used to
XX amplify 92kb gene fragment in human chromosome 17 at 17q21.
XX
XX Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
SQ
Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 932 TGGAGTCTGAGGCTGGAGAAAT 1013
DB 1 TGGAGGCTGGAGCAAGAGAAAT 22
RESULT 663
AAD31457
ID AAD31457 standard; DNA; 22 BP.
XX
XX AAD31457;
XX
XX 31-MAY-2002 (first entry)
XX
XX Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3R.
DE Human; Van Buchem's disease; genomic deletion; craniotubular hypertosis;
XX autosomal recessive disorder; chromosome 17; chromosome 17q21;
KW bone dysplasia; 92Kb gene fragment; PCR primer; ss.
XX
XX Homo sapiens.
OS WO200210455-A2.
XX

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XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US23968.
XX
XX 28-JUL-2000; 2000US-221855P.
XX
XX 06-JUL-2001; 2001US-303386P.
XX
XX (CELL-) CELLTECH R & D INC.
XX (STRA/) STRAEHLING HAMPTON K.
XX
XX Brunkow ME, Proll S, Paepers B;
XX WPI; 2002-227089/28.
XX
XX Methods for identifying subjects who are afflicted with or carriers of
XX diseases associated with genomic deletion(s), e.g. Van Buchem's
XX disease, by determining the presence of a deletion in the 92 kb region
XX of human chromosome 17 at 17q21 -
XX
XX Example 3; Page 26; 109pp; English.
XX
XX The present invention relates to methods for distinguishing between
XX individuals homozygous for and therefore afflicted with Van Buchem's
XX disease, individuals heterozygous for and therefore carriers of Van
XX Buchem's disease and individuals who are not afflicted with Van Buchem's
XX disease comprise identifying a large genomic deletion in chromosome 17 at
XX 17q21. The method is useful for identifying individuals who are afflicted
XX with or carriers of diseases associated with one or more genomic
XX deletion, particularly Van Buchem's disease, which is a rare autosomal
XX recessive disorder that results in a bone dysplasia referred to as
XX craniotubular hypertosis. The present sequence is a PCR primer used to
XX amplify 92kb gene fragment in human chromosome 17 at 17q21.
XX
XX Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 other;
SQ
Query Match 1.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 932 TGGAGTCTGAGGCTGGAGAAAT 1013
DB 1 TGGAGGCTGGAGCAAGAGAAAT 22
RESULT 664
AAD3452/c
ID AAA25452 standard; DNA; 17 BP.
XX
XX AAA25452;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
XX
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US08547.
XX
XX 20-APR-1998; 98US-0082404.
XX
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX

```

PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
PI Matulic-Adamic J;  
XX WPI; 2000-013248/01.  
XX  
XX New nucleic acids that interact, and optionally cleave, target  
PT sequences, used to treat cancer -  
XX  
XX Claim 77; Page 79; 148pp; English.  
XX  
XX The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphorodithioate  
CC link, having endonuclease activity. (A), and more generally any  
CC catalytic nucleic acid (A') that modulates expression of the oestrogen  
CC receptor gene, are used to treat cancer (particularly of breast or  
CC endometrium), in vivo or by transforming cells ex vivo and implanting  
CC treated cells, or for other conditions associated with levels of  
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)  
CC can also be used to correlate inhibition of gene expression with  
CC alterations in phenotype, particularly for identification of therapeutic  
CC targets, and as research reagents (for RNA, in the same way that  
CC restriction endonucleases are used with DNA). The combination of  
CC modifications in (A) improves resistance to nucleases, binding affinity  
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor  
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their  
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen  
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent  
CC their corresponding target sequences. AAA26219 to AAA26271 represent  
CC other ribozyme sequences and antisense oligonucleotides used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 other;  
SQ  
  
Query Match 1.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1084 AAAAAAAAAAAAAA 1100  
Db 17 AAAAAAAAAAAAAA 1  
  
RESULT 665  
AAA25453/C  
ID AAA25453 standard; DNA; 17 BP.  
XX  
XX AAA25453;  
XX  
XX 19-JUL-2000 (first entry)  
XX  
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.  
XX  
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
XX gene expression modification; cancer; phosphorothioate; endonuclease;  
XX anticancer; breast cancer; endometrium cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9954459-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 19-APR-1999; 99WO-US08547.  
XX  
XX 20-APR-1998; 98US-0082404.  
XX  
XX 23-JUN-1998; 98US-0103636.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulic-Adamic J;  
XX WPI; 2000-013248/01.  
XX  
XX New nucleic acids that interact, and optionally cleave, target  
PT sequences, used to treat cancer -  
XX  
XX Claim 77; Page 79; 148pp; English.  
XX  
XX The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphorodithioate  
CC link, having endonuclease activity. (A), and more generally any  
CC catalytic nucleic acid (A') that modulates expression of the oestrogen  
CC receptor gene, are used to treat cancer (particularly of breast or  
CC endometrium), in vivo or by transforming cells ex vivo and implanting  
CC treated cells, or for other conditions associated with levels of  
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)  
CC can also be used to correlate inhibition of gene expression with  
CC alterations in phenotype, particularly for identification of therapeutic  
CC targets, and as research reagents (for RNA, in the same way that  
CC restriction endonucleases are used with DNA). The combination of  
CC modifications in (A) improves resistance to nucleases, binding affinity  
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor  
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their  
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen  
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent  
CC their corresponding target sequences. AAA26219 to AAA26271 represent  
CC other ribozyme sequences and antisense oligonucleotides used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 other;  
SQ  
  
Query Match 1.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1083 TAAAAAAAAAAAAA 1099  
Db 17 TACAAAAAAAAAAAAA 1  
  
RESULT 666  
AAD44151/C  
ID AAD44151 standard; DNA; 17 BP.  
XX  
XX AAD44151;  
XX  
XX 13-DEC-2002 (first entry)  
XX  
XX Oligo-AT PCR primer #2 used to illustrate the method of the invention.  
XX  
XX Sequential consensus region-directed amplification; gene expression;  
XX disease diagnosis; gene analysis; human; matrix metalloproteinase;  
XX PCR; primer; ss.  
XX  
XX Unidentified.  
XX  
XX US6277571-B1.  
XX  
XX 21-AUG-2001.  
XX  
XX 30-SEP-1998; 98US-0163485.  
XX  
XX 03-OCT-1997; 97US-108152P.  
XX  
XX (UTVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
XX  
XX Fillmore H, Broadus W, Gillies G;  
XX WPI; 2002-412824/44.  
XX  
XX Sequential consensus region-directed amplification for sorting mixture  
PT of DNAs into 2 or more subsets or distinguishing gene expression

PT patterns in 2 samples, useful for disease diagnosis and gene analysis -  
 XX  
 XX Example; Fig 1D; 19pp; English.  
 XX  
 CC The invention relates to a method of sequential consensus region-directed  
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
 CC distinguishing gene expression patterns in 2 samples. The methods, kits  
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or  
 CC more subsets or distinguishing gene expression patterns in 2 samples  
 CC e.g. for disease diagnosis and gene analysis. The present sequence is  
 CC oligo AT PCR primer used to illustrate the method of the invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 1 other;  
 Query Match 1.4%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAA 1  
 RESULT 667  
 ABA91530/c  
 ID ABA91530 standard; DNA; 17 BP.  
 AC ABA91530;  
 DT 23-APR-2002 (first entry)  
 DE DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.  
 XX DNA-RNA hybrid; RNase H; nucleic acid detection; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT misc\_RNA 8  
 FT /\*tag= a  
 FT /label= "RNA"  
 PN WO200206531-A2.  
 PD 24-JAN-2002.  
 PF 12-JUL-2001; 2001WO-US22166.  
 PR 14-JUL-2000; 2000US-0616761.  
 PR 30-MAR-2001; 2001US-0823647.  
 XX (GENE-) APPLIED GENE TECHNOLOGIES INC.  
 PA Dattagupta N;  
 PI WPI; 2002-171819/22.  
 DR Probes for detecting target nucleotide sequence in sample, has sequence  
 PT that forms hairpin structure having a double-stranded segment and  
 PT single-stranded loop collectively forming region complementary to  
 PT target sequence -  
 XX Example 4; Page 49; 72pp; English.  
 XX The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide  
 CC AGT02014. This is one of a set of oligonucleotides (see  
 CC ABA91527-30) used to assess the minimum number of ribonucleotides  
 CC in DNA-RNA chimeric oligonucleotides required for RNase H cleavage.  
 CC Each oligonucleotide of the set had a different number of  
 CC ribonucleotides, 1 in the present case. The oligonucleotides were  
 CC mixed with target DNA oligonucleotide AGT02009 (see ABA91531) and  
 CC incubated with RNase H (5 U/ml) at 37 degrees C for 30 minutes.  
 CC The results showed that 4 ribonucleotides were the minimum number

CC for RNA cleavage. The invention provides probes for nucleic acid  
 CC hybridisation. The probes form a hairpin structure comprising a  
 CC double-stranded stem and a single-stranded loop, and are capable of  
 CC both intramolecular and intermolecular hybridisation. The  
 CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid  
 CC that is resistant to RNase H cleavage. When the probe hybridises  
 CC with a target DNA, the RNA strand in the DNA:RNA duplex becomes  
 CC sensitive to RNase H treatment and can be removed. Arrays and  
 CC methods for nucleic acid hybridisation using the probes are provided.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 other;  
 Query Match 1.4%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAA 1  
 RESULT 668  
 AAQ20108/c  
 ID AAQ20108 standard; DNA; 18 BP.  
 AC AAQ20108;  
 XX 01-APR-1992 (first entry)  
 DT Cross-linking oligomer 942 to target human TNF Receptor mRNA.  
 DE deoxyribonucleic acid; major groove; ethanoino group;  
 KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;  
 KW cross-linking group; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT modified\_base 5  
 FT /\*tag= a  
 FT /mod\_base= m5c  
 FT modified\_base 18  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "N4N4-ethanocytosine"  
 XX WO9118997-A.  
 PN 12-DEC-1991.  
 PD 24-MAY-1991; 91WO-1003680.  
 PF 14-JAN-1991; 91US-0640654.  
 PR 25-MAY-1990; 90US-0529346.  
 XX (GILE-) GILEAD SCIE INC.  
 PA Matteucci MD, Krawczyk S;  
 PI WPI; 1992-007480/01.  
 DR New sequence-specific non-photo-activated crosslinking agents -  
 PT bind to the major groove of duplex DNA and are esp. useful for  
 PT treating latent infections e.g. HIV  
 XX Example 4; Page 27; 42pp; English.  
 XX The oligomer was designed to target human TNF receptor mRNA  
 CC beginning at nucleotide 2354 and to covalently cross-link to  
 CC the target via the N4N4-ethanocytosine group. See also AAQ20109.  
 XX Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 other;  
 SQ

```

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAGAAAAA 1

RESULT 669
AAQ20109/c
ID AAQ20109 standard; DNA; 18 BP.
XX
AC AAQ20109;
XX
DT 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
DE Purine rich HUMNFR target duplex sequence.
XX
KW Target; human tumour necrosis factor receptor mRNA; AIDS; triplex;
KW HIV; hepatitis; malignancy; inflammation; ds.
XX
OS Synthetic.
XX
PN W09209705-A1.
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US08811.
XX
PR 23-NOV-1990; 90US-0617907.
PR 18-JAN-1991; 91US-0643382.
PR 08-APR-1991; 91US-0603420.
PR 17-APR-1991; 91US-0686544.
PR 17-APR-1991; 91US-0686546.
PR 17-APR-1991; 91US-0686547.
PR 27-SEP-1991; 91US-0766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with
PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
PT hepatitis, herpes, malignancy and inflammation
XX
PS Claim 11; Page 64; 77pp; English.
XX
CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC sequence contg. a purine-rich region concentrated on one chain of the
CC duplex. The sequence may be prepd. by standard DNA synthesis. The
CC HUMNFR duplex sequence is used as a target for novel oligomers which
CC are capable of forming a triplex at physiological pH by coupling into
CC the major groove of the DNA duplex. Three such oligomers TNFR 941-32
CC are capable of forming a triplex with this sequence. The oligomers
CC are used in the treatment of inflammation. Similar oligomers may
CC be used to target viral DNA duplexes specific for HIV, herpes and
CC other viruses. The triple helices form under mild conditions thus
CC assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer is able to inhibit gene expression,
CC as verified by in vitro systems.
CC See also AAQ25452-25500 and AAQ30226-448.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 other;

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAATATAA 1

RESULT 670
AAQ25501
ID AAQ25501 standard; DNA; 18 BP.
XX
AC AAQ25501;
XX
DT 25-MAR-2003 (updated)
DT 07-DEC-1992 (first entry)
XX
DE Purine rich HUMNFR target duplex sequence.
XX
KW Target; human tumour necrosis factor receptor mRNA; AIDS; triplex;
KW HIV; hepatitis; malignancy; inflammation; ds.
XX
OS Synthetic.
XX
PN W09209705-A1.
XX
PD 11-JUN-1992.
XX
PF 25-NOV-1991; 91WO-US08811.
XX
PR 23-NOV-1990; 90US-0617907.
PR 18-JAN-1991; 91US-0643382.
PR 08-APR-1991; 91US-0603420.
PR 17-APR-1991; 91US-0686544.
PR 17-APR-1991; 91US-0686546.
PR 17-APR-1991; 91US-0686547.
PR 27-SEP-1991; 91US-0766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with
PT G-C doublet in a DNA duplex, for treating and diagnosing HIV,
PT hepatitis, herpes, malignancy and inflammation
XX
PS Claim 11; Page 64; 77pp; English.
XX
CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC sequence contg. a purine-rich region concentrated on one chain of the
CC duplex. The sequence may be prepd. by standard DNA synthesis. The
CC HUMNFR duplex sequence is used as a target for novel oligomers which
CC are capable of forming a triplex at physiological pH by coupling into
CC the major groove of the DNA duplex. Three such oligomers TNFR 941-32
CC are capable of forming a triplex with this sequence. The oligomers
CC are used in the treatment of inflammation. Similar oligomers may
CC be used to target viral DNA duplexes specific for HIV, herpes and
CC other viruses. The triple helices form under mild conditions thus
CC assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer is able to inhibit gene expression,
CC as verified by in vitro systems.
CC See also AAQ25452-25500 and AAQ30226-448.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 16 A; 0 C; 2 G; 0 U; 0 other;

Query Match      1.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 671
AAQ30447/c
ID AAQ30447 standard; DNA; 18 BP.
XX
AC AAQ30447;

```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2004, 16:08:28 ; Search time 35 Seconds  
(without alignments)  
1.937 Million cell updates/sec

Title: us-09-904-568-1  
Perfect score: 1100  
Sequence: 1 gcacgagccacgacgacta.....attaaaaa1100

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1682 seqs, 30821 residues

Total number of hits satisfying chosen parameters: 3364

Minimum DB seq length: 12  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1690 summaries

Database : rng1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	1.9	21	1	AAQ75728 Reverse transcript
C 2	21	1.9	30	1	AAH71444 Human megain promo
C 3	20.2	1.8	25	1	AAH38447 SNP specific SNPE
C 4	20	1.8	20	1	AAQ75581 Reverse transcript
C 5	20	1.8	21	1	AAQ75727 Reverse transcript
C 6	20	1.8	21	1	AAQ75729 Reverse transcript
C 7	20	1.8	21	1	AAQ75730 Reverse transcript
C 8	19.6	1.8	27	1	AAV71936 Anchored poly T RT
C 9	19.6	1.8	27	1	ABK52620 Minority Genome me
C 10	19.4	1.8	21	1	AAQ75724 Reverse transcript
C 11	19.4	1.8	21	1	AAQ75732 Reverse transcript
C 12	19.4	1.8	21	1	AAQ75760 Reverse transcript
C 13	19.4	1.8	21	1	AAQ75696 Reverse transcript
C 14	19.4	1.8	21	1	AAQ75712 Reverse transcript
C 15	19.4	1.8	21	1	AAQ75720 Reverse transcript
C 16	19.4	1.8	21	1	AAQ75680 Reverse transcript
C 17	19.4	1.8	21	1	AAQ75675 Reverse transcript
C 18	19.4	1.8	21	1	AAQ75632 Reverse transcript
C 19	19.4	1.8	24	1	ABK12409 RT-PCR primer #1 f
C 20	19.4	1.8	24	1	ABK16361 Human phosphatidy
C 21	19.2	1.7	25	1	ABK86170 Oligo dt primer #3
C 22	19.2	1.7	27	1	ABX79828 EST polymorphic DN
C 23	19	1.7	19	1	AAQ75552 Reverse transcript
C 24	19	1.7	20	1	AAQ75580 Reverse transcript
C 25	19	1.7	20	1	AAQ75582 Reverse transcript
C 26	19	1.7	20	1	AAQ75579 Reverse transcript
C 27	19	1.7	21	1	AAQ75723 Reverse transcript
C 28	19	1.7	21	1	AAQ75725 Reverse transcript
C 29	19	1.7	21	1	AAQ75726 Reverse transcript
C 30	19	1.7	21	1	AAQ75731 Reverse transcript
C 31	19	1.7	21	1	AAQ75733 Reverse transcript
C 32	19	1.7	21	1	AAQ75734 Reverse transcript
C 33	19	1.7	21	1	AAQ75719 Reverse transcript

C 34	19	1.7	21	1	AAQ75721 Reverse transcript
C 35	19	1.7	21	1	AAQ75722 Reverse transcript
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C 37	19	1.7	24	1	ABK86169 Anchored poly T RT
C 38	19	1.7	27	1	AAV71935 Human gene specif
C 39	19	1.7	27	1	ABK65992 Human cyclophilin-PCR primer for hum
C 40	18.8	1.7	24	1	AAU47515 16s rRNA gene PCR
C 41	18.6	1.7	25	1	AAK84258 Human pancreatic p
C 42	18.6	1.7	25	1	AAC96240 Human BS124 specif
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C 48	18.4	1.7	20	1	AAQ75589 Reverse transcript
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C 74	18.2	1.7	25	1	AAH76998 SNP specific SNPE
C 75	18.2	1.7	25	1	AAH76998 Human amyloid prec
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C 77	18	1.6	25	1	AAC96085 16s rRNA gene PCR
C 78	18	1.6	18	1	AAH94667 Anchored poly (t) o
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C 84	18	1.6	20	1	AAH04916 Mammalian stem cel
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C 91	18	1.6	20	1	AAQ75576 Reverse transcript
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C 95	18	1.6	20	1	AAH10448 Human stem cell fa
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C 97	18	1.6	20	1	AAH04112 Human SCF (stem ce
C 98	18	1.6	20	1	AAH04213 Human SCF (stem ce
C 99	18	1.6	20	1	AAH23890 Human SCF (stem ce
C 100	18	1.6	20	1	AAH89092 Mammalian stem cel
C 101	18	1.6	20	1	ABK73849 SCF universal olig
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C 256	17	1.5	18	1	AA290646	Human adipose tias
C 257	17	1.5	18	1	AA287161	Oligoarabinonucleo
C 258	17	1.5	18	1	AA287162	Oligoarabinonucleo
C 259	17	1.5	18	1	AA287166	Deoxyarabinonucleo
C 260	17	1.5	18	1	AA287167	Deoxyarabinonucleo
C 261	17	1.5	18	1	AA200091	MRNA fragment used
C 262	17	1.5	18	1	AA282472	Phagemid vector PC
C 263	17	1.5	18	1	AA203565	Oligonucleotide #6
C 264	17	1.5	18	1	AA299708	Immunostimulatory
C 265	17	1.5	18	1	AA299734	Immunostimulatory
C 266	17	1.5	18	1	AA299734	Oligonucleotide A1
C 267	17	1.5	18	1	AA299734	Oligonucleotide A1
C 268	17	1.5	18	1	AA299734	Angiogenesis inhib
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C 270	17	1.5	18	1	AA299734	Poly d(T) primer
C 271	17	1.5	18	1	AA299734	Oligonucleotide us
C 272	17	1.5	18	1	AA299734	Rat secreted facto
C 273	17	1.5	18	1	AA299734	Adaptor oligonucle
C 274	17	1.5	18	1	AA299734	Immunostimulatory
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C 329	17	1.5	19	1	ABZ58336	Dye-coupled 3'-am
C 330	17	1.5	20	1	AAQ25565	Microsatellite seq
C 331	17	1.5	20	1	AAQ33554	Sequence of synthe
C 332	17	1.5	20	1	AAQ58578	Mammalian stem cel
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C 407	17	1.5	20	1	AAQ35464	Capture probe CP5	C 480	17	1.5	21	1	AAQ75643	Reverse transcript
C 408	17	1.5	20	1	AAQ35466	Rat SCF 5' cDNA am	C 481	17	1.5	21	1	AAQ75644	Reverse transcript
C 409	17	1.5	20	1	AAQ35466	Rat SCF 5' cDNA am	C 482	17	1.5	21	1	AAQ75645	Reverse transcript
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C 411	17	1.5	20	1	ABK65035	Nanoparticle-oligo	C 484	17	1.5	21	1	AAQ75615	Reverse transcript
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C 413	17	1.5	20	1	ABL45122	CD14 receptor PCR	C 486	17	1.5	21	1	AAQ75618	Reverse transcript
C 414	17	1.5	20	1	ABL62322	Oligonucleotide sy	C 487	17	1.5	21	1	AAQ75619	Reverse transcript
C 415	17	1.5	20	1	ABL38648	M tuberculosis rRN	C 488	17	1.5	21	1	AAQ75620	Reverse transcript
C 416	17	1.5	20	1	ABL39402	Immunostimulatory	C 489	17	1.5	21	1	AAQ75621	Reverse transcript
C 417	17	1.5	20	1	ABL39403	Immunostimulatory	C 490	17	1.5	21	1	AAQ75622	Reverse transcript
C 418	17	1.5	20	1	ABX92177	Immunostimulatory	C 491	17	1.5	21	1	AAQ75660	Reverse transcript
C 419	17	1.5	20	1	ABX79181	Nanoparticle-assoc	C 492	17	1.5	21	1	AAQ75661	Reverse transcript
C 420	17	1.5	20	1	ABZ22916	Thio-modified 20da	C 493	17	1.5	21	1	AAQ75662	Reverse transcript
C 421	17	1.5	20	1	ABZ59815	Phosphorothioate 2	C 494	17	1.5	21	1	AAQ75663	Reverse transcript
C 422	17	1.5	21	1	AAQ90391	Potato Gene PCR pr	C 495	17	1.5	21	1	AAQ75645	Reverse transcript
C 423	17	1.5	21	1	AAQ75665	CP-1 (synthetic DN	C 496	17	1.5	21	1	AAQ75646	Reverse transcript
C 424	17	1.5	21	1	AAQ75735	Reverse transcript	C 497	17	1.5	21	1	AAQ75647	Reverse transcript
C 425	17	1.5	21	1	AAQ75736	Reverse transcript	C 498	17	1.5	21	1	AAQ75649	Reverse transcript
C 426	17	1.5	21	1	AAQ75737	Reverse transcript	C 499	17	1.5	21	1	AAQ75650	Reverse transcript
C 427	17	1.5	21	1	AAQ75738	Reverse transcript	C 500	17	1.5	21	1	AAQ75651	Reverse transcript
C 428	17	1.5	21	1	AAQ75739	Reverse transcript	C 501	17	1.5	21	1	AAQ75652	Reverse transcript
C 429	17	1.5	21	1	AAQ75740	Reverse transcript	C 502	17	1.5	21	1	AAQ75653	Reverse transcript
C 430	17	1.5	21	1	AAQ75741	Reverse transcript	C 503	17	1.5	21	1	AAQ75654	Reverse transcript
C 431	17	1.5	21	1	AAQ75742	Reverse transcript	C 504	17	1.5	21	1	AAQ75655	Reverse transcript
C 432	17	1.5	21	1	AAQ75743	Reverse transcript	C 505	17	1.5	21	1	AAQ75656	Reverse transcript
C 433	17	1.5	21	1	AAQ75745	Reverse transcript	C 506	17	1.5	21	1	AAQ75657	Reverse transcript
C 434	17	1.5	21	1	AAQ75746	Reverse transcript	C 507	17	1.5	21	1	AAQ75658	Reverse transcript
C 435	17	1.5	21	1	AAQ75747	Reverse transcript	C 508	17	1.5	21	1	AAQ75659	Reverse transcript
C 436	17	1.5	21	1	AAQ75748	Reverse transcript	C 509	17	1.5	21	1	AAT10743	Oligonucleotide us
C 437	17	1.5	21	1	AAQ75749	Reverse transcript	C 510	17	1.5	21	1	AAT26268	Human polymorphic
C 438	17	1.5	21	1	AAQ75750	Reverse transcript	C 511	17	1.5	21	1	AAV35395	HIV-1 gag protein
C 439	17	1.5	21	1	AAQ75787	Reverse transcript	C 512	17	1.5	21	1	AAK81302	3' ribonucleoside
C 440	17	1.5	21	1	AAQ75788	Reverse transcript	C 513	17	1.5	21	1	AAZ26973	Primer used to rev
C 441	17	1.5	21	1	AAQ75789	Reverse transcript	C 514	17	1.5	21	1	AAZ44350	Protein kinase inh
C 442	17	1.5	21	1	AAQ75790	Reverse transcript	C 515	17	1.5	21	1	AAH42480	Oligonucleotide us
C 443	17	1.5	21	1	AAQ75791	Reverse transcript	C 516	17	1.5	21	1	AAF99707	Immunostimulatory
C 444	17	1.5	21	1	AAQ75792	Reverse transcript	C 517	17	1.5	21	1	ABL78428	Angiogenesis inh
C 445	17	1.5	21	1	AAQ75793	Reverse transcript	C 518	17	1.5	21	1	ABL39404	Immunostimulatory
C 446	17	1.5	21	1	AAQ75794	Reverse transcript	C 519	17	1.5	22	1	AAD51323	Regular oligo dr p
C 447	17	1.5	21	1	AAQ75795	Reverse transcript	C 520	17	1.5	22	1	AAQ64706	2',5'-linked tetra
C 448	17	1.5	21	1	AAQ75796	Reverse transcript	C 521	17	1.5	22	1	AAQ64724	2',5'-linked tetra
C 449	17	1.5	21	1	AAQ75797	Reverse transcript	C 522	17	1.5	22	1	AAA98276	Human mismatch rep
C 450	17	1.5	21	1	AAQ75798	Reverse transcript	C 523	17	1.5	23	1	AAQ17413	L1 cleavage site r
C 451	17	1.5	21	1	AAQ75773	Reverse transcript	C 524	17	1.5	23	1	AAQ0432	Oligomer IL6805 fo
C 452	17	1.5	21	1	AAQ75774	Reverse transcript	C 525	17	1.5	23	1	AAQ5360	Human protein-tyro
C 453	17	1.5	21	1	AAQ75775	Reverse transcript	C 526	17	1.5	23	1	AAQ75028	LCR oligo 2. Synt
C 454	17	1.5	21	1	AAQ75777	Reverse transcript	C 527	17	1.5	23	1	AAQ75029	LCR oligo 3. Synt
C 455	17	1.5	21	1	AAQ75779	Reverse transcript	C 528	17	1.5	23	1	AAT33701	Primer #1 for tiss
C 456	17	1.5	21	1	AAQ75779	Reverse transcript	C 529	17	1.5	23	1	AAT37316	RT-PCR Primer for
C 457	17	1.5	21	1	AAQ75781	Reverse transcript	C 530	17	1.5	23	1	AAV61555	Double-anchored ol
C 458	17	1.5	21	1	AAQ75782	Reverse transcript	C 531	17	1.5	23	1	AAV61556	Double-anchored ol
C 459	17	1.5	21	1	AAQ75783	Reverse transcript	C 532	17	1.5	23	1	AAV61554	Double-anchored ol
C 460	17	1.5	21	1	AAQ75784	Reverse transcript	C 533	17	1.5	23	1	AAC62450	Cleavage of nuclei
C 461	17	1.5	21	1	AAQ75785	Reverse transcript	C 534	17	1.5	23	1	AAC62451	Cleavage of nuclei
C 462	17	1.5	21	1	AAQ75786	Reverse transcript	C 535	17	1.5	23	1	AAO08407	Oligonucleotide pr
C 463	17	1.5	21	1	AAQ75767	Reverse transcript	C 536	17	1.5	23	1	AAF85497	PCR primer for DNA
C 464	17	1.5	21	1	AAQ75768	Reverse transcript	C 537	17	1.5	23	1	AAF16627	Gastric acid produ
C 465	17	1.5	21	1	AAQ75769	Reverse transcript	C 538	17	1.5	23	1	AAD33503	T7T18Apad PSL3-23-
C 466	17	1.5	21	1	AAQ75770	Reverse transcript	C 539	17	1.5	23	1	ABL95973	Probe #48 for asse
C 467	17	1.5	21	1	AAQ75666	Reverse transcript	C 540	17	1.5	23	1	ABA99682	Murine osteoporosi
C 468	17	1.5	21	1	AAQ75667	Reverse transcript	C 541	17	1.5	24	1	ABX97431	Glycosyltransferas
C 469	17	1.5	21	1	AAQ75668	Reverse transcript	C 542	17	1.5	24	1	AAH68615	DNA probe used in
C 470	17	1.5	21	1	AAQ75669	Reverse transcript	C 543	17	1.5	24	1	AAH43079	Nucleotide sequenc
C 471	17	1.5	21	1	AAQ75670	Reverse transcript	C 544	17	1.5	24	1	AAH24266	Human phosphatase
	17	1.5	21	1	AAQ75607	Reverse transcript		17	1.5	24	1	ABO79878	Human phosphatase

c 545	17	1.5	24	1	ABK86172	Oligo dT primer #4	c 618	16	1.5	18	1	ABK13935	5'-PCR primer used
c 546	17	1.5	24	1	ABN85073	Human S4 ribosomal	c 619	16	1.5	18	1	AAD52799	Primer used to pre
c 547	17	1.5	24	1	AAD33505	TT18Apad PS12-24-	620	16	1.5	20	1	AAS05714	Aminopurine substi
c 548	17	1.5	24	1	ABL55130	Human gonadotropin	c 621	16	1.5	20	1	AAC82923	Human S-9 derived
c 549	17	1.5	24	1	ABX79809	EST polymorphic DN	622	16	1.5	20	1	AAD33499	TT18Apad PS27-20-
c 550	16.8	1.5	20	1	AAZ37719	Human mdm2 phospho	c 623	16	1.5	20	1	ABA05917	Hepatitis B virus
c 551	16.8	1.5	20	1	AAS29488	Human mdm2 antisen	c 624	16	1.5	21	1	AAZ09196	Oligonucleotide 8
c 552	16.8	1.5	20	1	AAF83959	BAP28 gene fragmen	625	16	1.5	21	1	AAD33500	TT18Apad PS26-21-
c 553	16.8	1.5	20	1	AAF80873	Human mdm2 phospho	626	16	1.5	22	1	AAD33501	TT18Apad PS25-22-
c 554	16.8	1.5	20	1	AAS97833	Murine SAC1 gene-s	627	15.8	1.4	19	1	AAT29081	Primer for tyrosin
c 555	16.8	1.5	20	1	AAS97860	Murine SAC1 gene-s	628	15.8	1.4	19	1	AAV01125	Elastin PCR primer
c 556	16.8	1.5	21	1	AAZ28500	Human polymorphic	c 629	15.8	1.4	19	1	ABT13587	Liver regeneration
c 557	16.8	1.5	21	1	AAH88803	Human polymorphic	c 630	15.8	1.4	20	1	AAT32535	Primer for exon 12
c 558	16.8	1.5	23	1	AAA64547	Nucleotide sequenc	c 631	15.8	1.4	20	1	AAZ44829	Human FADD primer
c 559	16.8	1.5	24	1	AAV06320	Human prollyl 4-hyd	c 632	15.8	1.4	20	1	AAS05713	Polypyrimidine Cri
c 560	16.8	1.5	24	1	ABN85224	Human translation	c 633	15.8	1.4	21	1	AAT48469	Third-strand oligo
c 561	16.4	1.5	18	1	AAQ30446	Oligomer TNFR941 f	634	15.8	1.4	21	1	AAZ26632	Human polymorphic
c 562	16.4	1.5	18	1	AAF75598	Binary encoded seq	c 635	15.8	1.4	21	1	AAZ14729	Triple helix third
c 563	16.4	1.5	20	1	AAS05715	8-aminopurine subs	c 636	15.8	1.4	22	1	AAZ27844	PCR primer for hum
c 564	16.4	1.5	20	1	AAAF99943	Synthetic oligonuc	637	15.8	1.4	22	1	AAS63416	Oligonucleotide-na
c 565	16.4	1.5	20	1	ABA05916	Hepatitis B virus	638	15.8	1.4	22	1	AAS63419	Oligonucleotide-na
c 566	16.4	1.5	23	1	AAZ33577	Deletion sequence	c 639	15.8	1.4	22	1	AAS10359	Oligonucleotide-go
c 567	16.4	1.5	23	1	AAZ39753	Synthetic oligonuc	640	15.8	1.4	22	1	AAZ10362	Oligonucleotide-go
c 568	16.4	1.5	23	1	AAH30031	Human interleukin	641	15.8	1.4	22	1	AAZ28471	Random oligonucleo
c 569	16.4	1.5	23	1	AAH30035	Human myelin prote	642	15.8	1.4	22	1	AAZ28474	Random oligonucleo
c 570	16.2	1.5	18	1	AAZ18389	RT-PCR primer of t	643	15.8	1.4	22	1	ABT54436	Silver staining me
c 571	16.2	1.5	21	1	AAZ26563	Human polymorphic	644	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 572	16.2	1.5	22	1	AAZ26563	Polymorphic sequen	645	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 573	16	1.5	16	1	AAZ07568	Homo sapiens fetal	646	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 574	16	1.5	16	1	AAZ07568	DNA chip primer #4	647	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 575	16	1.5	16	1	AAZ07568	Human polymorphic	648	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 576	16	1.5	16	1	AAZ42481	Oligonucleotide us	649	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 577	16	1.5	16	1	AAZ42481	Oligonucleotide po	650	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 578	16	1.5	16	1	AAZ42481	Oligonucleotide-mi	651	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 579	16	1.5	16	1	AAZ42481	Oligonucleotide #5	652	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 580	16	1.5	16	1	AAZ42481	Nucleotide sequenc	653	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 581	16	1.5	16	1	AAZ42481	Oligo-homodeoxyrib	654	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 582	16	1.5	17	1	AAZ42481	Human flt1 VEGF re	655	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 583	16	1.5	17	1	AAZ42481	Human flt1 VEGF re	656	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 584	16	1.5	17	1	AAZ42481	Human eosinophil c	657	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 585	16	1.5	17	1	AAZ42481	RT-PCR primer of t	658	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 586	16	1.5	17	1	AAZ42481	PCR anchor primer,	659	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 587	16	1.5	17	1	AAZ42481	PCR anchor primer,	660	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 588	16	1.5	17	1	AAZ42481	PCR anchor primer,	661	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 589	16	1.5	17	1	AAZ42481	PCR anchor primer,	662	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 590	16	1.5	17	1	AAZ42481	PCR anchor primer,	663	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 591	16	1.5	17	1	AAZ42481	Human IgA nephropa	664	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 592	16	1.5	17	1	AAZ42481	PCR primer GT15A u	665	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 593	16	1.5	17	1	AAZ42481	Oestrogen receptor	666	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 594	16	1.5	17	1	AAZ42481	Oestrogen receptor	667	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 595	16	1.5	17	1	AAZ42481	Oestrogen receptor	668	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 596	16	1.5	17	1	AAZ42481	Anchored oligo(dT)	669	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 597	16	1.5	17	1	AAZ42481	Human polinosis-a	670	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 598	16	1.5	17	1	AAZ42481	PCR anchor primer,	671	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 599	16	1.5	17	1	AAZ42481	Human polinosis-a	672	15.8	1.4	22	1	ABT54436	Nucleic acid detec
c 600	16	1.5	17	1	AAZ42481	Nucleotide sequenc	673	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 601	16	1.5	17	1	AAZ42481	Human B153 expres	674	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 602	16	1.5	17	1	AAZ42481	Allergic disease e	675	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 603	16	1.5	17	1	AAZ42481	Nucleotide sequenc	676	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 604	16	1.5	17	1	AAZ42481	Human allergic dis	677	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 605	16	1.5	17	1	AAZ42481	Human atopic transf	678	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 606	16	1.5	17	1	AAZ42481	Human atopic derma	679	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 607	16	1.5	17	1	AAZ42481	5'-PCR primer used	680	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 608	16	1.5	17	1	AAZ42481	Primer, Synthetic	681	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 609	16	1.5	18	1	AAZ42481	Sequence derived f	682	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 610	16	1.5	18	1	AAZ42481	Nucleotide sequenc	683	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 611	16	1.5	18	1	AAZ42481	Nucleotide sequenc	684	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 612	16	1.5	18	1	AAZ42481	Nucleotide sequenc	685	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 613	16	1.5	18	1	AAZ42481	Human adipose tiss	686	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 614	16	1.5	18	1	AAZ42481	Human adipose tiss	687	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 615	16	1.5	18	1	AAZ42481	Human adipose tiss	688	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 616	16	1.5	18	1	AAZ42481	Binary encoded seq	689	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
c 617	16	1.5	18	1	AAZ42481	Binary encoded seq	690	15.8	1.4	22	1	ABT54436	Nucleotide sequenc
					Human cytomagalovi								

C 691	15.2	1.4	16	1	AAH27758	Primer used in hum	C 764	15	1.4	15	1	ABK98184	Triple helix formi
C 692	15.2	1.4	16	1	AAF82119	RN-PCR primer of t	C 765	15	1.4	15	1	ABL57054	Hydrazide phosphor
C 693	15.2	1.4	17	1	AAH18388	Human TSA7005 gene	C 766	15	1.4	15	1	ABL57056	Hydrazide phosphor
C 694	15.2	1.4	17	1	AAH14174	Modified Poly-1 Pr	C 767	15	1.4	15	1	ABL57059	Hydrazide phosphor
C 695	15.2	1.4	20	1	AAZ09195	Oligonucleotide 7	C 768	15	1.4	15	1	ABL57060	Hydrazide precurs
C 696	15.2	1.4	20	1	AAH58043	Human PRO1410 forw	C 769	15	1.4	15	1	ABL57061	Hydrazide precurs
C 697	15.2	1.4	20	1	ABA82154	Zmax1 gene region	C 770	15	1.4	15	1	ABL57063	Hydrazide precurs
C 698	15.2	1.4	20	1	AAH54523	Primer #132 used i	C 771	15	1.4	15	1	ABL57064	Hydrazide precurs
C 699	15.2	1.4	20	1	AAH82913	Human beta-actin d	C 772	15	1.4	15	1	ABL57066	Hydrazide precurs
C 700	15.2	1.4	20	1	AAH82918	Human S-9 derived	C 773	15	1.4	15	1	ABL57066	Hydrazide precurs
C 701	15.2	1.4	20	1	ABN80967	Mouse caspase 7 ph	C 774	15	1.4	15	1	ABA40743	Amino-C6-modified
C 702	15.2	1.4	20	1	ABK44387	Human onco-gene p1	C 775	15	1.4	15	1	ABA97403	Chicken heparanase
C 703	15.2	1.4	20	1	ABK22951	Human Zmax1 CDNA f	C 776	15	1.4	15	1	ABD29506	Nucleotide sequenc
C 704	15.2	1.4	20	1	ABA05915	Hepatitis B virus	C 777	15	1.4	15	1	ABD22531	Primer used for th
C 705	15.2	1.4	20	1	ABL45369	Capture oligonucle	C 778	15	1.4	15	1	ABD237501	Retroviral reverse
C 706	15.2	1.4	20	1	ABL45369	Human chromsome 2	C 779	15	1.4	15	1	ABV75865	Oligonucleotide SE
C 707	15.2	1.4	20	1	AAH53968	Human HBM SFS mark	C 780	15	1.4	15	1	ABV74141	Oligonucleotide T1
C 708	15.2	1.4	21	1	AAZ26499	DNA mutation detec	C 781	15	1.4	16	1	ABV74142	Oligonucleotide us
C 709	15.2	1.4	21	1	AAH79922	Human polymorphic	C 782	15	1.4	16	1	ABX18368	5' End of cDNA lib
C 710	15.2	1.4	21	1	AAH91374	PCR primer used to	C 783	15	1.4	16	1	AAH18369	RT-PCR primer of t
C 711	15.2	1.4	21	1	AAH91374	Oligo JT-296 for c	C 784	15	1.4	16	1	ABU57075	RT-PCR primer of t
C 712	15.2	1.4	21	1	ABK15655	Anchored oligo-dt	C 785	15	1.4	17	1	AAU69799	Molecular beacon t
C 713	15	1.4	15	1	AAQ79184	Nuclease resistant	C 786	15	1.4	17	1	AAU69802	Human flt1 VEGF re
C 714	15	1.4	15	1	AAQ79184	Nuclease resistant	C 787	15	1.4	17	1	AAV37934	Human flt1 VEGF re
C 715	15	1.4	15	1	AAH52136	Human ICAM hammerh	C 788	15	1.4	17	1	AAV19118	Primer of the spec
C 716	15	1.4	15	1	AAH52136	Human ICAM hammerh	C 789	15	1.4	17	1	AAH64162	Anchored oligo (T)
C 717	15	1.4	15	1	AAV01603	Oligonucleotide co	C 790	15	1.4	17	1	AAH64163	PCR anchor primer,
C 718	15	1.4	15	1	AAV01604	Oligonucleotide co	C 791	15	1.4	17	1	AAH64172	PCR anchor primer,
C 719	15	1.4	15	1	AAV07431	Synthetic peptide-	C 792	15	1.4	17	1	AAH64173	PCR anchor primer,
C 720	15	1.4	15	1	AAH86605	Oligonucleotide se	C 793	15	1.4	17	1	AAH64182	PCR anchor primer,
C 721	15	1.4	15	1	AAH86675	Oligonucleotide li	C 794	15	1.4	17	1	AAH64183	PCR anchor primer,
C 722	15	1.4	15	1	AAH00787	N3-P5 phosphoramid	C 795	15	1.4	17	1	AAH64203	PCR anchor primer,
C 723	15	1.4	15	1	AAH00787	N3-P5 phosphoramid	C 796	15	1.4	17	1	AAH64204	PCR anchor primer,
C 724	15	1.4	15	1	AAH5048	Primer used to rev	C 797	15	1.4	17	1	AAH64214	PCR anchor primer,
C 725	15	1.4	15	1	AAH62347	Oligonucleotide #3	C 798	15	1.4	17	1	AAH64231	PCR anchor primer,
C 726	15	1.4	15	1	AAH62348	Oligonucleotide #4	C 799	15	1.4	17	1	AAH64232	PCR anchor primer,
C 727	15	1.4	15	1	AAH62350	Oligonucleotide #2	C 800	15	1.4	17	1	AAH82721	PCR anchor primer,
C 728	15	1.4	15	1	AAH46502	PCR primer used to	C 801	15	1.4	17	1	AAH82722	Human IGA nephropa
C 729	15	1.4	15	1	AAH07788	Nucleic acid sequ	C 802	15	1.4	17	1	AAH82722	Human IGA nephropa
C 730	15	1.4	15	1	AAH07789	Nucleic acid sequ	C 803	15	1.4	17	1	AAA30180	PCR primer GT15C u
C 731	15	1.4	15	1	AAH07790	Nucleic acid sequ	C 804	15	1.4	17	1	AAA30181	PCR primer GT15C u
C 732	15	1.4	15	1	AAH07791	Nucleic acid sequ	C 805	15	1.4	17	1	AAZ25448	Oestrogen receptor
C 733	15	1.4	15	1	AAH07792	Nucleic acid sequ	C 806	15	1.4	17	1	AAZ36740	Anchored oligo(dT)
C 734	15	1.4	15	1	AAH07793	Nucleic acid sequ	C 807	15	1.4	17	1	AAZ35714	Murine gene anchor
C 735	15	1.4	15	1	AAH07794	Nucleic acid sequ	C 808	15	1.4	17	1	AAH82875	Human pollinosis-a
C 736	15	1.4	15	1	AAH07795	Nucleic acid sequ	C 809	15	1.4	17	1	AAH82876	Human pollinosis-a
C 737	15	1.4	15	1	AAH07796	Nucleic acid sequ	C 810	15	1.4	17	1	AAH91720	PCR anchor primer,
C 738	15	1.4	15	1	AAH07797	Nucleic acid sequ	C 811	15	1.4	17	1	AAH91721	PCR anchor primer,
C 739	15	1.4	15	1	AAH07798	Nucleic acid sequ	C 812	15	1.4	17	1	AAH92293	Human pollinosis-a
C 740	15	1.4	15	1	AAH07799	Nucleic acid sequ	C 813	15	1.4	17	1	AAH92294	Human pollinosis-a
C 741	15	1.4	15	1	AAH07800	Nucleic acid sequ	C 814	15	1.4	17	1	AAH47127	Human pollinosis-a
C 742	15	1.4	15	1	AAH07801	Nucleic acid sequ	C 815	15	1.4	17	1	AAH47128	Nucleotide sequenc
C 743	15	1.4	15	1	AAH07802	Nucleic acid sequ	C 816	15	1.4	17	1	AAH49949	Nucleotide sequenc
C 744	15	1.4	15	1	AAH07803	Nucleic acid sequ	C 817	15	1.4	17	1	AAH49950	Human B153 expres
C 745	15	1.4	15	1	AAH07825	Nucleic acid sequ	C 818	15	1.4	17	1	AAH47235	Human B153 expres
C 746	15	1.4	15	1	AAH07828	Nucleic acid sequ	C 819	15	1.4	17	1	AAH47236	Allergic disease e
C 747	15	1.4	15	1	AAH07831	Nucleic acid sequ	C 820	15	1.4	17	1	ABL59039	Allergic disease e
C 748	15	1.4	15	1	AAH07834	Nucleic acid sequ	C 821	15	1.4	17	1	ABL59040	Nucleotide sequenc
C 749	15	1.4	15	1	AAH261854	Nucleic acid sequ	C 822	15	1.4	17	1	ABN99830	Human allergic dis
C 750	15	1.4	15	1	AAH264910	HCV 3' non core re	C 823	15	1.4	17	1	ABN99831	Human allergic dis
C 751	15	1.4	15	1	AAH20308	Substrate for HH r	C 824	15	1.4	17	1	ABK49635	Human Acetyltransf
C 752	15	1.4	15	1	AAH20311	Oligo dT15 EDTA la	C 825	15	1.4	17	1	ABK49636	Human Acetyltransf
C 753	15	1.4	15	1	AAH20311	Oligonucleotide b)	C 826	15	1.4	17	1	ABK49757	Human atopic derma
C 754	15	1.4	15	1	AAF53331	IGF-I oligonucleot	C 827	15	1.4	17	1	ABK49758	Human atopic derma
C 755	15	1.4	15	1	AAF53332	IGF-I oligonucleot	C 828	15	1.4	17	1	ABK79793	EST polymorphic DN
C 756	15	1.4	15	1	AAF16603	Gastric acid produ	C 829	15	1.4	18	1	AAV54171	Nucleotide sequenc
C 757	15	1.4	15	1	AAF30882	Oligonucleotide po	C 830	15	1.4	18	1	AAV54172	Nucleotide sequenc
C 758	15	1.4	15	1	AAH49243	PNA-forming oligon	C 831	15	1.4	18	1	AAV54174	Nucleotide sequenc
C 759	15	1.4	15	1	ABX00240	Hepatitis C virus	C 832	15	1.4	18	1	AAV54175	Nucleotide sequenc
C 760	15	1.4	15	1	ABX03406	Hepatitis C virus	C 833	15	1.4	18	1	AAV53531	HIV-1 gag protein
C 761	15	1.4	15	1	AAQ82140	Acceptor vector pH	C 834	15	1.4	18	1	AAV53539	Polynucleotide # 1
C 762	15	1.4	15	1	AAH49453	Mutation detection	C 835	15	1.4	18	1	AAV58386	Polynucleotide # 2
C 763	15	1.4	15	1	AAH49455	Triple helix formi	C 836	15	1.4	18	1	AAZ90641	Human adipose tiss
												AAZ90642	Human adipose tiss

C 837	15	1.4	18	1	AAZ90650	Human adipose tiss
C 838	15	1.4	18	1	AAZ90651	Human adipose tiss
C 839	15	1.4	18	1	ABT11136	Human 5-lipoxygena
C 840	15	1.4	20	1	AAZ73293	Primer for pUC19 D
C 841	15	1.4	20	1	AAZ32003	MSH2 gene specific
C 842	15	1.4	20	1	AAZ32010	MSH2 gene specific
C 843	15	1.4	20	1	AAZ32010	Human beta-actin d
C 844	15	1.4	20	1	AAZ32010	Human beta-actin d
C 845	15	1.4	20	1	AAZ32010	Human beta-actin d
C 846	15	1.4	20	1	AAZ32010	Human beta-actin d
C 847	15	1.4	20	1	AAZ32010	Human beta-actin d
C 848	15	1.4	20	1	AAZ32010	Human beta-actin d
C 849	15	1.4	20	1	AAZ32010	Human S-9 derived
C 850	15	1.4	20	1	AAZ32010	Human S-9 derived
C 851	15	1.4	20	1	AAZ32010	Human S-9 derived
C 852	15	1.4	20	1	AAZ32010	Human S-9 derived
C 853	15	1.4	20	1	AAZ32010	Human S-9 derived
C 854	15	1.4	20	1	AAZ32010	Human glutathione
C 855	15	1.4	20	1	AAZ32010	HT15-C downstream
C 856	15	1.4	20	1	AAZ32010	Molecular beacon t
C 857	15	1.4	20	1	AAZ32010	Human GLUT10 SSCP
C 858	15	1.4	20	1	AAZ32010	Capture oligonucle
C 859	15	1.4	20	1	AAZ32010	Human gene single
C 860	15	1.4	20	1	AAZ32010	Histamine N-methyl
C 861	15	1.4	20	1	AAZ32010	Histamine N-methyl
C 862	15	1.4	20	1	AAZ32010	Molecular beacon t
C 863	15	1.4	20	1	AAZ32010	Cross-linking olig
C 864	15	1.4	20	1	AAZ32010	Oligomer HUM beta
C 865	15	1.4	20	1	AAZ32010	Oligomer HUM beta
C 866	15	1.4	20	1	AAZ32010	Human inhibitor of
C 867	15	1.4	20	1	AAZ32010	Human inhibitor of
C 868	15	1.4	20	1	AAZ32010	Mouse GPR4 cDNA am
C 869	15	1.4	20	1	AAZ32010	Toxicologically re
C 870	15	1.4	20	1	AAZ32010	TYR 1 PCR primer f
C 871	15	1.4	20	1	AAZ32010	PCR primer used to
C 872	15	1.4	20	1	AAZ32010	Human ZS1G-11 DNA
C 873	15	1.4	20	1	AAZ32010	Human G713 PCR pri
C 874	15	1.4	20	1	AAZ32010	Reverse PCR primer
C 875	15	1.4	20	1	AAZ32010	Reverse PCR primer
C 876	15	1.4	20	1	AAZ32010	Primer #52. Homo
C 877	15	1.4	20	1	AAZ32010	Linker #52. Uniden
C 878	15	1.4	20	1	AAZ32010	Human PI3 kinase p
C 879	15	1.4	20	1	AAZ32010	Caspase 6 antisens
C 880	15	1.4	20	1	AAZ32010	Arabidopsis chromo
C 881	15	1.4	20	1	AAZ32010	Thale cress HY2 DN
C 882	15	1.4	20	1	AAZ32010	V-beta-a primer.
C 883	15	1.4	20	1	AAZ32010	Human polymorphic
C 884	15	1.4	20	1	AAZ32010	Human polymorphic
C 885	15	1.4	20	1	AAZ32010	PCR primer used to
C 886	15	1.4	20	1	AAZ32010	Human UDP-glucuron
C 887	15	1.4	20	1	AAZ32010	Human corticotropi
C 888	15	1.4	20	1	AAZ32010	Human GSR allele s
C 889	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 890	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 891	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 892	15	1.4	20	1	AAZ32010	Oligo-dT PCR prime
C 893	15	1.4	20	1	AAZ32010	Primer MGH1 for m
C 894	15	1.4	20	1	AAZ32010	Endothelial nitric
C 895	15	1.4	20	1	AAZ32010	ECORV private prox
C 896	15	1.4	20	1	AAZ32010	Endothelial nitric
C 897	15	1.4	20	1	AAZ32010	Human endothelial
C 898	15	1.4	20	1	AAZ32010	Low adenosine anti
C 899	15	1.4	20	1	AAZ32010	Oestrogen receptor
C 900	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 901	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 902	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 903	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 904	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 905	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 906	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 907	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 908	15	1.4	20	1	AAZ32010	PCR primer ZC24271
C 909	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 910	15	1.4	20	1	AAZ32010	Human adipose tiss
C 911	15	1.4	20	1	AAZ32010	Human adipose tiss
C 912	15	1.4	20	1	AAZ32010	Human 5-lipoxygena
C 913	15	1.4	20	1	AAZ32010	Primer for pUC19 D
C 914	15	1.4	20	1	AAZ32010	MSH2 gene specific
C 915	15	1.4	20	1	AAZ32010	MSH2 gene specific
C 916	15	1.4	20	1	AAZ32010	Human beta-actin d
C 917	15	1.4	20	1	AAZ32010	Human beta-actin d
C 918	15	1.4	20	1	AAZ32010	Human beta-actin d
C 919	15	1.4	20	1	AAZ32010	Human beta-actin d
C 920	15	1.4	20	1	AAZ32010	Human beta-actin d
C 921	15	1.4	20	1	AAZ32010	Human S-9 derived
C 922	15	1.4	20	1	AAZ32010	Human S-9 derived
C 923	15	1.4	20	1	AAZ32010	Human S-9 derived
C 924	15	1.4	20	1	AAZ32010	Human S-9 derived
C 925	15	1.4	20	1	AAZ32010	Human S-9 derived
C 926	15	1.4	20	1	AAZ32010	Human glutathione
C 927	15	1.4	20	1	AAZ32010	HT15-C downstream
C 928	15	1.4	20	1	AAZ32010	Molecular beacon t
C 929	15	1.4	20	1	AAZ32010	Human GLUT10 SSCP
C 930	15	1.4	20	1	AAZ32010	Capture oligonucle
C 931	15	1.4	20	1	AAZ32010	Human gene single
C 932	15	1.4	20	1	AAZ32010	Histamine N-methyl
C 933	15	1.4	20	1	AAZ32010	Histamine N-methyl
C 934	15	1.4	20	1	AAZ32010	Molecular beacon t
C 935	15	1.4	20	1	AAZ32010	Cross-linking olig
C 936	15	1.4	20	1	AAZ32010	Oligomer HUM beta
C 937	15	1.4	20	1	AAZ32010	Oligomer HUM beta
C 938	15	1.4	20	1	AAZ32010	Human inhibitor of
C 939	15	1.4	20	1	AAZ32010	Human inhibitor of
C 940	15	1.4	20	1	AAZ32010	Mouse GPR4 cDNA am
C 941	15	1.4	20	1	AAZ32010	Toxicologically re
C 942	15	1.4	20	1	AAZ32010	TYR 1 PCR primer f
C 943	15	1.4	20	1	AAZ32010	PCR primer used to
C 944	15	1.4	20	1	AAZ32010	Human ZS1G-11 DNA
C 945	15	1.4	20	1	AAZ32010	Human G713 PCR pri
C 946	15	1.4	20	1	AAZ32010	Reverse PCR primer
C 947	15	1.4	20	1	AAZ32010	Reverse PCR primer
C 948	15	1.4	20	1	AAZ32010	Primer #52. Homo
C 949	15	1.4	20	1	AAZ32010	Linker #52. Uniden
C 950	15	1.4	20	1	AAZ32010	Human PI3 kinase p
C 951	15	1.4	20	1	AAZ32010	Caspase 6 antisens
C 952	15	1.4	20	1	AAZ32010	Arabidopsis chromo
C 953	15	1.4	20	1	AAZ32010	Thale cress HY2 DN
C 954	15	1.4	20	1	AAZ32010	V-beta-a primer.
C 955	15	1.4	20	1	AAZ32010	Human polymorphic
C 956	15	1.4	20	1	AAZ32010	Human polymorphic
C 957	15	1.4	20	1	AAZ32010	PCR primer used to
C 958	15	1.4	20	1	AAZ32010	Human UDP-glucuron
C 959	15	1.4	20	1	AAZ32010	Human corticotropi
C 960	15	1.4	20	1	AAZ32010	Human GSR allele s
C 961	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 962	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 963	15	1.4	20	1	AAZ32010	RT-PCR primer of t
C 964	15	1.4	20	1	AAZ32010	Oligo-dT PCR prime
C 965	15	1.4	20	1	AAZ32010	Primer MGH1 for m
C 966	15	1.4	20	1	AAZ32010	Endothelial nitric
C 967	15	1.4	20	1	AAZ32010	ECORV private prox
C 968	15	1.4	20	1	AAZ32010	Endothelial nitric
C 969	15	1.4	20	1	AAZ32010	Human endothelial
C 970	15	1.4	20	1	AAZ32010	Low adenosine anti
C 971	15	1.4	20	1	AAZ32010	Oestrogen receptor
C 972	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 973	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 974	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 975	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 976	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 977	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 978	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 979	15	1.4	20	1	AAZ32010	Adenosine deaminas
C 980	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 981	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 982	15	1.4	20	1	AAZ32010	PCR primer ZC24271
C 983	15	1.4	20	1	AAZ32010	Antisense oligonuc
C 984	15	1.4	20	1	AAZ32010	Human adipose tiss
C 985	15	1.4	20	1	AAZ32010	Human adipose tiss
C 986	15	1.4	20	1	AAZ32010	Human 5-lipoxygena
C 987	15	1.4	20	1	AAZ32010	Primer for pUC19 D
C 988	15	1.4	20	1	AAZ32010	MSH2 gene specific
C 989	15	1.4	20	1	AAZ32010	MSH2 gene specific
C 990	15	1.4	20	1	AAZ32010	Human beta-actin d
C 991	15	1.4	20	1	AAZ32010	Human beta-actin d
C 992	15	1.4	20	1	AAZ32010	Human beta-actin d
C 993	15	1.4	20	1	AAZ32010	Human beta-actin d
C 994	15	1.4	20	1	AAZ32010	Human S-9 derived
C 995	15	1.4	20	1	AAZ32010	Human S-9 derived
C 996	15	1.4	20	1	AAZ32010	Human S-9 derived
C 997	15	1.4	20	1	AAZ32010	Human S-9 derived
C 998	15	1.4	20	1	AAZ32010	Human glutathione
C 999	15	1.4	20	1	AAZ32010	HT15-C downstream
C 1000	15	1.4	20	1	AAZ32010	Molecular beacon t

Murine IL-5 antise  
Ribonucleotide red  
Human S-9 derived  
Gene 216 SSCP sequ  
Human helicase-moi  
Human calreticulin  
Capture oligonucle  
Human matrix metal  
Human gene 216 pol  
Human matrix metal  
Mouse interleukin  
Oligo d(T) primer  
RT-PCR primer of t  
Escherichia coli 2  
Human biallelic ma  
Legionella 23S rRN  
C. trachomatis 23S  
Fungal 28S rRNA sp  
Universal probe 10  
Probe d. Unidenti  
Bacteriophage M4 v  
Cross-linking olig  
Oligomer HUM beta  
Oligomer HUM beta  
Gene detection seq  
Antisense oligonuc  
Human papilloma vi  
Human chromosome 1  
Internal PCR prime  
Auxotrophic ORF TR  
Retinoblastoma 1 p  
Probe for detectin  
Internal PCR prime  
Variant #5 of univ  
N-ras probe 665T  
Primer MY48 for hu  
Human mdm2 phospho  
Human mdm2 phospho  
PCR primer used to  
PCR primer used to  
PCR primer used to  
PCR primer used to  
PCR primer used to  
PCR primer used to  
Primer 128 for PDZ  
Human ras oncogene  
Human ras oncogene  
Human STAT3 phosph  
Human Ig H chain s  
Human TNFalpha ant  
Reverse primer for  
PCR primer for bet  
Human mdm2 antise  
Human mdm2 antise  
Human c-ski oncop  
Follicular conjunc  
Human E2F-2 gene p  
Human mdm2 antise  
Human mdm2 phospho  
Human mdm2 phospho  
Oligonucleotide in  
Human PLA2, group  
Human RECD1 antis  
Human RAIDD antis  
Mouse syntaxin 4 i  
Human Her-1 antise  
Human Stat3 antise  
DST CHS1 23 cDNA s  
Murine SAC1 gene-s  
Mouse pancreatic p

983	14.2	1.3	20	1	AA956792	Human STAT3 antisense	1056	13.8	1.3	17	1	ABA78137	BRCA1 mutation cor
984	14.2	1.3	20	1	ABL44478	Human chromosome 1	c1057	13.8	1.3	17	1	ABA78138	BRCA1 mutation cor
985	14.2	1.3	20	1	ABW77208	PCR primer used to	c1058	13.8	1.3	17	1	AA511599	Porcine reproducti
986	14	1.3	20	1	AAQ33508	Sequence of micros	c1059	13.8	1.3	17	1	AAH95016	Human Chk1 ribozym
c 987	14	1.3	14	1	AAV09230	3' poly(T) primer	1060	13.8	1.3	17	1	AAH80147	Oligonucleotide hy
c 988	14	1.3	14	1	AAV12222	Poly(T) oligonucle	1061	13.8	1.3	17	1	ABK02484	Human NOGO Ambery
c 989	14	1.3	14	1	AAK57019	WO9923258 oligonuc	1062	13.8	1.3	17	1	ABS74958	Human PAPP-Ea asso
c 990	14	1.3	14	1	AAK19465	Human senescence f	1063	13.8	1.3	17	1	ABT06038	Human IgM heavy ch
c 991	14	1.3	14	1	AAK14688	Triple helix formi	c1064	13.8	1.3	17	1	ABN08387	Human IgM heavy ch
c 992	14	1.3	14	1	AAK14689	Triple helix formi	c1065	13.8	1.3	17	1	ABN08389	Human GDMPLP-1 17-m
c 993	14	1.3	14	1	AAK14689	Triple helix third	c1066	13.8	1.3	17	1	ABN08390	Human GDMPLP-1 17-m
c 994	14	1.3	14	1	AAK62349	Oligonucleotide #1	c1067	13.8	1.3	17	1	ABN08391	Human GDMPLP-1 17-m
c 995	14	1.3	14	1	AAK84160	Oligonucleotide #2	c1068	13.8	1.3	17	1	ABN08662	Human GDMPLP-1 17-m
c 996	14	1.3	14	1	AAK83821	RNA oligonucleotid	c1069	13.8	1.3	17	1	ABT34448	Tumour suppression
c 997	14	1.3	14	1	ABO833269	EG1 cDNA tag relat	1070	13.8	1.3	17	1	ABT39664	Tumour suppression
c 998	14	1.3	14	1	ABO833275	EG1 cDNA tag relat	c1071	13.8	1.3	17	1	ABZ65528	Human HER2 DNzyme
c 999	14	1.3	14	1	ABO833278	EG1 cDNA tag relat	c1072	13.8	1.3	17	1	AAZ29451	Primer for laci
c 1000	14	1.3	14	1	ABU88471	Light dr 3p1 prime	c1073	13.8	1.3	18	1	AAZ41089	Calcium ion channe
c 1001	14	1.3	14	1	AAU93701	Light responsive o	c1074	13.8	1.3	18	1	AAZ06604	Human ELK-1 phosph
c 1002	14	1.3	14	1	AAU24492	Retinoid-regulated	c1075	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1003	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1076	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1004	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1077	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1005	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1078	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1006	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1079	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1007	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1080	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1008	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1081	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1009	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1082	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1010	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1083	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1011	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1084	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1012	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1085	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1013	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1086	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1014	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1087	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1015	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1088	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1016	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1089	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1017	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1090	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1018	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1091	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1019	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1092	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1020	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1093	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1021	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1094	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1022	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1095	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1023	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1096	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1024	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1097	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1025	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1098	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1026	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1099	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1027	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1100	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1028	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1101	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1029	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1102	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1030	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1103	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1031	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1104	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1032	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1105	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1033	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1106	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1034	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1107	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1035	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1108	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1036	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1109	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1037	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1110	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1038	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1111	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1039	14	1.3	15	1	AAU52140	Human ICAM hammerh	c1112	13.8	1.3	18	1	AAZ57824	ELK-1 expression m
c 1040	13.8	1.3	17	1	AAQ33914	Probe yz30 to N-ra	c1113	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1041	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1114	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1042	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1115	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1043	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1116	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1044	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1117	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1045	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1118	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1046	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1119	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1047	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1120	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1048	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1121	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1049	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1122	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1050	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1123	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1051	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1124	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1052	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1125	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1053	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1126	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1054	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1127	13.4	1.2	15	1	ABX01462	Hepatitis C virus
c 1055	13.8	1.3	17	1	AAQ33914	Detection probe fo	c1128	13.4	1.2	15	1	ABX01462	Hepatitis C virus



1129	13.4	1.2	17	1	ABA80869	LDLR mutation corr	c1202	13.2	1.2	18	1	AAF61167	Human betal-adreno
c1130	13.4	1.2	17	1	ABA80872	LDLR mutation corr	1203	13.2	1.2	18	1	AAF94707	Rho C antisense ph
1131	13.4	1.2	17	1	ABA80873	LDLR mutation corr	1204	13.2	1.2	18	1	AAC99280	Probe sequence use
1132	13.4	1.2	17	1	AAH80145	Oligonucleotide hy	c1205	13.2	1.2	18	1	AAH47615	Human Her-3 mRNA 1
1133	13.4	1.2	17	1	AAH80146	Oligonucleotide hy	1206	13.2	1.2	18	1	ABX96552	Human genomic DNA
c1134	13.4	1.2	17	1	ABK01296	Human NOGO Inozyme	1207	13.2	1.2	18	1	ABT06253	Synthetic DNA sell
c1135	13.4	1.2	17	1	ABK01700	Human NOGO Inozyme	1208	13.2	1.2	18	1	ABT04732	End-labelled probe
1136	13.4	1.2	17	1	ABN07676	Human NOGO Inozyme	1209	13.2	1.2	18	1	ABN99785	DNA probe #39 for
1137	13.4	1.2	17	1	ABN07677	Human NOGO Inozyme	1210	13.2	1.2	18	1	ABN72477	Sample orionucleo
1138	13.4	1.2	17	1	ABN07678	Human NOGO Inozyme	1211	13.2	1.2	18	1	ABL59674	Oligonucleotide pr
c1139	13.4	1.2	17	1	ABN08388	Human NOGO Inozyme	c1212	13.2	1.2	18	1	ABL58280	Oligonucleotide pr
c1140	13.4	1.2	17	1	ABN08660	Human NOGO Inozyme	1213	13.2	1.2	18	1	ABL58280	Probe #4 used in a
c1141	13.4	1.2	17	1	ABN08661	Human NOGO Inozyme	1214	13.2	1.2	18	1	ABL58280	Probe #4 used in a
c1142	13.4	1.2	17	1	ABK18426	Human ERG hammerhe	1215	13.2	1.2	18	1	ABL54939	Human tumour suppr
1143	13.4	1.2	17	1	ABK18426	Human ERG hammerhe	1216	13.2	1.2	18	1	ABL54939	Human tumour suppr
c1144	13.4	1.2	17	1	ABK19435	Human ERG hammerhe	c1217	13.2	1.2	18	1	ABL55132	Human chromosome 1
c1145	13.4	1.2	17	1	ABK19435	Human ERG hammerhe	1218	13.2	1.2	18	1	ABL55132	Nucleic acid synth
c1146	13.4	1.2	17	1	ABK19436	Human ERG hammerhe	c1219	13.2	1.2	18	1	ABZ21485	Synthetic probe SE
1147	13.4	1.2	17	1	ABK26751	Reduced palmitate	1219	13.2	1.2	18	1	AAQ34018	Microsatellite seq
c1148	13.4	1.2	17	1	ABK26752	Reduced palmitate	c1220	13.2	1.2	18	1	AAQ34128	Sequence of a micr
c1149	13.4	1.2	17	1	ABT34751	Tumour suppression	c1221	13.2	1.2	18	1	AAQ54278	Antineoplastic oli
c1150	13.4	1.2	17	1	ABT38926	Tumour suppression	c1222	13.2	1.2	18	1	AAV03386	Enhanced specifici
c1151	13.4	1.2	17	1	ABZ65372	Human HER2 DNAzyme	c1223	13.2	1.2	18	1	AAV43768	Cancer associated
c1152	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1224	13.2	1.2	18	1	AAV78231	MALDI-analysis oli
c1153	13.4	1.2	18	1	AAQ38707	First chimeric pri	1225	13.2	1.2	18	1	AAV77992	Electrospray mass
1154	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1226	13.2	1.2	18	1	AAZ32598	DNA oligomer A-13S
c1155	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1227	13.2	1.2	18	1	AAZ34665	RT primer A0 used
c1156	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1228	13.2	1.2	18	1	AAZ34665	3' PCR primer used
c1157	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1229	13.2	1.2	18	1	AAZ34665	Immunostimulatory
c1158	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1230	13.2	1.2	18	1	AAZ34665	Immunostimulatory
c1159	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1231	13.2	1.2	18	1	AAZ34665	Fragment 1 #2. Un
1160	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1232	13.2	1.2	18	1	AAZ34665	Model sequence, s
c1161	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1233	13.2	1.2	18	1	AAZ34665	Sequence with 2'-O
c1162	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1234	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1163	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1235	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1164	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1236	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1165	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1237	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1166	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1238	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1167	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1239	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1168	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1240	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1169	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1241	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1170	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1242	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1171	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1243	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1172	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1244	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1173	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1245	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1174	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1246	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1175	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1247	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1176	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1248	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1177	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1249	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1178	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1250	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1179	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1251	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1180	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1252	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1181	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1253	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1182	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1254	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1183	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1255	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1184	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1256	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1185	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1257	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1186	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1258	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1187	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1259	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1188	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1260	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1189	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1261	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1190	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1262	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1191	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1263	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1192	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1264	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1193	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1265	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1194	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1266	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1195	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1267	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1196	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1268	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1197	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1269	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1198	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1270	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1199	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1271	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
1200	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1272	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
c1201	13.4	1.2	18	1	AAQ38707	First chimeric pri	c1273	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE
							c1274	13.2	1.2	18	1	AAZ34665	Oligonucleotide SE

Poly(7) oligonucle

13	1.2	1348	12.8	1.2	16	1	AAA33723	Low adenosine anti
13	1.2	1349	12.8	1.2	16	1	ABL57868	Human ABCA7 gene p
13	1.2	1350	12.8	1.2	17	1	AAQ13796	Probe 83-4A for ce
13	1.2	1351	12.8	1.2	17	1	AAQ20006	Oligonucleotide #2
13	1.2	1352	12.8	1.2	17	1	AAQ20005	Oligonucleotide #1
13	1.2	1353	12.8	1.2	17	1	AAQ26203	HIA-DR beta sub-ty
13	1.2	1354	12.8	1.2	17	1	AAQ75070	Mouse flt-1 VEGF r
13	1.2	1355	12.8	1.2	17	1	AAQ71001	Human KDR VEGF rec
13	1.2	1356	12.8	1.2	17	1	AAQ70072	Human flt1 VEGF re
13	1.2	1357	12.8	1.2	17	1	AAQ69805	Human flt1 VEGF re
13	1.2	1358	12.8	1.2	17	1	AAQ69438	Human flt1 VEGF re
13	1.2	1359	12.8	1.2	17	1	AAQ69439	Human flt1 VEGF re
13	1.2	1360	12.8	1.2	17	1	AAQ62988	Delta-9 desaturase
13	1.2	1361	12.8	1.2	17	1	AAQ62274	Granule bound star
13	1.2	1362	12.8	1.2	17	1	AAQ57442	DNA probe 1 specif
13	1.2	1363	12.8	1.2	17	1	AAQ97477	Human EGF-R target
13	1.2	1364	12.8	1.2	17	1	AAQ96673	Potato citrate syn
13	1.2	1365	12.8	1.2	17	1	AAQ19046	Human IIE-2 substr
13	1.2	1366	12.8	1.2	17	1	AAQ21123	Integrin alpha 6 s
13	1.2	1367	12.8	1.2	17	1	AAQ22609	Integrin subunit b
13	1.2	1368	12.8	1.2	17	1	AAQ22830	Integrin subunit b
13	1.2	1369	12.8	1.2	17	1	AAQ22974	Integrin subunit b
13	1.2	1370	12.8	1.2	17	1	AAQ25179	Human A-Raf substr
13	1.2	1371	12.8	1.2	17	1	AAQ25181	Hammerhead ribozym
13	1.2	1372	12.8	1.2	17	1	AAQ25555	Hammerhead ribozym
13	1.2	1373	12.8	1.2	17	1	AAQ20213	Hammerhead ribozym
13	1.2	1374	12.8	1.2	17	1	AAQ22208	Hammerhead ribozym
13	1.2	1375	12.8	1.2	17	1	AAQ2388	Hammerhead ribozym
13	1.2	1376	12.8	1.2	17	1	AAQ03227	Hammerhead ribozym
13	1.2	1377	12.8	1.2	17	1	AAQ6314	Hammerhead ribozym
13	1.2	1378	12.8	1.2	17	1	AAQ36578	Hammerhead ribozym
13	1.2	1379	12.8	1.2	17	1	AAQ25179	Human genomic SNP
13	1.2	1380	12.8	1.2	17	1	AAQ25181	Oestrogen receptor
13	1.2	1381	12.8	1.2	17	1	AAQ25444	Oestrogen receptor
13	1.2	1382	12.8	1.2	17	1	AAQ25456	Oestrogen receptor
13	1.2	1383	12.8	1.2	17	1	ABA77753	Retinoblastoma mut
13	1.2	1384	12.8	1.2	17	1	ABA77754	Retinoblastoma mut
13	1.2	1385	12.8	1.2	17	1	AAH76222	Human prostaglandi
13	1.2	1386	12.8	1.2	17	1	AAH95015	Human Chk1 ribozym
13	1.2	1387	12.8	1.2	17	1	AAH95046	Human Chk1 ribozym
13	1.2	1388	12.8	1.2	17	1	AAH80148	Human Chk1 ribozym
13	1.2	1389	12.8	1.2	17	1	AAH80148	Oligonucleotide hy
13	1.2	1390	12.8	1.2	17	1	AAQ03856	PCR primer 415 use
13	1.2	1391	12.8	1.2	17	1	ABK01170	Human NCO inozyme
13	1.2	1392	12.8	1.2	17	1	ABK01424	Human NCO inozyme
13	1.2	1393	12.8	1.2	17	1	ABK01891	Human NCO Zinzyne
13	1.2	1394	12.8	1.2	17	1	ABK01940	Human NCO Zinzyne
13	1.2	1395	12.8	1.2	17	1	ABK02483	Human NCO Zinzyne
13	1.2	1396	12.8	1.2	17	1	ABK03593	Human CD20 DNazyme
13	1.2	1397	12.8	1.2	17	1	ABK74957	Human P



c1567	12.4	1.1	15	1	AAZ64408	Substrate for ham	1640	12.4	1.1	17	1	ABN07679	Human GDMPL-1 17-m
c1568	12.4	1.1	15	1	AAF92685	HLA-DR typing prob	c1641	12.4	1.1	17	1	ABN07800	Human GDMPL-1 17-m
1569	12.4	1.1	15	1	AAF95031	Mutant capture oli	c1642	12.4	1.1	17	1	ABN07801	Human GDMPL-1 17-m
c1570	12.4	1.1	15	1	AAF60455	Oligonucleotide c1	c1643	12.4	1.1	17	1	ABN07802	Human GDMPL-1 17-m
c1571	12.4	1.1	15	1	AAF81000	PTGS2 allele speci	c1644	12.4	1.1	17	1	ABN07803	Human GDMPL-1 17-m
1572	12.4	1.1	15	1	AAF41502	IGFBP2 oligonucleo	c1645	12.4	1.1	17	1	ABN08111	Human GDMPL-1 17-m
c1573	12.4	1.1	15	1	AAF46504	IGFBP2 oligonucleo	c1646	12.4	1.1	17	1	ABN08112	Human GDMPL-1 17-m
c1574	12.4	1.1	15	1	AAF49043	IGF-I oligonucleot	c1647	12.4	1.1	17	1	ABN08113	Human GDMPL-1 17-m
1575	12.4	1.1	15	1	AAF51980	IGF-I oligonucleot	c1648	12.4	1.1	17	1	ABN08114	Human GDMPL-1 17-m
1576	12.4	1.1	15	1	AAF51981	IGF-I oligonucleot	c1649	12.4	1.1	17	1	ABN08393	Human GDMPL-1 17-m
c1577	12.4	1.1	15	1	AAF53299	IGF-I oligonucleot	c1650	12.4	1.1	17	1	ABN08394	Human GDMPL-1 17-m
c1578	12.4	1.1	15	1	AAF53300	IGF-I oligonucleot	c1651	12.4	1.1	17	1	ABN08659	Human GDMPL-1 17-m
c1579	12.4	1.1	15	1	ABX01316	Hepatitis C virus	c1652	12.4	1.1	17	1	ABN08659	GAPDH cDNA PCR pri
c1580	12.4	1.1	15	1	ABX01461	Hepatitis C virus	c1653	12.4	1.1	17	1	ABN08659	Human ERG hammarhe
1581	12.4	1.1	15	1	ABK41344	Human eIF2gamma r	c1654	12.4	1.1	17	1	ABK17554	Human ERG hammarhe
1582	12.4	1.1	15	1	ABK41344	Human colon cancer	c1655	12.4	1.1	17	1	ABK17718	Human ERG hammarhe
1583	12.4	1.1	15	1	ABK32012	Human colon cancer	c1656	12.4	1.1	17	1	ABK17723	Human ERG hammarhe
c1584	12.4	1.1	15	1	ABK32522	Human pancreatic c	c1657	12.4	1.1	17	1	ABK17724	Human ERG hammarhe
c1585	12.4	1.1	15	1	ABZ76549	Lactobacillus brev	c1658	12.4	1.1	17	1	ABK18431	Human ERG hammarhe
1586	12.4	1.1	16	1	AAV14166	Probe HBP21 for g	c1659	12.4	1.1	17	1	ABK18608	Human ERG G-cleave
1587	12.4	1.1	16	1	AAV48906	Complementary huma	c1660	12.4	1.1	17	1	ABK19084	Human ERG DNazyme
c1588	12.4	1.1	16	1	AAV57828	PCR primer for mar	c1661	12.4	1.1	17	1	ABK19427	Human ERG DNazyme
c1589	12.4	1.1	16	1	AAV36683	PCR primer for mar	c1662	12.4	1.1	17	1	ABK26199	Increased starch p
c1590	12.4	1.1	16	1	AAV32000	Human HLA-A/HLA-B	c1663	12.4	1.1	17	1	ABK26200	Increased starch p
1591	12.4	1.1	16	1	AAA46246	Interphotoreceptor	c1664	12.4	1.1	17	1	ABT34415	Tumour suppression
c1592	12.4	1.1	16	1	AAZ36573	Probe hybridising	c1665	12.4	1.1	17	1	ABT35404	Tumour suppression
1593	12.4	1.1	16	1	AAH91937	Human inflammatory	c1666	12.4	1.1	17	1	ABT35974	Tumour suppression
c1594	12.4	1.1	16	1	ABT11146	Human 5-lipoxygasa	c1667	12.4	1.1	17	1	ABT36096	Tumour suppression
c1595	12.4	1.1	16	1	ABK41462	Human proteasome a	c1668	12.4	1.1	17	1	ABT36562	Tumour suppression
c1596	12.4	1.1	16	1	ACA58253	Human familial bip	c1669	12.4	1.1	17	1	ABT37233	Tumour suppression
1597	12.4	1.1	17	1	AAQ26112	HLA-DR beta sub-ty	c1670	12.4	1.1	17	1	ABT37801	Tumour suppression
c1598	12.4	1.1	17	1	AAQ26233	HLA-DR beta sub-ty	c1671	12.4	1.1	17	1	ABT39985	Tumour suppression
c1599	12.4	1.1	17	1	AAQ26331	HLA-DR beta sub-ty	c1672	12.4	1.1	17	1	ACA06427	Tumour suppression
c1600	12.4	1.1	17	1	AAQ47606	Human D HUMDUR/C	c1673	12.4	1.1	17	1	ABZ60277	NFKB sub-unit modu
c1601	12.4	1.1	17	1	AAV71613	Human KDR VEGF rec	c1674	12.4	1.1	17	1	ABZ60283	Human K-Ras DNazym
c1602	12.4	1.1	17	1	AAV41179	Probe HBP50 for g	c1675	12.4	1.1	17	1	ABZ61269	Human K-Ras DNazym
c1603	12.4	1.1	17	1	AAV97635	Human EGF-R target	c1676	12.4	1.1	17	1	ABZ61967	Human H-Ras DNazym
1604	12.4	1.1	17	1	AAV95304	Human c-fos target	c1677	12.4	1.1	17	1	ABZ64762	Human H-Ras DNazym
1605	12.4	1.1	17	1	AAV95305	Human c-fos target	c1678	12.4	1.1	17	1	ABZ64765	Human HER2 DNazyme
1606	12.4	1.1	17	1	AAV96425	Human c-fos target	c1679	12.4	1.1	17	1	ABZ64766	Human HER2 DNazyme
1607	12.4	1.1	17	1	AAV48869	Potato citrate syn	c1680	12.4	1.1	17	1	ABZ64806	Human HER2 DNazyme
c1608	12.4	1.1	17	1	AAV20398	BrB-2 gene antise	c1681	12.4	1.1	17	1	ABZ64876	Human HER2 DNazyme
1609	12.4	1.1	17	1	AAV91019	Integrin alpha 6 s	c1682	12.4	1.1	17	1	ABZ64877	Human HER2 DNazyme
1610	12.4	1.1	17	1	AAV91020	Human C-raf target	c1683	12.4	1.1	17	1	ABZ64901	Human HER2 DNazyme
c1611	12.4	1.1	17	1	AAV91021	Human C-raf target	c1684	12.4	1.1	17	1	ABZ64966	Human HER2 DNazyme
1612	12.4	1.1	17	1	AAV91021	PCR primer used to	c1685	12.2	1.1	18	1	AAV16025	Human HER2 DNazyme
1613	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1686	12.2	1.1	18	1	AAV16025	PCR primer used to
1614	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1687	12.2	1.1	18	1	AAV16025	PCR primer for Hum
1615	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1688	12.2	1.1	18	1	AAV16025	PCR primer D-F use
1616	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1689	12.2	1.1	18	1	AAV16025	Murine Sox2 gene p
c1617	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1690	12.2	1.1	21	1	AAV16025	Reverse transcript
c1618	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1690	12.2	1.1	22	1	AAV16025	Oligonucleotide-na
c1619	12.4	1.1	17	1	AAV91021	Hammerhead ribozym	c1690	12.2	1.1	22	1	AAV16025	
1620	12.4	1.1	17	1	AAV91021	Primer IPWTF for i							
1621	12.4	1.1	17	1	AAV91021	Human genomic SNP							
c1622	12.4	1.1	17	1	AAV91021	Human frataxin gen							
1623	12.4	1.1	17	1	AAV91021	Factor VIII mutati							
c1624	12.4	1.1	17	1	AAV91021	Factor VIII mutati							
1625	12.4	1.1	17	1	AAV91021	Human Chk1 ribozym							
1626	12.4	1.1	17	1	AAV91021	Human Chk1 ribozym							
1627	12.4	1.1	17	1	AAV91021	Oligonucleotide hy							
c1628	12.4	1.1	17	1	AAV91021	Human NOGO Hamerh							
1629	12.4	1.1	17	1	AAV91021	Human pp-GaNTase 1							
c1630	12.4	1.1	17	1	AAV91021	Human pp-GaNTase 1							
c1631	12.4	1.1	17	1	AAV91021	Human pp-GaNTase 1							
c1632	12.4	1.1	17	1	AAV91021	Human pp-GaNTase 1							
c1633	12.4	1.1	17	1	AAV91021	Murine Ikbk exon							
c1634	12.4	1.1	17	1	AAV91021	Human CLCA1 gene e							
1635	12.4	1.1	17	1	AAV91021	Human CLCA1 gene e							
1636	12.4	1.1	17	1	AAV91021	Human CLCA1 gene e							
1637	12.4	1.1	17	1	AAV91021	Human CLCA1 gene e							
1638	12.4	1.1	17	1	AAV91021	Human CLCA1 gene e							
1639	12.4	1.1	17	1	AAV91021	Human GDMPL-1 17-m							

## ALIGNMENTS

RESULT 1  
AAQ75728/c  
ID AAQ75728 standard; DNA; 21 BP.  
XX  
AC AAQ75728;  
XX  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
PN JP06303997-A.  
XX

PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 XX WPI; 1995-018287/03.  
 XX  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested cDNAs with restriction  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;  
 Query Match 1.9%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAAATAAAAAAAAAA 1100  
 DB 21 TATTAAAAAATAAAAAAAAAA 1  
 RESULT 2  
 AAA71444/c  
 ID AAA71444 standard; DNA; 30 BP.  
 AC AAA71444;  
 XX  
 DT 01-DEC-2000 (first entry)  
 XX  
 DE Human megisin promoter PCR primer SEQ ID NO: 11.  
 KW Promoter; megisin; human; protein isolation; screening. PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200043528-A1.  
 PN  
 XX 27-JUL-2000.  
 PD  
 XX 25-JAN-2000; 2000WO-JP00350.  
 PF  
 XX 25-JAN-1999; 99JP-0015667.  
 PR  
 XX (KURO/) KUROKAWA K.  
 PA (MIYA/) MIYATA T.  
 XX  
 XX Miyata T;  
 PI  
 XX WPI; 2000-543257/49.  
 DR  
 XX DNA for promoter region of megisin useful for screening proteins -  
 PT  
 XX Example 5; Page 38; 45pp; Japanese.  
 PS  
 XX This invention describes a novel DNA sequence (I) representing a  
 CC promoter region having part or all of a specific base sequence. The  
 CC invention also describes (1) a vector containing (I); (2) a cell  
 CC transformed by the above vector; and (3) protein produced using (I). (I)

CC is useful for screening and isolating proteins (especially transcription  
 CC factors). AAA71434-A71469 represent PCR primers used in the method  
 CC described in the invention.  
 XX

SQ Sequence 30 BP; 6 A; 10 C; 5 G; 9 T; 0 other;  
 Query Match 1.9%; Score 21; DB 1; Length 30;  
 Best Local Similarity 82.8%; Pred. No. 65;  
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 266 GAGCACCTTCAGAAAGTTGTTGAAACTTG 294  
 |||||  
 DB 30 GAGCACCTTCAGATAGGAGCTGAAACTTG 2

RESULT 3

AAH38447

ID AAH38447 standard; DNA; 25 BP.

XX  
 AC AAH38447;  
 XX

DT 14-AUG-2001 (first entry)  
 XX

DE SNP specific SNPE primer SEQ ID 1243.  
 XX

KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 XX

OS Homo sapiens.  
 XX

PN WO200129262-A2.  
 XX

PD 26-APR-2001.  
 XX

PF 13-OCT-2000; 2000WO-US28436.  
 XX

PR 15-OCT-1999; 99US-0160096.  
 XX

PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX

PI Picoult-Newburg L, Pohl M;  
 XX

DR WPI; 2001-290930/30.  
 XX

XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample -  
 XX

PS Claim 1; Page 56; 83pp; English.  
 XX

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence.

XX Sequence 25 BP; 6 A; 2 C; 13 G; 4 T; 0 other;

Query Match 1.8%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 74;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAGTCTGAGGCTGAGGATGG 1015  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 TTGGAGGCTGAGGCTGAGGATGG 25

## RESULT 4

AAQ75581/c  
 ID AAQ75581 standard; DNA; 20 BP.

XX AC

XX AAQ75581;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENSEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;  
 Query Match 1.8%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100  
 ||||| ||||| ||||| ||||| |||||  
 Db 20 ATTAAAAAATAAAAAAAAAA 1

## RESULT 5

AAQ75727/c

ID AAQ75727 standard; DNA; 21 BP.

XX AAQ75727;  
 AC  
 XX 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENSEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.8%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAAATAAAAAAAAAA 1100  
 ||||| ||||| ||||| ||||| |||||  
 Db 20 ATTAAAAAATAAAAAAAAAA 1

## RESULT 6

AAQ75729/c

ID AAQ75729 standard; DNA; 21 BP.

XX AC

XX AAQ75729;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes..The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.8%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 66;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100

Db 20 ATTAAAAA1100

RESULT 7

AAQ75730/c

ID AAQ75730 standard; DNA; 21 BP.

XX AC AAQ75730;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes..The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;

Query Match

Best Local Similarity 1.8%; Score 20; DB 1; Length 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 ATTAAAAA1100

Db 20 ATTAAAAA1100

RESULT 8

AAV71936/c

ID AAV71936 standard; DNA; 27 BP.

XX AC AAV71936;

XX DT 18-FEB-1999 (first entry)

XX DE Anchored poly T RT-PCR primer.

XX Normalised; cDNA library; mRNA cloning; reverse transcription;  
 KW immobilise; screening; hybridisation; nucleic acid amplification;  
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.

OS Synthetic.

XX WO9851789-A2.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-DK00186.

XX PR 27-MAR-1998; 98DK-0000432.

XX PR 13-MAY-1997; 97DK-0000547.

XX PR 19-MAY-1997; 97US-0871030.

XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.

XX PI Warthoe PR;

XX WPI; 1999-009772/01.

XX Preparation of normalised, subdivided cDNA libraries from mRNA - by  
 PT reverse transcription and amplification, used to screen for new  
 PT genes and interacting proteins, potential drugs, and for diagnosis

XX Example 1; Page 29; 71pp; English.

XX The invention relates to preparation of a normalised, subdivided library  
 CC of amplified cDNA from the coding regions of mRNA in a sample. The  
 CC method involves reverse transcription, with at least one cDNA primer of  
 CC formula 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any  
 CC sequence of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3  
 CC and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second  
 CC strand cDNA synthesis using the first strand as template and a second  
 CC cDNA primer of a similar formula, in the presence of DNA polymerase I (or  
 CC its Klenow fragment) and amplification of double-stranded cDNA with a set  
 CC of amplification primers. Comparison of cDNA in the prepared library with  
 CC a database (a computer-generated list of molecular weights of restricted  
 CC DNA fragments of known sequence) is used to determine presence of an  
 CC expressed protein in a cell, also to detect changes in such expression  
 CC (particularly for diagnosis of disease). Surfaces (chip) having  
 CC amplified cDNA stably immobilised on it, obtained by a similar method,  
 CC are used to screen for genes of a particular family, by hybridisation  
 CC with nucleic acid from the family (to identify new genes) and to detect  
 CC differences in expression patterns between cells. The polypeptides  
 CC expressed by the libraries can be used for drug development. Sequences  
 CC AAV71935 to AAV71946 represent primers used to exemplify the method of  
 CC the invention.

XX Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 other;

Query Match

1.8%; Score 19.6; DB 1; Length 27;

Best Local Similarity 84.6%; Pred. No. 1e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1075 GCAACTATTAAAAA 1100  
DB 27 GCAAAAAA 2

RESULT 9  
ABK52620/C  
ID ABK52620 standard; DNA; 27 BP.  
XX AC  
XX ABK52620;  
XX DT 27-AUG-2002 (first entry)  
XX DE Minority genome method VFA-MUT-11 DNA sequence.  
XX KW Minority genome method; viral quasi-species; majority genome;  
XX KW genetic diagnosis; viral infection; human immune deficiency virus;  
XX KW hepatitis B; hepatitis C; antiviral therapy; ss.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT misc\_difference 1  
FT /tag= a  
FT /label= unknown  
FT /note= "C6 aminolinker sequence"  
XX PN W200183815-AL.  
XX PD 08-NOV-2001.  
XX PF 27-APR-2001; 2001WO-ES00165.  
XX PR 27-APR-2000; 2000ES-0001068.  
XX PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.  
XX PI Arias Esteban A, Baranowski E, Briones Llorente C, Domingo Solans E;  
XX PI Escarnis Homs C, Gomez Castilla J, Martin Ruiz-jarabo C;  
XX PI Parro Garcia V;  
XX WP1; 2002-147445/19.  
XX PT Detecting minority genomes in viral quasi-species, useful for  
XX PT identifying mutants responsible for drug resistance and to  
XX PT individualise therapy -  
XX PS Example 1; Page 53; 107pp; Spanish.  
XX CC The present invention relates to a new method for detecting minority  
XX CC genomes, present at less than 50%, in a population of nucleic acids of  
XX CC a viral quasi-species and having at least one mutation with respect to  
XX CC the majority genome. The invention can be used for genetic diagnosis of  
XX CC viral infections, especially human immune deficiency virus and  
XX CC hepatitis B or C, particularly to detect memory minority genomes that are  
XX CC implicated in failure of antiviral therapy, so the method may make  
XX CC possible design of therapies customised for individual patients. The  
XX CC present nucleic acid sequence represents the VFA-MUT-11 DNA sequence that  
XX CC was used in the methods of the invention.  
XX SQ Sequence 27 BP; 2 A; 4 C; 2 G; 18 T; 1 other;

Query Match 1.8%; Score 19.6; DB 1; Length 27;  
Best Local Similarity 84.6%; Pred. No. 1e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1073 AGCAACTATTAAAAA 1098  
DB 27 ACCGAGGATTAAAAA 2

RESULT 10  
AAQ75724/C  
ID AAQ75724 standard; DNA; 21 BP.  
XX AC  
XX AAQ75724;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.  
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WP1; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
XX PT followed by digestion with restriction enzymes  
XX PS Disclosure; Page 8; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an  
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
XX CC and a plural type of labelled reverse transcription primers  
XX CC (GENSEQ files AAQ75547-Q7598) and using the aggregate of mRNAs as the  
XX CC template for each reverse transcription primer; (b) digesting each of  
XX CC the prepared aggregates of the double-stranded cDNAs with restriction  
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
XX CC separate lanes. The method can be used to analyse gene expression  
XX CC rapidly and easily.  
XX SQ Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.8%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 85;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1100  
DB 21 TTTAAAAA 1

RESULT 11  
AAQ75732/C  
ID AAQ75732 standard; DNA; 21 BP.  
XX AC  
XX AAQ75732;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.



```
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TGTAAAAA 1
RESULT 12
AAQ75760/c
ID AAQ75760 standard; DNA; 21 BP.
XX
AC AAQ75760;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
```

```
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TATGAAAAA 1
RESULT 13
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TACTAAAAA 1
RESULT 14
AAQ75712/c
ID AAQ75712 standard; DNA; 21 BP.
XX
AC AAQ75712;
XX
```

DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 XX 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 7; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 85;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA 1100  
 DB 21 TACTAAAAA 1  
 RESULT 15  
 AAQ75720/c  
 ID AAQ75720 standard; DNA; 21 BP.  
 XX AAQ75720;  
 AC  
 XX 04-AUG-1995 (first entry)  
 DT Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 XX 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 DR

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 8; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;  
 SQ Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 85;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA 1100  
 DB 21 TCCTAAAAA 1  
 RESULT 16  
 AAQ75680/c  
 ID AAQ75680 standard; DNA; 21 BP.  
 XX AAQ75680;  
 AC  
 XX 04-AUG-1995 (first entry)  
 DT Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 OS JP06303997-A.  
 XX 01-NOV-1994.  
 PD 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 7; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;  
 SQ Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 85;

OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-0112515.

XX 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA

XX followed by digestion with restriction enzymes

XX Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an

XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX and a plural type of labelled reverse transcription primers

XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the

XX template for each reverse transcription primer; (b) digesting each of

XX the prepared aggregates of the double-stranded cDNAs with restriction

XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX separate lanes. The method can be used to analyse gene expression

XX rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;

SQ

Query Match 1.8%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 85;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1080 TATTAAAAAATAAAAAAAAA 1100

Db 21 TATCAAAAAAAAAAAAAAAAAA 1

RESULT 19

ABK12409

ID ABK12409 standard; DNA; 24 BP.

XX AC ABK12409;

XX 18-JUN-2002 (first entry)

XX RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.

XX Polypeptide-laminin B210.67; embryo development teratogenesis;

XX cytotstatic; reverse transcriptase-PCR; RT-PCR; primer; ss.

XX Unidentified.

XX CN1328013-A.

XX 26-DEC-2001.

XX 14-JUN-2000; 2000CN-0116514.

XX 14-JUN-2000; 2000CN-0116514.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-270054/32.

XX Polypeptide-laminin B210.67, useful for treating diseases such as

XX embryo development teratogenesis -

XX Example 2; Page 18 (disclosure); 33pp; Chinese.

```
XX The present invention relates to the isolation of polypeptide-laminin
CC B210.67, and the polynucleotide encoding it. Also described is
CC the process for preparing the protein by DNA recombination. The
CC polypeptide is useful for treating diseases such as embryo
CC development teratogenesis. The present sequence for reverse
CC transcriptase (RT)-PCR primer #1 is used with RT-PCR primer #2
CC (ABK12410) for isolating cDNA encoding polypeptide-laminin B210.67.
XX Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 other;
SQ
Query Match 1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 3 TCTTAAAAA 23
RESULT 20
AAI66361/c
ID AAI66361 standard; DNA; 24 BP.
XX
AC AAI66361;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
KW Human; phosphatidylinositol-3 kinase 35; PTINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175014-A2.
XX
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN003328.
XX
PR 17-MAR-2000; 2000CN-0114973.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
WPI; 2002-025836/03.
XX
New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations -
XX
Example 2; Page 12; 34pp; Chinese.
XX
The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention.
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;
Query Match 1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
Db 24 TCTTAAAAA 4
```

```
RESULT 21
ABK86170/c
ID ABK86170 standard; DNA; 25 BP.
XX
AC ABK86170;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #3 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
FN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US45401.
XX
PR 01-NOV-2000; 2000US-244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
WPI; 2002-508123/54.
XX
Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end -
XX
Example 2; Page 21; 45pp; English.
XX
The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dT primer used in the method of the
CC invention.
XX
SQ Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 other;
Query Match 1.7%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 11e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
Db 24 AACCAAAAAA 1
RESULT 22
ABX79828/c
```

ID ABX79828 standard; cDNA; 27 BP.  
 AC ABX79828;  
 XX 17-APR-2003 (first entry)  
 XX EST polymorphic DNA repeat polynucleotide #153.  
 DE  
 XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6472154-B1.  
 PN  
 XX 29-OCT-2002.  
 PD  
 XX 31-DEC-1999; 99US-0475947.  
 XX  
 XX 31-DEC-1999; 99US-0475947.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Garner HR, Wren JD, Minna JD, Fondon JW;  
 XX WPI; 2003-208816/20.  
 XX  
 XX Identifying a candidate polymorphic repeat within a coding sequence,  
 PT for understanding or treating genetic disease, comprises detecting  
 PT tandem repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability -  
 XX  
 XX Examples; Column 717; 588pp; English.  
 PS  
 XX The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs.  
 XX  
 SQ Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 other;  
 Query Match 1.7%; Score 19.2; DB 1; Length 27;  
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 1077 AACTATTATAAAAAAAAAAAAAA 1100  
 DB 27 AATATAAAAAAAAAAAAAAAAAAAAA 4  
 RESULT 23  
 ID AAQ75552/c  
 XX AAQ75552 standard; DNA; 19 BP.  
 AC AAQ75552;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT

DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 other;  
 SQ  
 Query Match 1.7%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TTAATAAAAAAAAAAAAAA 1  
 RESULT 24  
 ID AAQ75580/c  
 XX AAQ75580 standard; DNA; 20 BP.  
 AC AAQ75580;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT

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PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 other;
Query Match 1.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 25
AAQ75582/c
ID AAQ75582 standard; DNA; 20 BP.
AC AAQ75582;
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
FN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 26
AAQ75579/c
ID AAQ75579 standard; DNA; 20 BP.
AC AAQ75579;
XX
XX 04-AUG-1995 (first entry)
DT
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
FN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 27
AAQ75723/c
ID AAQ75723 standard; DNA; 21 BP.
AC AAQ75723;
XX
XX 04-AUG-1995 (first entry)
DT
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
```

```
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 28
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX
AC AAQ75725;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 28
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX
AC AAQ75725;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 30
AAQ75731/c
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SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match      1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAACAAAAA 1100
DB 19 TTAACAAAAA 1

RESULT 33
AAQ75719/c
ID AAQ75719 standard; DNA; 21 BP.
XX AC AAQ75719;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression - by amplification of mRNA
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match      1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAACAAAAA 1100
DB 19 TTAACAAAAA 1

RESULT 34
AAQ75721/c
ID AAQ75721 standard; DNA; 21 BP.
XX AC AAQ75721;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression - by amplification of mRNA
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match      1.7%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAACAAAAA 1100
DB 19 TTAACAAAAA 1

RESULT 35
AAQ75722/c
ID AAQ75722 standard; DNA; 21 BP.
XX AC AAQ75722;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PS followed by digestion with restriction enzymes
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XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
XX
XX Query Match 1.7%; Score 19; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1082 TTAATAAAAAAAAAAAAAA 1100
XX Db 19 TTAATAAAAAAAAAAAAAA 1
XX
XX RESULT 36
XX ID ABK86168/c
XX AC ABK86168 standard; DNA; 24 BP.
XX AC ABK86168;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #1 used in method to study gene expression.
XX EX Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX PN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US45401.
XX PR 01-NOV-2000; 2000US-244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for
XX PT identifying mRNAs expressed at different levels, comprises employing an
XX PT identifier having a oligo-dT primer of a specific sequence and a
XX PT detectable marker at its 5' end -
XX PS Disclosure; Page 11; 45pp; English.
XX
XX The invention relates to systems for identification and characterisation
XX of gene expression in one or more samples, comprising an identifier having
XX a specific oligo-dT primer sequence, where the identifier comprises a
XX detectable marker at its 5' end. The system is useful for identifying any
XX or all genes expressed in a given in vivo or in vitro RNA sample, as well
XX as the relative differences in mRNA between 2 or more samples, where
XX that are expressed at different levels of new genes, and for identifying mRNAs
XX system or method addresses limitations of prior methods by comprising
XX compositions and systems that incorporate new strategies where molecular
XX or biochemical assay compositions and systems are linked to DNA or RNA
XX sequence databases for optimal resource efficiency in assaying gene
XX expression. The system has the following advantages over existing
XX methods: (a) prior sequence information or clone library construction is
XX not needed to enable the assay; (b) provides immediate sequence
XX information in addition to information concerning changes or differences
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CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dT primer used in the method of the
CC invention.
XX SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 other;
XX
XX Query Match 1.7%; Score 19; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1082 TTAATAAAAAAAAAAAAAA 1100
XX Db 22 TTAATAAAAAAAAAAAAAA 4
XX
XX RESULT 37
XX ID ABK86169
XX AC ABK86169 standard; DNA; 24 BP.
XX AC ABK86169;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #2 used in method to study gene expression.
XX EX Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX PN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US45401.
XX PR 01-NOV-2000; 2000US-244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX PI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for
XX PT identifying mRNAs expressed at different levels, comprises employing an
XX PT identifier having a oligo-dT primer of a specific sequence and a
XX PT detectable marker at its 5' end -
XX PS Disclosure; Page 11; 45pp; English.
XX
XX The invention relates to systems for identification and characterisation
XX of gene expression in one or more samples, comprising an identifier having
XX a specific oligo-dT primer sequence, where the identifier comprises a
XX detectable marker at its 5' end. The system is useful for identifying any
XX or all genes expressed in a given in vivo or in vitro RNA sample, as well
XX as the relative differences in mRNA between 2 or more samples, where
XX that are expressed at different levels of new genes, and for identifying mRNAs
XX system or method addresses limitations of prior methods by comprising
XX compositions and systems that incorporate new strategies where molecular
XX or biochemical assay compositions and systems are linked to DNA or RNA
XX sequence databases for optimal resource efficiency in assaying gene
XX expression. The system has the following advantages over existing
XX methods: (a) prior sequence information or clone library construction is
XX not needed to enable the assay; (b) provides immediate sequence
XX information in addition to information concerning changes or differences
```

CC in mRNA level, to determine mRNA expression level and mRNA identification  
 CC in one assay; (c) generates cDNA fragments from all mRNAs present in the  
 CC sample for subsequent investigation by common molecular biology  
 CC techniques; and (d) does not require prior knowledge of the sequence of  
 CC the genome of the organism under investigation and can be employed in  
 CC organisms lacking significant genomic sequence information. The present  
 CC sequence represents an oligo dT primer used in the method of the  
 CC invention.

XX SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 other;  
 Query Match 1.7%; Score 19; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 |||||  
 Db 3 TTAATAAAAAAAAAAAAAA 21

## RESULT 39

AAV71935/c

ID AAV71935 standard; DNA; 27 BP.

XX AC AAV71935;

XX DT 18-FEB-1999 (first entry)

XX DE Anchored poly T RT-PCR primer.

XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;  
 KW immobilise; screening; hybridisation; nucleic acid amplification;  
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.  
 XX OS Synthetic.

XX PN WO9851789-A2.

XX PD 19-NOV-1998.

XX PF 13-MAY-1999; 98WO-DK00186.

XX PR 27-MAR-1998; 98DK-0000432.

XX PR 13-MAY-1997; 97DK-0000547.

XX PR 19-MAY-1997; 97US-0871030.

XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.

XX PI Warthoe PR;

XX PS WPI; 1999-009772/01.

XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by  
 PT reverse transcription and amplification, used to screen for new  
 PT genes and interacting proteins, potential drugs, and for diagnosis

XX PS Example 1; Page 29; 71pp; English.

XX CC The invention relates to preparation of a normalised, subdivided library  
 CC of amplified cDNA from the coding regions of mRNA in a sample. The  
 CC method involves reverse transcription, with at least one cDNA primer of  
 CC formula 5'-Con1-dTn2-Vn3-Nn4 to form first strand cDNA where Con1 = any  
 CC sequence of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3  
 CC and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second  
 CC strand cDNA synthesis using the first strand as template and a second  
 CC cDNA primer of a similar formula, in the presence of DNA polymerase I (or  
 CC its Klenow fragment) and amplification of double-stranded cDNA with a set  
 CC of amplification primers. Comparison of cDNA in the prepared library with  
 CC a database (a computer-generated list of molecular weights of restricted  
 CC DNA fragments of known sequence) is used to determine presence of an  
 CC expressed protein in a cell, also to detect changes in such expression  
 CC (particularly for diagnosis of disease). Surfaces (chip) having  
 CC amplified cDNA stably immobilised on it, obtained by a similar method,

CC are used to screen for genes of a particular family, by hybridisation  
 CC with nucleic acid from the family (to identify new genes) and to detect  
 CC differences in expression patterns between cells. The polypeptides  
 CC expressed by the libraries can be used for drug development. Sequences  
 CC AAV71935 to AAV71946 represent primers used to exemplify the method of  
 CC the invention.

XX SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 other;  
 Query Match 1.7%; Score 19; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 |||||  
 Db 27 TTAATAAAAAAAAAAAAAA 9

## RESULT 39

ABK65992/c

ID ABK65992 standard; DNA; 27 BP.

XX AC ABK65992;

XX DT 02-JUL-2002 (first entry)

XX DE Human gene specific PCR primer #80.

XX KW Primer; ss; DNA microarray; differential expression analysis; human.

XX OS Homo sapiens.

XX PN US6352829-B1.

XX PD 05-MAR-2002.

XX PF 05-JAN-1999; 99US-0225928.

XX PR 21-MAY-1997; 97US-0859998.

XX PR (CLON-) CLONTECH LAB INC.

XX PI Chenchik A, Johhadze G, Bibilashvili R;

XX PS WPI; 2002-314699/35.

XX PT Producing sub-population of labeled nucleic acids, useful for analysing  
 XX differences in RNA profiles between several different physiological  
 XX sources, using set of distinct gene specific primers  
 XX Example 3; SEQ ID No 80; 11pp; English.  
 XX CC The invention relates to producing a sub-population of labeled nucleic  
 XX acids (NAs) comprising contacting a NA sample from a physiological  
 XX source, with a pool of 50 distinct gene specific primers under suitable  
 XX conditions to enzymatically generate sub-population of NAs, where  
 XX each gene specific primer has a sequence complementary to a distinct  
 XX mRNA, and each labeled NA is generated using a single gene specific  
 XX primer. The method is useful for producing a sub-population of labeled  
 XX NAs which is useful for analysing the differences in the RNA profiles  
 XX between several different physiological sources, where the method  
 XX comprises producing subpopulation of labeled NAs for the different  
 XX physiological sources, comprising the populations for each physiological  
 XX source to identify differences in the population, where the comparison  
 XX is preferably performed by hybridising the labeled NAs for each of the  
 XX distinct physiological sources to an array of probe NAs stably  
 XX associated with the surface of a substrate to produce a hybridisation  
 XX pattern for each of the sources, and comparing the patterns for each of  
 XX the sources, where differential gene expression assays are  
 XX utilised in differential expression analysis of diseased a normal  
 XX tissue e.g. neoplastic a normal tissue, or different tissue or  
 XX subissue types. The present sequence is a human gene specific PCR  
 XX primer used in the method of the invention.



XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences  
PT of specific length -  
XX  
PS Claim 14; Page 47; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular.  
XX  
SQ Sequence 25 BP; 3 A; 4 C; 1 G; 17 T; 0 other;  
  
Query Match 1.7%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 1.4e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1072 AAGCACTATTAAAAA 1096  
DB 25 AAGGAGGTATCAAAAAA 1  
  
RESULT 43  
AAX78723/c  
ID AAX78723 standard; DNA; 26 BP.  
XX  
AC AAX78723;  
XX  
DT 03-SEP-1999 (first entry)  
XX  
DE Human pancreatic PA153 EST-specific clone primer 12.  
XX  
KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;  
KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;  
KW gene therapy; EST; expressed sequence tag; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9931274-A2.  
XX  
PD 24-JUN-1999.  
XX  
PF 11-DEC-1998; 98WO-US26441.  
XX  
PR 15-DEC-1997; 97US-0990568.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;  
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
PI Roberts-Rapp L, Russell JC, Stroupe SD;  
XX  
WPI; 1999-405041/34.  
XX  
PT PA153 cDNA transcribed from pancreatic tissue  
XX  
PS Example 2; Page 121; 123pp; English.  
XX  
CC This invention describes novel contiguous and partially overlapping  
CC cDNA sequences and their encoded polypeptides, designated PA153,  
CC transcribed from human pancreatic tissue and which have cytostatic  
CC activity. The PA153 polynucleotides, proteins and antibodies are all  
CC useful in methods of detection. Detection of PA153 polynucleotide,  
CC antigens or anti-PA153 antibodies in a sample is indicative of  
CC pancreatic disease. PA153 antibodies (antagonists) can also be used in  
CC vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours  
CC or metastases. Antisense PA153 polynucleotides can be used in gene

CC therapy of pancreatic diseases. AAX78712-X78725 represent primers used  
CC in the method of the invention.  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;  
  
Query Match 1.7%; Score 18.6; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1.5e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1076 CAACCTATTAAAAA 1100  
DB 26 CAAAAA 2  
  
RESULT 44  
AAX07466/c  
ID AAX07466 standard; cDNA; 26 BP.  
XX  
AC AAX07466;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Human BS124 specific EST clone oligonucleotide.  
XX  
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
KW EST; ss.  
XX  
OS Synthetic.  
XX  
PN WO9859049-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US12862.  
XX  
PR 20-JUN-1997; 97US-0879354.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;  
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;  
XX  
WPI; 1999-105623/09.  
XX  
PT New isolated BS124 polynucleotides and polypeptides - used for  
PT detecting, diagnosing, preventing or treating diseases or conditions  
PT of the breast, such as breast cancer  
XX  
PS Disclosure; Page 97; 125pp; English.  
XX  
CC The sequence is that of an oligonucleotide used in the isolation of a  
CC BS124-specific EST clone. It is useful for detecting, diagnosing,  
CC staging, preventing or treating, or determining predisposition to  
CC diseases or conditions of the breast, such as breast cancer.  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 other;  
  
Query Match 1.7%; Score 18.6; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1.5e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1076 CAACCTATTAAAAA 1100  
DB 26 CAAAAA 2  
  
RESULT 45  
AAQ75597/c  
ID AAQ75597 standard; DNA; 20 BP.  
XX  
AC AAQ75597;  
XX

DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 XX  
 XX JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;  
 SQ  
 Query Match 1.7%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1081 ATTAAAAA 1100  
 XX 20 ATGAAAAA 1  
 Db  
 RESULT 46  
 AAQ75584/c  
 ID AAQ75584 standard; DNA; 20 BP.  
 XX  
 XX AAQ75584;  
 AC  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;  
 SQ  
 Query Match 1.7%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1081 ATTAAAAA 1100  
 XX 20 ATGAAAAA 1  
 Db  
 RESULT 46  
 AAQ75584/c  
 ID AAQ75584 standard; DNA; 20 BP.  
 XX  
 XX AAQ75584;  
 AC  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 other;  
 SQ  
 Query Match 1.7%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1080 TATTAAAA 1099  
 XX 20 TATAAAAA 1  
 Db  
 RESULT 47  
 AAQ75585/c  
 ID AAQ75585 standard; DNA; 20 BP.  
 XX  
 XX AAQ75585;  
 AC  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 XX  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 XX Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 other;  
 SQ  
 Query Match 1.7%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;



Qy	1081	ATTAAAAA	AAAAA	1100
D <sub>b</sub>	21	ATTGAAAA	AAAAA	2

XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993;







```

OY 1081 ATTAAAAA1100
DB 20 ACTAAAAA1

RESULT 59
AAQ75713/c
ID AAQ75713 standard; DNA; 21 BP.
XX
XX AAQ75713;
AC
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX 16-APR-1993; 93JP-0112515.
PS
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX 16-APR-1993; 93JP-0112515.
PS
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS

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XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DT
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
PT
XX Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
SQ

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Query Match 1.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1081 ATTAAAAA1100
DB 20 ACTAAAAA1

RESULT 61
AAQ75678/c
ID AAQ75678 standard; DNA; 21 BP.
XX
XX AAQ75678;
AC
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DT
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
PT
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;
SQ

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RESULT 63

16-APR-1993;

X  
TO-FAFX  
TO-FAF

PR 16-APR-1993; 93JP-0112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1081 ATTAAAAA 1100  
DB 20 AATAAAAA 1  
RESULT 65  
AAQ75676/c  
ID AAQ75676 standard; DNA; 21 BP.  
XX AC AAQ75676;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-0112515.  
XX 16-APR-1993; 93JP-0112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-0112515.  
XX 16-APR-1993; 93JP-0112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.

XX SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 other;  
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1080 TATTA 1099  
DB 20 TATTA 1  
RESULT 66  
AAQ75677/c  
ID AAQ75677 standard; DNA; 21 BP.  
XX AC AAQ75677;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-0112515.  
XX 16-APR-1993; 93JP-0112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
XX rapidly and easily.  
XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 other;  
XX Query Match 1.7%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1080 TATTA 1099  
DB 20 TATTA 1  
RESULT 67  
AAQ75629/c  
ID AAQ75629 standard; DNA; 21 BP.  
XX AC AAQ75629;  
XX  
XX 04-AUG-1995 (first entry)  
XX



QY 1081 ATTAAAAA 1100  
 Db 20 ATCAAAAAA 1

RESULT 70  
 AAQ75634/c  
 ID AAQ75634 standard; DNA; 21 BP.

XX AC AAQ75634;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.

XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1100  
 Db 20 ATCAAAAAA 1

RESULT 71  
 ABA93238  
 ID ABA93238 standard; DNA; 22 BP.

XX AC ABA93238;

XX DT 18-APR-2002 (first entry)

XX DE Polya adaptor oligonucleotide SEQ ID NO:1.

XX KW Detection; comparative detection; adaptor; ss.

XX OS Synthetic.

XX PN JP200133800-A.

XX PD 04-DEC-2001.  
 XX PF 30-MAY-2000; 2000JP-0160324.  
 XX PR 30-MAY-2000; 2000JP-0160324.  
 XX PA (UNIT-) UNITECH CO LTD.  
 XX DR WPI; 2002-135950/18.  
 XX DT Comparative detection of the amounts of RNA and DNA -  
 XX PT Disclosure; Page 9; 9pp; Japanese.  
 XX PS

CC The present invention describes a method for the comparative detection  
 of the amount of an RNA. The method comprises: (a) cDNAs obtained by  
 transcribing respectively from at least two tissue RNAs are respectively  
 fragmented by using a same restriction enzyme; (b) each different adaptor  
 and a common adaptor are added to each of the cDNA fragments derived from  
 the same or different tissues by the step (a); (c) the resultant adaptor-  
 added cDNAs are mixed together; (d) an adaptor primer having the common  
 sequence to said different adaptor and a gene-specific adaptor are used  
 to amplify said adaptor-added cDNAs containing no region derived from  
 polyadenylic acid of the mRNA before the addition of the adaptor among  
 the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
 cDNA amounts are measured between the tissues; (f) the RNA is detected  
 from the measured result; (g) each different adaptor and a common adaptor  
 are added to each of the genomic DNA fragments derived from a same or  
 different individuals; (h) the resultant adaptor-added genomic DNAs are  
 mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
 an adaptor primer having the common sequence to the different adaptor and  
 a sequence-specific adaptor; and (j) the ratios of the amplified amounts  
 of the genomic DNAs are measured between the individuals. The method is  
 used for the detection of the amounts of RNA and DNA. The present  
 sequence represents an oligonucleotide which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 other;

Query Match 1.7%; Score 18.4; DB 1; Length 22;  
 Best Local Similarity 95.0%; Pred. No. 1.3e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1100  
 Db 2 ATCAAAAAA 21

RESULT 72  
 ABV77669/c  
 ID ABV77669 standard; DNA; 24 BP.

XX AC ABV77669;

XX DT 03-FEB-2003 (first entry)

XX DE Human zinc finger protein 9.79 PCR primer #1.

XX KW Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;  
 anti-HIV; PCR; primer; ss.

XX OS Homo sapiens.

XX PN CN1343710-A.

XX PD 10-APR-2002.

XX PF 19-SEP-2000; 2000CN-0125246.

XX PR 19-SEP-2000; 2000CN-0125246.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX  
PI Mao Y, Xie Y;  
XX WPI; 2002-548879/59.  
XX  
XX A novel human zinc finger protein 9.79 polypeptide, useful for treating  
XX several diseases e.g. cancer and HIV infection -  
XX  
XX Example 2; Page 16 (Disclosure); 31pp; Chinese.  
XX  
XX The present invention relates to human zinc finger protein 9.79 (see  
XX AB59011). The zinc finger protein is useful for treating several  
XX diseases e.g. cancer and HIV infection. The present sequence is a PCR  
XX primer, which was used in an example from the invention.  
XX  
XX Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 other;  
SQ

Query Match 1.7%; Score 18.4; DB 1; Length 24;  
Best Local Similarity 95.0%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1100  
Dd 23 ATGAAAAA 4

RESULT 73  
AAH39959  
ID AAH39959 standard; DNA; 25 BP.  
XX  
XX AAH39959;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific SNPE primer SEQ ID 2755.  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 13-OCT-2000; 2000WO-US28436.  
XX  
XX 15-OCT-1999; 99US-0160096.  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoult-Newburg L, Pohl M;  
XX  
XX WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
XX absence or identity of single polynucleotide polymorphism in a nucleic  
XX acid sample -  
XX  
XX Claim 1; Page 64; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX primer extension (SNPE) primers, and the sequences of regions flanking  
XX sites of single nucleotide polymorphisms SNPs. The present invention  
XX includes kits for determining the presence or absence of a SNP, using the  
XX oligonucleotides of the invention. The PCR primers are used to amplify a  
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
XX performing a single-nucleotide primer extension reaction. The

CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC diseases of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence.  
XX  
SQ Sequence 25 BP; 16 A; 2 C; 2 G; 5 T; 0 other;  
Query Match 1.7%; Score 18.4; DB 1; Length 25;  
Best Local Similarity 95.0%; Pred. No. 1.5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1079 CTATTA 1098  
Dd 5 CTCTTA 24

RESULT 74  
AAH76998/c  
ID AAH76998 standard; DNA; 24 BP.  
XX  
XX AAH76998;  
XX  
DT 15-DEC-2001 (first entry)  
XX  
DE Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.  
XX  
XX Human, amyloid precursor protein 9; recombinant production;  
XX malignant tumour; cancer; blood disease; HIV infection;  
XX human immunodeficiency virus; immune disorder; inflammatory  
XX cytostatic; anti-HIV; antiinflammatory; immunomodulator;  
XX reverse transcription-PCR; RT-PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200174878-A1.  
XX  
XX 11-OCT-2001.  
XX  
XX 23-MAR-2001; 2001WO-CN00391.  
XX  
XX 24-MAR-2000; 2000CN-0115106.  
XX  
XX (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2001-626386/72.  
XX  
XX New human amyloid precursor protein 9 and encoded polynucleotide,  
XX applicable in diagnosis and treatment of cancer, hemopathy, human  
XX immunodeficiency virus infection, immunological diseases and various  
XX inflammations -  
XX  
XX Example 2; Page 16; 37pp; Chinese.  
XX  
XX The invention relates to human amyloid precursor protein 9 (AAG66809),  
XX nucleic acids encoding it (AAH76998), and a method for the recombinant  
XX production of amyloid precursor protein 9. The protein has a molecular  
XX weight of 9 kD. The present invention additionally discloses an  
XX antagonist of amyloid precursor protein 9 for therapeutic use, and an  
XX antibody which specifically binds to amyloid precursor protein 9. Amyloid





XX OS Synthetic.

XX PN WO9732023-A1.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-AU00124.

XX PR 01-MAR-1996; 96AU-0008386.

XX PA (FLOR-) FLORIGENE LTD.

XX PI Brugliera F, Holton TA, Michael MZ;

XX PX WPI; 1997-440691/41.

XX DR

XX PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and

XX PT corresponding DNA, used in the manipulation of pigmentation in

XX PT plants

XX PS Example 15; Page 59; 234pp; English.

XX PX

XX CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC

XX CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream

XX CC region of a polyadenylation sequence. They were used to prime cDNA

XX CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA,

XX CC and were also utilised in the PCR amplification of plant

XX CC cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see

XX CC AAT94657) encoding flavonoid 3' hydroxylase (see AAW35704) was isolated

XX CC using a differential display approach. This can be used to

XX CC manipulate the pigmentation of transgenic plants.

XX SX

XX SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TTAATAAAAAAAAAAAAAA 1100

DB 18 TTAATAAAAAAAAAAAAAA 1

RESULT 78

AAAX18372/c

ID AAAX18372 standard; DNA; 18 BP.

AC AAAX18372;

XX DT 11-MAY-1999 (first entry)

XX DE

XX DE RT-PCR primer of the invention SEQ ID 13.

XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX OS Synthetic.

XX PN JP11032765-A.

XX PD 09-FEB-1999.

XX PF 18-JUL-1997; 97JP-0208312.

XX PR 18-JUL-1997; 97JP-0208312.

XX PX (TAKI ) TAKARA SHUZO CO LTD.

XX PA

XX DR WPI; 1999-183822/16.

XX PT Peptides having at least two new nucleotides - useful as primers in

XX PT RT-PCR

PS Disclosure; Page 11; 19pp; Japanese.

XX

XX CC This sequence represents a primer of the invention. The invention relates

XX CC to sequences of at least two nucleotides of formula:

XX CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where

XX CC X = a labelled compound and/or a nucleotide with voluntary sequence;

XX CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition

XX CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;

XX CC N = adenine, guanine, cytosine or thymine; gamma = thymine;

XX CC k = natural number of 3 or over indicating the repetition of gamma, in

XX CC which thymine expressed by gamma indicating the repetition of gamma, in

XX CC guanine and/or cytosine. The new nucleotides are useful as primers for

XX CC RT-PCR and determination of base sequences. The new sequences allow for

XX CC reproducible and highly efficient analysis of gene sequences.

XX SX

XX SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1099

DB 18 TTAATAAAAAAAAAAAAAA 1

RESULT 79

AAQ75553/c

ID AAQ75553 standard; DNA; 19 BP.

XX AC AAQ75553;

XX DT 04-AUG-1995 (first entry)

XX DE

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX XX

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA

XX PT followed by digestion with restriction enzymes

XX PS Disclosure; Page 5; 11pp; Japanese.

XX CC

XX CC A method for the analysis of cDNA comprises (a) preparing an

XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

XX CC and a plural type of labelled reverse transcription primers

XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the

XX CC template for each reverse transcription primer; (b) digesting each of

XX CC the prepared aggregates of the double-stranded cDNAs with restriction

XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

XX CC separate lanes. The method can be used to analyse gene expression

XX CC rapidly and easily.

XX SX

XX SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 80
AAQ75554/c
ID AAQ75554 standard; DNA; 19 BP.
XX
AC AAQ75554;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 81
AAQ75551/c
ID AAQ75551 standard; DNA; 19 BP.
XX
AC AAQ75551;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.

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XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 82
AAQ49436/c
ID AAQ49436 standard; cDNA; 20 BP.
XX
AC AAQ49436;
XX
DT 25-MAR-2003 (updated)
DT 27-APR-1994 (first entry)
XX
XX Cytochrome P450 sequence amplification PCR primer polyT.
XX
XX Transgenic plants; altered petal colour;
XX polymerase chain reaction; ss.
XX
XX Synthetic.
XX
XX WO9320206-A1.
XX
XX 14-OCT-1993.
XX
XX 25-MAR-1993; 93WO-AU00127.
XX
XX 27-MAR-1992; 92AU-0001538.
XX
XX 07-JAN-1993; 93AU-0006698.
XX
XX (ITFL-) INT FLOWER DEV PTY LTD.
XX
XX Cornish EC, Holton TA, Tanaka Y;
XX
XX WPI; 1993-336914/42.
XX
XX Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
XX create transgenic plants with altered petal colour
XX

```

PS Disclosure; Page 25; 86pp; English.

XX The sequence is that of a PCR primer which was used in polymerase

CC chain reactions for the amplification of cloned cytochrome P450

CC sequences.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1100

DB 18 TAAAAAATAAAAAA 1

RESULT 83

AA04916/c

ID AA04916 standard; cDNA; 20 BP.

XX

AC AA04916;

XX

DT 25-MAR-2003 (updated)

DT 15-MAY-1996 (first entry)

XX

DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.

XX

KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;

KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;

KW transplant; neoplasia; myelosuppression; bone marrow; ss.

XX

OS Synthetic.

XX

PN BP676470-A1.

XX

PD 11-OCT-1995.

XX

PF 04-OCT-1990; 95EP-0105391.

XX

PR 01-OCT-1990; 90US-0589701.

PR 16-OCT-1989; 89US-0422383.

PR 11-JUN-1990; 90US-0537198.

PR 24-AUG-1990; 90US-0573616.

PR 28-SEP-1990; 90WO-US05548.

XX

PA (AMGE-) AMGEN INC.

XX

PI Rosselman RA, Martin FH, Suggs SV, Zsebo KM;

XX

DR WPI; 1995-346090/45.

XX

PT New stem cell factor polypeptide(s) - for stimulating the growth of

PT primitive progenitor cells, esp. for treating disorders involving

PT blood cells

XX

PS Example 3; Fig 12C; 127pp; English.

XX

CC AA04915-T04922 are oligonucleotide primers and probes used for the

CC amplification and sequencing of mammalian stem cell factor (SCF).

CC Non-naturally occurring SCF and C-terminally truncated polypeptides,

CC having amino acid sequences sufficiently duplicative of naturally

CC occurring SCF, stimulate growth of primitive progenitors such as

CC haematopoietic progenitor cells, neural stem cells and primordial

CC germ stem cells. The peptides can be used in a composition for

CC treating leucopenia, anaemia or thrombocytopenia, for enhancing

CC engraftment of bone marrow during transplantation or for bone marrow

CC recovery after chemotherapy or radiation-induced bone marrow aplasia

CC or myelosuppression. They can also be used for treating neoplasia,

CC nerve damage, infertility, intestinal damage or myeloproliferative

CC disorders. Antibodies may be raised against the peptides for use in

CC detection or neutralisation of SCF in serum. SCF may be useful for

CC the treatment of AIDS and severe combined immunodeficiency (SCID)

CC states alone or in combination with other factors such as IL-7.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1100

DB 19 TAAAAAATAAAAAA 2

RESULT 84

AAQ75583/c

ID AAQ75583 standard; DNA; 20 BP.

XX

AC AAQ75583;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX

OS Synthetic.

XX

PN JP06303997-A.

XX

PD 01-NOV-1994.

XX

PF 16-APR-1993; 93JP-0112515.

XX

PR 16-APR-1993; 93JP-0112515.

XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

DR WPI; 1995-018287/03.

XX

PT Analysis of cDNA and gene expression - by amplification of mRNA

PT followed by digestion with restriction enzymes

XX

PS Disclosure; Page 5; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers

CC (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the

CC template for each reverse transcription primer; (b) digesting each of

CC the prepared aggregates of the double-stranded cDNAs with restriction

CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in

CC separate lanes. The method can be used to analyse gene expression

CC rapidly and easily.

XX

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAA 1100

DB 18 TAAAAAATAAAAAA 1

RESULT 85

AAQ75586/c

ID AAQ75586 standard; DNA; 20 BP.

XX

AC AAQ75586;

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XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75587-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 86
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
AC AAQ75587;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75587-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 86
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
AC AAQ75587;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75587-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

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```

DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 87
AAQ75588/c
ID AAQ75588 standard; DNA; 20 BP.
AC AAQ75588;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;

```

Query Match

KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 91

AAQ75578/c  
 ID AAQ75578 standard; DNA; 20 BP.

XX AC AAQ75578;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.

XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 92

AAV07752/c

ID AAV07752 standard; DNA; 20 BP.

XX AC AAV07752;

DT 07-DEC-1998 (first entry)

XX Phosphorothioate oligonucleotide.

XX Phosphorothioate; sulphurisation; heterocycle; automated synthesis;  
 KW antisense; EDIH; Beaucage reagent; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc\_feature 1..20

FT /tag= a

FT /note= "phosphorothioate internucleotide linkages"

XX PN WO9741130-A2.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-US07118.

XX PR 30-APR-1996; 96US-0641920.

XX PA (LOU) UNIV LOUISIANA STATE & AGRIC.

XX PB (MINU) UNIV MINNESOTA.

XX PI Barany G, Chen L, Hammer RP, Musier-Forsyth K, Xu Q;

XX WPI; 1997-549671/50.

XX Sulphurisation of phosphorus-containing compounds, e.g.

PT oligo:nucleotide(s) - by contacting the compound with a

PT di:sulphide-containing five-membered heterocycle

XX Example 7; Page 30; 51pp; English.

XX The present invention provides a method for sulphurising phosphorus-  
 CC containing compounds. It comprises contacting the phosphorus-containing  
 CC compound with a 1,2,4-dithiazolidine-2,5-dione compound or a  
 CC 3-substituted-1,2,4-dithiazolin-5-one compound. The method is especially  
 CC useful for incorporation of phosphorothioate linkages into biologically  
 CC important molecules such as DNA, RNA and phosphopeptides. Molecules  
 CC containing such linkages are useful e.g. as antisense compounds for  
 CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-  
 CC protein interactions, or as catalytic RNA. The present sequence  
 CC represents an oligonucleotide with phosphorothioate linkages prepared by  
 CC the method of the invention.

XX Sequence 20 BP; 1 A; 0 C; 0 G; 19 U; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 20 TAAAAAAAAAAAAAAAAA 3

RESULT 93

AAAI3753/c

ID AAAI3753 standard; DNA; 20 BP.

XX AC AAAI3753;

XX DT 27-JUL-2000 (first entry)

DE Stem cell factor universal oligonucleotide 220-7.  
 XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;  
 KW primitive progenitor cell; haematopoietic disorder; syngeneic;  
 KW allogeneic; autologous bone marrow transplant; gene therapy;  
 KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;  
 KW cancer; ss.  
 XX Synthetic.  
 OS EP992579-A1.  
 XX PN 12-APR-2000.  
 XX PD 04-OCT-1990; 99EP-0122861.  
 XX PF 16-OCT-1989; 89US-0422383.  
 XX PR 11-JUN-1990; 90US-0537198.  
 XX PR 24-AUG-1990; 90US-0573616.  
 XX PR 28-SEP-1990; 90WO-US05548.  
 XX PR 01-OCT-1990; 90US-0589701.  
 XX PR 04-OCT-1990; 90EP-0310899.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Zeebo KM, Suggs SV, Bosselmann RA, Martin FH;  
 XX WPI; 2000-259135/23.  
 XX DR Production of hematopoietic cells suitable for administration to a  
 PT subject using progenitor cells and expanding the cells using stem cell  
 PT factor -  
 XX Example 3; Fig 12C; 123pp; English.  
 XX A method has been developed of making haematopoietic cells suitable for  
 CC administration to a subject. The method comprises: (a) obtaining  
 CC haematopoietic progenitor cells from a donor; and (b) expanding the  
 CC cells by adding to the cells a haematopoietically effective dose of a  
 CC polypeptide product having at least part of the primary structural  
 CC confirmation and one or more of the biological properties of naturally  
 CC occurring stem cell factor (SCF). The method is useful for stimulating  
 CC primitive progenitor cells including early haematopoietic progenitor  
 CC cells which are capable of maturing to erythroid, megakaryocyte,  
 CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute  
 CC increases in haematopoietic cells of both myeloid and lymphoid lineages.  
 CC SCF is useful for treating haematopoietic disorders. The method is  
 CC useful for expanding early haematopoietic progenitors in syngeneic,  
 CC allogeneic or autologous bone marrow transplant. SCF is useful for  
 CC enhancing the efficiency of gene therapy based on transfecting the  
 CC haematopoietic stem cells. SCF is also useful for combating the  
 CC myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing  
 CC haematopoietic recovery after acute blood loss and as a boost to the  
 CC immune system for fighting neoplasia (cancer). The present sequence  
 CC represents a universal oligonucleotide which is used in an example from  
 CC the present invention.  
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 DB 19 TAAAAAATAAAAAAAAAA 2  
 RESULT 94  
 AAS10448/c  
 ID AAS10448 standard; DNA; 20 BP.  
 XX AC AAS10448;

XX 24-OCT-2001 (first entry)  
 DT Human stem cell factor (SCF) cDNA universal PCR primer 220-7.  
 XX Human; stem cell factor; SCF; haematopoietic progenitor cell;  
 DE blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.  
 KW Homo sapiens.  
 OS US6248319-B1.  
 XX PN 19-JUN-2001.  
 XX PD 24-MAY-1995; 95US-0449653.  
 XX PF 10-APR-1991; 91US-0684535.  
 XX PR 25-NOV-1992; 92US-0982255.  
 XX PR 16-OCT-1989; 89US-0422383.  
 XX PR 11-JUN-1990; 90US-0537198.  
 XX PR 24-AUG-1990; 90US-0573616.  
 XX PR 01-OCT-1990; 90US-0589701.  
 XX PR 21-DEC-1993; 93US-0172329.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (WART/) MARTIN F H.  
 XX Zeebo KM, Bosselmann RA, Suggs SV, Martin FH;  
 XX WPI; 2001-407312/43.  
 XX Increasing the number of early haematopoietic progenitor cells in the  
 CC peripheral blood useful for the treatment of blood disorders including  
 CC Hodgkin's disease comprises the administration of human stem cell  
 CC factor -  
 XX Example 3; Fig 12C; 210pp; English.  
 XX The present sequence for universal PCR primer 220-7 is 1 of 19  
 CC PCR primers (AAS10435-AAS10453) used to amplify various portions of  
 CC the human SCF cDNA sequence. The sequence is described in an  
 CC invention relating to novel stem cell factors, the polynucleotides  
 CC encoding them and methods for producing the stem cell factors. The  
 CC methods involve increasing the number of early haematopoietic progenitor  
 CC cells in human peripheral blood by administering a haematopoietically  
 CC effective human stem cell factor polypeptide. The methods are useful for  
 CC the treatment of blood disorders, including myelofibrosis,  
 CC myelocytosis, osteopetrosis, metastatic carcinoma, acute leukaemia,  
 CC multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease,  
 CC Niemann-Pick disease, refractory anaemia, malaria, vitamin B12 and folic  
 CC acid deficiency, hypopigmentation disorders i.e. piebaldism and viral  
 CC induced disorders, including AIDS.  
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 DB 19 TAAAAAATAAAAAAAAAA 2  
 RESULT 95  
 AAH41332/c  
 ID AAH41332 standard; DNA; 20 BP.  
 XX AC AAH41332;  
 XX



DT 21-AUG-2001 (first entry)  
 XX Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.  
 DE Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;  
 XX gene therapy; PCR primer; mutagenesis; probe; ss.  
 KW Synthetic.  
 XX OS  
 XX US6207454-B1.  
 PN 27-MAR-2001.  
 XX 31-DEC-1998; 98US-0224681.  
 XX 21-DEC-1993; 93US-0172329.  
 PR 24-MAY-1995; 95US-0049653.  
 PR 12-JAN-1998; 98US-0005893.  
 PR 25-NOV-1992; 92US-0982255.  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI MPI; 2001-366062/38.  
 DR Enhancing efficiency of transfer of polynucleotide into a target  
 PT mammalian cell in vitro, involves exposing cell that expresses a stem  
 PT cell factor receptor to stem cell factor, and introducing  
 PT polynucleotide into cell in vitro -  
 XX Example 3; Fig 12C; 210pp; English.  
 PS The present invention describes a method for enhancing (E) the  
 XX efficiency of transfer of a polynucleotide (I) into a target mammalian  
 CC cell (II) in vitro, comprising exposing (II) that expresses a stem cell  
 CC factor (SCF) receptor to a biologically active SCF, its analogue or  
 CC fragment, which induces cell proliferation, and introducing (I) to (II)  
 CC in vitro. Exposure of SCF to (II) results in increased uptake of (I)  
 CC into the cell. The method is useful for enhancing the efficiency of the  
 CC transfer of a polynucleotide into a target mammalian cell in vitro.  
 CC The method is useful in gene therapy techniques. AAH41301 to AAH41364  
 CC and AAB98351 to AAB98390 represent sequences used in the exemplification  
 CC of the present invention.  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1083 TAAAAA AAAAAAAAAA 1100  
 Db 19 TAAAAA AAAAAAAAAA 2  
 RESULT 96  
 AAS04112/c  
 ID AAS04112 standard; DNA; 20 BP.  
 XX AAS04112;  
 AC 29-AUG-2001 (first entry)  
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

KW PCR primer; ss.  
 XX OS Homo sapiens.  
 XX PN US6207417-B1.  
 XX PD 27-MAR-2001.  
 XX 07-JUN-1995; 95US-0482918.  
 XX 21-DEC-1993; 93US-0172329.  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSERMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI MPI; 2001-298941/31.  
 DR Novel nucleic acids encoding stem cell factor useful for treating  
 PT disorders involving blood cells, e.g. leukaemia, splenomegaly, Hodgkin's  
 PT disease, Kala azar, anaemia and septicemia -  
 XX Example 3; Fig 12C; 209pp; English.  
 PS The present sequence for universal PCR primer 220-7 is 1 of 8  
 XX universal oligonucleotides (AAS04110-AAS04117) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAU02453-AAU02458, AAU02460, AAU02461) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAU02462-AAU02481) and the oligonucleotides  
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, Kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1083 TAAAAA AAAAAAAAAA 1100  
 Db 19 TAAAAA AAAAAAAAAA 2  
 RESULT 97  
 AAS04213/c  
 ID AAS04213 standard; DNA; 20 BP.  
 XX AAS04213;  
 AC 29-AUG-2001 (first entry)  
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS US6218148-B1.  
 PN XX  
 XX 17-APR-2001.  
 PD XX  
 XX 21-DEC-1993; 93US-0172329.  
 XX 25-NOV-1992; 92US-0982255.  
 XX 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-291051/29.  
 PI Isolated DNA sequence, encoding polypeptide product useful for  
 DR stimulating growth of early haematopoietic progenitor cells -  
 XX Example 3; Fig 12C; 167pp; English.  
 PS The present sequence for universal PCR primer 220-7 is 1 of 8  
 CC universal oligonucleotides (AA04211-AA04218) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAU02777-AAU02794) and the oligonucleotides  
 CC (AA04182-AA04210) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 DB 19 TAAAAAATAAAAAAAAAA 2  
 RESULT 98  
 AAH23890/c  
 ID AAH23890 standard; DNA; 20 BP.  
 XX AAH23890;  
 AC 07-AUG-2001 (first entry)  
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
 DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX

OS Homo sapiens.  
 XX US6204363-B1.  
 PN XX  
 XX 20-MAR-2001.  
 PD XX  
 XX 25-NOV-1992; 92US-0982255.  
 XX 10-APR-1991; 91US-0684535.  
 PR 16-OCT-1989; 89US-0422383.  
 PR 11-JUN-1990; 90US-0537198.  
 PR 24-AUG-1990; 90US-0573616.  
 PR 01-OCT-1990; 90US-0589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-256683/26.  
 PI New stem cell factor polypeptides and their analogs which stimulate  
 DR growth of early hematopoietic progenitors, useful for treating aplastic  
 XX anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's  
 PS disease -  
 XX Example 3; Fig 12C; 166pp; English.  
 CC The present sequence for universal PCR primer 220-7 is 1 of 8  
 CC universal oligonucleotides (AAH23888-AAH23895) used in the  
 CC isolation of the human SCF (stem cell factor) cDNA sequence. The  
 CC present invention relates to novel stem cell factors  
 CC (AAH23861-AAH23868, AAH23871-AAH23876) and the polynucleotides  
 CC encoding them. SCF stimulate primitive progenitor cells including early  
 CC haematopoietic progenitor cells. The invention also describes SCF  
 CC peptides (AAH23878-AAH23897) and the oligonucleotides  
 CC (AAH23859-AAH23887) used in the isolation of human and rat SCF  
 CC sequences. The polynucleotide encoding SCF is useful for producing SCF  
 CC and useful in gene therapy. It is useful for treating disorders  
 CC involving blood cells such as myelofibrosis, metastatic carcinoma,  
 CC acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma,  
 CC Gaucher's disease, anaemia, congestive splenomegaly, kala azar,  
 CC sarcoidosis, military tuberculosis, disseminated fungus disease,  
 CC fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, and hypopigmentation disorders such as  
 CC piebaldism and vitiligo.  
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 SQ Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 DB 19 TAAAAAATAAAAAAAAAA 2  
 RESULT 99  
 AAF89092/c  
 ID AAF89092 standard; DNA; 20 BP.  
 XX AAF89092;  
 AC 13-JUL-2001 (first entry)  
 XX Mammalian stem cell factor PCR primer SEQ ID NO: 33.  
 DE Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
 XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
 KW severe combined immunodeficiency; PCR primer; ss.  
 XX Mammalia.  
 OS

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XX PN US6207802-B1.
XX PD 27-MAR-2001.
XX XX
XX PF 09-NOV-1994; 94US-0336728.
XX XX
XX PR 25-NOV-1992; 92US-0982255.
XX PR 16-OCT-1989; 89US-0422383.
XX PR 11-JUN-1990; 90US-0537198.
XX PR 24-AUG-1990; 90US-0573616.
XX PR 01-OCT-1990; 90US-0589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX
XX DR WPI; 2001-353108/37.
XX XX
XX PT Novel isolated non-human mammalian stem cell factor polypeptide
XX PT stimulating growth of early haematopoietic progenitor cells, useful for
XX PT treating aplastic anaemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX PT sarcoidosis -
XX XX
XX PS Example 3; Fig 12C; 209pp; English.
XX XX
XX CC The present invention provides the protein and coding sequences of
XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the
XX CC growth of early haematopoietic progenitor cells, neural stem cells and
XX CC primordial germ stem cells. The sequences are useful in the treatment of
XX CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX CC and intestinal damage, infertility, AIDS and severe combined
XX CC immunodeficiency (SCID). The present sequence is primer used to amplify
XX CC an SCF in the exemplification of the invention.
XX XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
XX XX
XX Query Match 1.6%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd |||||
19 TAAAAAATAAAAAAAAAA 2

RESULT 100
ABS73849/C
ID ABS73849 standard; DNA; 20 BP.
XX AC ABS73849;
XX DT 05-DEC-2002 (first entry)
XX XX
XX DE SCF universal oligonucleotide 220-7.
XX XX
XX KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
XX KW haematopoietic system; metastatic carcinoma; acute leukaemia;
XX KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
XX KW refractory erythroblastic anaemia; lymphoma; Gaucher's disease;
XX KW disseminated fungus disease; haematopoietic; tuberculostatic;
XX KW anticanceric; antifungal; antimalarial; dermatological; ss.
XX XX
XX OS Synthetic.
XX XX
XX EN EP1241258-A2.
XX XX
XX PD 18-SEP-2002.
XX XX
XX PF 04-OCT-1990; 2002EP-0008587.
XX XX
XX PR 16-OCT-1989; 89US-0422383.
XX XX

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PR 11-JUN-1990; 90US-0537198.
PR 24-AUG-1990; 90US-0573616.
PR 28-SEP-1990; 90US-0589701.
PR 01-OCT-1990; 90US-0589701.
PR 04-OCT-1990; 90EP-0310899.
PR 04-OCT-1990; 95EP-0105391.
XX (AMGE-) AMGEN INC.
XX PA
XX XX
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX XX
XX DR WPI; 2002-684093/74.
XX XX
XX PT Production of a human stem cell factor (SCF) polypeptide for treating
XX PT disorders involving blood cells, such as leukaemia, comprises culturing
XX PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
XX PT encoding the human SCF -
XX XX
XX PS Example 3; Fig 12C; 120pp; English.
XX XX
XX CC The present invention relates to novel stem cell factors (SCFs),
XX CC polynucleotide sequences encoding the SCFs, and methods of producing
XX CC them. SCFs are involved in the blood-forming (haematopoietic)
XX CC system in mammals, particularly humans. The method of the invention
XX CC is useful for the production of human SCF. The stem cell factors are
XX CC useful to treat disorders involving blood cells e.g. metastatic
XX CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
XX CC lymphoma, refractory erythroblastic anaemia, multiple myeloma,
XX CC disseminated fungus disease, malaria, and vitiligo. The present
XX CC sequence representing a universal oligonucleotide for SCF DNA is
XX CC used in the examples of the present invention.
XX XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;
XX XX
XX Query Match 1.6%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd |||||
19 TAAAAAATAAAAAAAAAA 2

RESULT 101
RAD35465/C
ID RAD35465 standard; DNA; 20 BP.
XX AC RAD35465;
XX DT 25-JUL-2002 (first entry)
XX XX
XX DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX XX
XX KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
XX KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
XX KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
XX KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
XX KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
XX KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
XX KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
XX KW disseminated fungus disease; Fulminating septicemia; piebaldism; AIDS;
XX KW acquired immune deficiency syndrome; malaria; military tuberculosis;
XX KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
XX KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
XX KW primer; ss.
XX XX
XX OS Rattus sp.
XX XX
XX EN US2002018763-A1.
XX XX
XX PD 14-FEB-2002.
XX XX
XX PF 12-JAN-1998; 98US-0005243.
XX XX

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XX PR 24-MAY-1995; 95US-0449653.  
 XX PA (ZSEB/) ZSEBO K M.  
 XX PA (BOSS/) BOSSSELMAN R A.  
 XX PA (SUGG/) SUGGS S V.  
 XX PA (MART/) MARTIN F H.  
 XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX XX WPI; 2002-350789/38.  
 XX PT Novel non-naturally-occurring stem cell factor polypeptide, useful for  
 XX PT treating leucopenia, thrombocytopenia, anemia and for enhancing  
 XX PT engraftment of bone marrow during transplantation in a mammal -  
 XX PS Example 3; Fig 12C; 217pp; English.  
 XX CC The present invention relates to novel non-naturally-occurring stem cell  
 XX CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
 XX CC duplicative of that of naturally-occurring SCF to allow possession of  
 XX CC haematopoietic biological activity of naturally occurring SCF. Sequences  
 XX CC of the invention are useful for treating leucopenia, thrombocytopenia,  
 XX CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
 XX CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
 XX CC are also useful for treating acquired immune deficiency in a human, nerve  
 XX CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
 XX CC active polymer polypeptide adduct, for enhancing biological activity  
 XX CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
 XX CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,  
 XX CC Hodgkin's disease, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 XX CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
 XX CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
 XX CC splenic pancytopenia, disseminated fungus disease, malaria, military  
 XX CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin  
 XX CC B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
 XX CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
 XX CC and vitiligo. The present sequence is a PCR primer which is used for  
 XX CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
 XX CC exemplification of the invention.  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 other;  
 Query Match 1.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAA...AAAAAAAAA 1100  
 Db 19 TAAAAA...AAAAAAAAA 2  
 RESULT 102  
 AAQ75691/c  
 ID AAQ75691 standard; DNA; 21 BP.  
 XX AC AAQ75691;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX OS aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX PA WPI; 1995-018287/03.  
 XX DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX CC and a plural type of labelled reverse transcription primers  
 XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX CC template for each reverse transcription primer; (b) digesting each of  
 XX CC the prepared aggregates of the double-stranded cDNAs with restriction  
 XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX CC separate lanes. The method can be used to analyse gene expression  
 XX CC rapidly and easily.  
 XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 Query Match 1.6%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. NO. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAA...AAAAAAAAA 1100  
 Db 18 TAAAAA...AAAAAAAAA 1  
 RESULT 103  
 AAQ75692/c  
 ID AAQ75692 standard; DNA; 21 BP.  
 XX AC AAQ75692;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX OS aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX PA WPI; 1995-018287/03.  
 XX DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX CC and a plural type of labelled reverse transcription primers  
 XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX CC template for each reverse transcription primer; (b) digesting each of  
 XX CC the prepared aggregates of the double-stranded cDNAs with restriction

XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX XX WPI; 1995-018287/03.  
 XX DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX CC and a plural type of labelled reverse transcription primers  
 XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX CC template for each reverse transcription primer; (b) digesting each of  
 XX CC the prepared aggregates of the double-stranded cDNAs with restriction  
 XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX CC separate lanes. The method can be used to analyse gene expression  
 XX CC rapidly and easily.  
 XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 Query Match 1.6%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. NO. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAA...AAAAAAAAA 1100  
 Db 18 TAAAAA...AAAAAAAAA 1  
 RESULT 103  
 AAQ75692/c  
 ID AAQ75692 standard; DNA; 21 BP.  
 XX AC AAQ75692;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX OS aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-0112515.  
 XX PR 16-APR-1993; 93JP-0112515.  
 XX XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX PA WPI; 1995-018287/03.  
 XX DR Analysis of cDNA and gene expression - by amplification of mRNA  
 XX PT followed by digestion with restriction enzymes  
 XX PS Disclosure; Page 7; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an  
 XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX CC and a plural type of labelled reverse transcription primers  
 XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX CC template for each reverse transcription primer; (b) digesting each of  
 XX CC the prepared aggregates of the double-stranded cDNAs with restriction



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DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAAAAAA 1100
DB 18 TAAAAAAAAAAAAAAAAA 1
RESULT 107
AAQ75700/c
ID AAQ75700 standard; DNA; 21 BP.
XX
XX AC AAQ75700;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-0112515.
XX
XX PR 16-APR-1993; 93JP-0112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-0112515.
XX
XX PR 16-APR-1993; 93JP-0112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAAAAAA 1100
DB 18 TAAAAAAAAAAAAAAAAA 1
RESULT 108
AAQ75701/c
ID AAQ75701 standard; DNA; 21 BP.
XX
XX AC AAQ75701;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-0112515.
XX
XX PR 16-APR-1993; 93JP-0112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 TAAAAAAAAAAAAAAAAA 1100
DB 18 TAAAAAAAAAAAAAAAAA 1
RESULT 109
AAQ75702/c
ID AAQ75702 standard; DNA; 21 BP.
XX
XX AC AAQ75702;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
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RESULT 112
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX
XX AAQ75705;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 113
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX
XX AAQ75706;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX

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PF 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 114
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX
XX AAQ75707;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-0112515.
PF
XX
XX 16-APR-1993; 93JP-0112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
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XX Disclosure; Page 7; 11pp; Japanese.
PS
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XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;
SQ
Query Match 1.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAAAAAAAAAAAAA 1100
Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 115
AAQ75708/c
ID AAQ75708 standard; DNA; 21 BP.
XX
XX AAQ75708;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX

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CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;  
  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1083 TAAAAA...AAAAA 1100  
Db 18 TAAAAA...AAAAA 1  
  
RESULT 115  
AAQ75708/c  
ID AAQ75708 standard; DNA; 21 BP.  
XX  
AC AAQ75708;  
XX  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
FN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
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XX  
PS Disclosure; Page 7; 11pp; Japanese.  
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CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;  
  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1083 TAAAAA...AAAAA 1100  
Db 18 TAAAAA...AAAAA 1  
  
RESULT 116  
AAQ75709/c  
ID AAQ75709 standard; DNA; 21 BP.  
XX  
AC AAQ75709;  
XX  
XX

DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
FN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA  
followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
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aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;  
  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1083 TAAAAA...AAAAA 1100  
Db 18 TAAAAA...AAAAA 1  
  
RESULT 117  
AAQ75710/c  
ID AAQ75710 standard; DNA; 21 BP.  
XX  
AC AAQ75710;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
FN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

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XX Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
    Query Match      1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 118
AAQ75715/c
ID AAQ75715 standard; DNA; 21 BP.
XX
AC AAQ75715;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
    Query Match      1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 120
AAQ75717/c
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 119
AAQ75716/c
ID AAQ75716 standard; DNA; 21 BP.
XX
AC AAQ75716;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
PT followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
    Query Match      1.6%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 1.5e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Dd 18 TAAAAAATAAAAAAAAAA 1

RESULT 120
AAQ75717/c
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

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RESULT 123  
AAQ75684/c  
ID AAQ75684 standard; DNA; 21 BP.  
XX AC AAQ75684;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes  
XX PS Disclosure; Page 7; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.  
XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
Db 18 TAAAAA AAAAAAAAAA 1  
RESULT 124  
AAQ75685/c  
ID AAQ75685 standard; DNA; 21 BP.  
XX AC AAQ75685;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes  
XX PS Disclosure; Page 7; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.  
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
Db 18 TAAAAA AAAAAAAAAA 1  
RESULT 125  
AAQ75686/c  
ID AAQ75686 standard; DNA; 21 BP.  
XX AC AAQ75686;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes  
XX PS Disclosure; Page 7; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.  
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
Db 18 TAAAAA AAAAAAAAAA 1  
RESULT 126  
AAQ75687/c  
ID AAQ75687 standard; DNA; 21 BP.  
XX AC AAQ75687;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes  
XX PS Disclosure; Page 7; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.  
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
Db 18 TAAAAA AAAAAAAAAA 1  
RESULT 127  
AAQ75688/c  
ID AAQ75688 standard; DNA; 21 BP.  
XX AC AAQ75688;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-0112515.  
XX PR 16-APR-1993; 93JP-0112515.

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CC rapidly and easily.
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;
SQ
  Query Match      1.6%; Score 18; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 126
AAQ75687/c
ID AAQ75687 standard; DNA; 21 BP.
XX AC AAQ75687;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;

  Query Match      1.6%; Score 18; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 127
AAQ75688/c
ID AAQ75688 standard; DNA; 21 BP.
XX AC AAQ75688;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
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XX Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

  Query Match      1.6%; Score 18; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
DB 18 TAAAAAATAAAAAAAAAA 1

RESULT 128
AAQ75689/c
ID AAQ75689 standard; DNA; 21 BP.
XX AC AAQ75689;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
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PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
 DB 18 TAAAAA...AAAAA 1

RESULT 129  
 AAQ75690/c  
 ID AAQ75690 standard; DNA; 21 BP.  
 AC AAQ75690;  
 XX  
 DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.  
 Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.  
 Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 Disclosure; Page 7; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
 DB 18 TAAAAA...AAAAA 1

RESULT 130  
 AAQ75671/c  
 ID AAQ75671 standard; DNA; 21 BP.  
 AC AAQ75671;  
 XX  
 DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.  
 Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.  
 Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 Disclosure; Page 7; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
 DB 18 TAAAAA...AAAAA 1

RESULT 131  
 AAQ75672/c  
 ID AAQ75672 standard; DNA; 21 BP.  
 AC AAQ75672;  
 XX  
 DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.  
 Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX Disclosure; Page 7; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX and a plural type of labelled reverse transcription primers  
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs  
 XX template for each reverse transcription primer; (b) digesting each of  
 XX the prepared aggregates of the double-stranded cDNAs with restriction  
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX separate lanes. The method can be used to analyse gene expression  
 XX rapidly and easily.  
 XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;  
 XX  
 XX Query Match 1.6%; Score 18; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1083 TAAAAAATAAAAAAAAAA 1100  
 XX 18 TAAAAAATAAAAAAAAAA 1  
 XX  
 XX RESULT 132  
 XX AAQ75673/C  
 XX ID AAQ75673 standard; DNA; 21 BP.  
 XX AC AAQ75673;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX Disclosure; Page 7; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX and a plural type of labelled reverse transcription primers  
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs  
 XX template for each reverse transcription primer; (b) digesting each of  
 XX the prepared aggregates of the double-stranded cDNAs with restriction  
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX separate lanes. The method can be used to analyse gene expression  
 XX rapidly and easily.  
 XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;  
 XX  
 XX Query Match 1.6%; Score 18; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1083 TAAAAAATAAAAAAAAAA 1100  
 XX 18 TAAAAAATAAAAAAAAAA 1  
 XX  
 XX RESULT 132  
 XX AAQ75673/C  
 XX ID AAQ75673 standard; DNA; 21 BP.  
 XX AC AAQ75673;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX Disclosure; Page 7; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs

CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;  
 CC  
 CC Query Match 1.6%; Score 18; DB 1; Length 21;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1083 TAAAAAATAAAAAAAAAA 1100  
 CC 18 TAAAAAATAAAAAAAAAA 1  
 CC  
 CC RESULT 133  
 CC AAQ75674/C  
 CC ID AAQ75674 standard; DNA; 21 BP.  
 CC AC AAQ75674;  
 CC DT 04-AUG-1995 (first entry)  
 CC DE Reverse transcription primer used in cDNA analysis technique.  
 CC Analysis; gene expression; reverse transcription; primer; cDNA;  
 CC aggregate; restriction enzyme; ss.  
 CC Synthetic.  
 CC JP06303997-A.  
 CC 01-NOV-1994.  
 CC 16-APR-1993; 93JP-0112515.  
 CC 16-APR-1993; 93JP-0112515.  
 CC (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 CC WPI; 1995-018287/03.  
 CC Analysis of cDNA and gene expression - by amplification of mRNA  
 CC followed by digestion with restriction enzymes  
 CC Disclosure; Page 7; 11pp; Japanese.  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;  
 CC  
 CC Query Match 1.6%; Score 18; DB 1; Length 21;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1083 TAAAAAATAAAAAAAAAA 1100  
 CC 18 TAAAAAATAAAAAAAAAA 1  
 CC  
 CC RESULT 134

AAQ30430/C  
ID AAQ30430 standard; DNA; 23 BP.  
AC AAQ30430;  
XX  
DT 25-MAR-2003 (updated)  
DT 07-DEC-1992 (first entry)  
XX  
DE Oligomer IL6803 for forming triplex with HUMIL6 target duplex.  
XX  
XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;  
KW RSV; HPV; malignancy; hepatitis; inflammation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
FT modified\_base 23  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
FT misc\_feature 12..23  
FT /tag= c  
FT /label= inverted\_polarity\_region  
FT /notes= "see comments"  
FT misc\_feature 11..12  
FT /tag= d  
FT /note= "o-xyloso dimer synthon linkage"  
XX  
XX WO9209705-A1.  
XX  
PD 11-JUN-1992.  
XX  
XX 25-NOV-1991; 91WO-US08811.  
XX  
PR 23-NOV-1990; 90US-0617907.  
PR 18-JAN-1991; 91US-0643382.  
PR 08-APR-1991; 91US-0683420.  
PR 17-APR-1991; 91US-0686544.  
PR 17-APR-1991; 91US-0686546.  
PR 17-APR-1991; 91US-0686547.  
PR 27-SEP-1991; 91US-0766733.  
XX  
PA (GILE-) GILEAD SCI INC.  
XX  
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
XX WPI; 1992-217083/26.  
XX  
XX New oligomers contg. modified bases - which form a triplex with  
FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,  
FT hepatitis, herpes, malignancy and inflammation  
XX  
PS Claim 12; Page 71; 77pp; English.  
XX  
CC The synthetic oligomer is capable of forming a triplex at  
CC physiological pH with a purine rich target sequence by coupling  
CC into the major groove of the duplex. The specific target sequence  
CC of this oligomer is the human interleukin 6 gene untranslated  
CC sequence contg. a purine rich sequence concd. on one strand  
CC of the duplex. The oligomer, and others like it are useful in  
CC diagnosis and therapy of diseases characterised by specific DNA  
CC duplex targets, e.g. HPV, HIV, hepatitis B, herpes, malignant  
CC tumours and inflammation. The triple helices form under mild conditions  
CC thus assays may be carried out without subjecting the test specimen to  
CC harsh conditions. The oligomer contains an inverted polarity region  
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso  
CC (nucleotides have the 3' positions of xylose sugars linked via the o-  
CC xylene ring). Two nucleotides are coupled through a xyloso residue  
CC to form the dimer synthon. This additional modifications may render

CC the oligomer stable to nuclease activity. The oligomer is able to  
CC inhibit gene expression, as verified by in vitro systems.  
CC See also AAQ25452-25501 and AAQ30296-448.  
CC (Updated on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 other;  
XX  
Query Match 1.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1083 TAAAAAATAAAAAA 1100  
DB 23 TAAAAAATAAAAAA 6  
XX  
RESULT 135  
AAQ30431/C  
ID AAQ30431 standard; DNA; 23 BP.  
XX  
AC AAQ30431;  
XX  
DT 25-MAR-2003 (updated)  
DT 07-DEC-1992 (first entry)  
XX  
DE Oligomer IL6804 for forming triplex with HUMIL6 target duplex.  
XX  
XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV;  
KW RSV; HPV; malignancy; hepatitis; inflammation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= N4 N4 ethanocytosine"  
FT modified\_base 23  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
FT misc\_feature 12..23  
FT /tag= c  
FT /label= inverted\_polarity\_region  
FT /note= "see comments"  
FT misc\_feature 11..12  
FT /tag= d  
FT /note= "o-xyloso dimer synthon linkage"  
XX  
XX WO9209705-A1.  
XX  
PD 11-JUN-1992.  
XX  
XX 25-NOV-1991; 91WO-US08811.  
XX  
PR 23-NOV-1990; 90US-0617907.  
PR 18-JAN-1991; 91US-0643382.  
PR 08-APR-1991; 91US-0683420.  
PR 17-APR-1991; 91US-0686544.  
PR 17-APR-1991; 91US-0686546.  
PR 17-APR-1991; 91US-0686547.  
PR 27-SEP-1991; 91US-0766733.  
XX  
PA (GILE-) GILEAD SCI INC.  
XX  
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
XX WPI; 1992-217083/26.  
XX  
XX New oligomers contg. modified bases - which form a triplex with  
FT G-C doublet in a DNA duplex, for treating and diagnosing HIV,  
FT hepatitis, herpes, malignancy and inflammation  
XX



comprising screening a DNA sample for the variant MLH1 or MSH2 gene where presence of the variant indicates presence of, or susceptibility to HNPCC; (2) a method of identifying mutants in splice donor or acceptor sites of the human MLH1 gene, comprising sequencing splice donor or acceptor sites of the gene with intronic primers for the human MLH1 gene and analysing the sequence to identify any mutants; (3) a method of identifying mutants in splice donor or acceptor sites of a human MSH2 gene, comprising sequencing splice donor or acceptor sites of the gene with intronic primers for the human MSH2 gene and analysing the sequence to identify any mutants; and (4) a transgenic model system for colorectal cancer comprising cells expressing the variant MLH1 or MSH2 gene. The MLH1 and MSH2 variants are used to diagnose or determine a patient's susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene fragments from the present invention. ABL01832 to ABL01839 represent mutagenic primers used in the exemplification of the present invention.

Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
DB 2 TAAAAA...AAAAA 19

RESULT 137  
AAV42215/c  
ID AAV42215 standard; DNA; 25 BP.  
XX AC AAV42215;  
XX DT 16-OCT-1998 (first entry)  
XX DE Sequencing primer used to exemplify the invention.  
XX KW Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.  
XX OS Synthetic.  
XX PH Key  
XX FT modified\_base 1  
XX FT /tag= a  
XX FT /note= "labelled with the donor carboxyfluorescein"  
XX FT modified\_base 7  
XX FT /tag= b  
XX FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"  
XX FT modified\_base 14  
XX FT /tag= b  
XX FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"  
XX FT modified\_base 17  
XX FT /tag= b  
XX FT /note= "optionally labelled with the acceptor 6-carboxyrhodamine"  
XX FT modified\_base 17  
XX FT /tag= a  
XX FT /note= "optionally labelled with the donor carboxyfluorescein"

WO9831834-A1.  
23-JUL-1998.  
12-DEC-1997; 97WO-US22914.  
15-JAN-1997; 97US-0784162.  
(INCY-) INCYTE PHARM INC.

Claim 12; Page 71; 77pp; English.  
The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions such assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthn. The linking gp. is o-xyloso (nucleotides have the 3' positions of xylose sugars linked via the o-xyloso ring). Two nucleotides are coupled through a xylene residue to form the dimer synthn. This additional modification may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems.  
See also AAQ25452-25501 and AAQ30226-448.  
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 other;

Query Match 1.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
DB 23 TAAAAA...AAAAA 6

RESULT 136  
ABL01773  
ID ABL01773 standard; DNA; 23 BP.  
XX AC ABL01773;  
XX DT 18-MAR-2002 (first entry)  
XX DE Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.  
XX KW Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;  
XX KW hereditary non-polyposis colorectal cancer; ds.  
XX OS Homo sapiens.  
XX FN US200104936-A1.  
XX PD 22-NOV-2001.  
XX PF 22-OCT-1999; 99US-0426548.  
XX PR 22-OCT-1998; 98US-105180P.  
XX PA (ROBB/) ROBBINS D.  
XX PA (LING/) LIN-GOERKE J L.  
XX PA (LING/) LING J C.  
XX PI Robbins D, Lin-Goerke JL, Ling JC;  
XX WPI; 2002-105577/14.  
XX New variants of the human MLH1 and MSH2 genes for diagnosing or determining a predisposition for hereditary non-polyposis colorectal cancer -  
XX Disclosure; Page 4; 38pp; English.  
XX The present invention describes a variant human MLH1 or MSH2 gene. Also described are: (1) a method for diagnosing or predicting susceptibility to hereditary non-polyposis colorectal cancer (HNPCC),

XX  
PI  
XX  
XX  
DR  
XX  
XX  
WPI; 1998-414127/35.  
XX  
Set of energy-transfer fluorescent labels with donor and acceptor at  
PT different separations - useful for DNA sequencing allows use of  
PT fewer analysing wavelengths or an increased throughput  
XX  
XX  
PS  
PS  
Example 1; Page 14; 30pp; English.  
XX  
The present sequence exemplified the primer of the invention, and  
CC is used to sequence Incyte clone 1 (AAV42737). The primer of the  
CC invention is labelled with a set of at least 2 different fluorescent  
CC labels. The set comprises an energy-transfer fluorescent label with at  
CC least 1 each of a donor fluorophore and an acceptor fluorophore capable  
CC of energy transfer, and separated by a distance x, and a second similar  
CC fluorescent label in which the separation distance is y, x and y being  
CC sufficiently different for the two fluorescent labels to produce  
CC distinct fluorescent signals. Fluorescent labels are useful in  
CC multicomponent analyses, e.g. as probes for fluorescent in situ  
CC hybridisation or especially as primers for DNA sequencing.  
XX  
SQ  
Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
DB 24 TAAAAA AAAAAAAAAA 7  
RESULT 138  
AAx84259/c  
ID AAX84259 standard; DNA; 25 BP.  
XX  
AC AAX84259;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE PCR primer for human Nck associated protein 1 coding sequence.  
XX  
KW Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
KW therapy; PCR primer; ss.  
XX  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9931239-A1.  
XX  
PD 24-JUN-1999.  
XX  
XX 14-DEC-1998; 98WO-JP05646.  
XX  
XX 15-DEC-1997; 97JP-0363183.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX (SAKA/) SAKAKI Y.  
XX  
XX Sakaki Y;  
XX  
DR WPI; 1999-395181/33.  
XX  
XX Protein inhibiting apoptosis, useful in the diagnosis and treatment  
PT of Alzheimer's disease  
XX  
XX Disclosure; Page 76; 90pp; Japanese.  
XX  
XX This sequence represents a PCR primer used to isolate DNA encoding the  
CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits  
CC apoptosis. The protein can be used in the investigation, diagnosis and

CC treatment (e.g. by gene therapy) of Alzheimer's disease.  
XX  
SQ  
Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 other;  
Query Match 1.6%; Score 18; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1083 TAAAAA AAAAAAAAAA 1100  
DB 25 TAAAAA AAAAAAAAAA 8  
RESULT 139  
AAx69640/c  
ID AAT69640 standard; DNA; 19 BP.  
XX  
AC AAT69640;  
XX  
DT 20-FEB-1998 (first entry)  
XX  
DE Telomerase Oligo-dT-Primer P3.  
XX  
KW Telomerase; substrate; primer; detection; 5'-region; retrovirus;  
KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;  
KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.  
XX  
OS Synthetic.  
XX  
PN DE19644302-A1.  
XX  
PD 05-JUN-1997.  
XX  
PF 24-OCT-1996; 96DE-1044302.  
XX  
PR 28-NOV-1995; 95DE-1044317.  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Erich T, Hinzpeter M, Karl G, Leying H;  
XX WPI; 1997-299542/28.  
XX  
XX Measuring telomerase activity, useful for tumour diagnosis and  
PT compound screening - by extending substrate primer, followed by  
PT amplification and immobilising product for detection  
XX  
XX Example; Page 11; 21pp; German.  
XX  
XX The present sequence is a telomerase Oligo-dT-Primer, which can  
CC be used in a novel method for detecting telomerase activity. The  
CC method comprises adding to a test sample a 1st primer, that  
CC serves as telomerase substrate, and nucleoside triphosphate (dNTP)  
CC and incubating to allow primer extension by the telomerase,  
CC amplifying the extension product, immobilising the amplification  
CC product (AP) on a solid phase and qualitative and/or quantitative  
CC detection of AP, where the substrate primer is preferably from the  
CC 5'-region of the long terminal repeat 2 (LTR-2) sequence of a  
CC retrovirus. The method can be used to diagnose tumours and screen  
CC compounds for effector activity. Immobilisation of AP provides a  
CC signal that is reproducibly representative of telomerase activity,  
CC eliminates the need for gel electrophoretic separation and  
CC provides high sensitivity. Radioactive labels are not required and  
CC the method can be automated for routine use. Specific detection is  
CC achieved by proper choice of hybridisation conditions, without  
CC separation of the telomerase extension product. A specific signal  
CC is generated by 1-10 cell equivalents, but for tumour analysis  
CC 10-1000 ng of tissue is usually used.  
XX  
SQ  
Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 2 other;  
Query Match 1.6%; Score 17.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.5e+02;

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Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100
Db 19 DKAAAAAAAAAAAAAAAAAAAA 1

RESULT 140
AAQ75744/c
ID AAQ75744 standard; DNA; 21 BP.
XX
AC AAQ75744;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;
WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAAAAAAAAAAAAA 1100
Db 21 TACGAAAAAAAAAAAAAAAAAAAA 1

RESULT 141
AAQ75752/c
ID AAQ75752 standard; DNA; 21 BP.
XX
AC AAQ75752;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

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OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAAAAAAAAAAAAA 1100
Db 21 TCTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 142
AAQ75792/c
ID AAQ75792 standard; DNA; 21 BP.
XX
AC AAQ75792;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-0112515.
XX
PR 16-APR-1993; 93JP-0112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an

```

CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA...AAAAA 1100  
 DB 21 TAGGAAAAA...AAAAA 1  
 RESULT 143  
 AAQ75771/C  
 ID AAQ75771 standard; DNA; 21 BP.  
 AC AAQ75771;  
 DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; lipp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX and a plural type of labelled reverse transcription primers  
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX template for each reverse transcription primer; (b) digesting each of  
 XX the prepared aggregates of the double-stranded cDNAs with restriction  
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX separate lanes. The method can be used to analyse gene expression  
 XX rapidly and easily.  
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1079 CTATTAAAAA...AAAAA 1099  
 DB 21 CTAGAAAAA...AAAAA 1

RESULT 144  
 AAQ75776/C  
 ID AAQ75776 standard; DNA; 21 BP.  
 AC AAQ75776;  
 DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 XX followed by digestion with restriction enzymes  
 XX Disclosure; Page 9; lipp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 XX and a plural type of labelled reverse transcription primers  
 XX (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 XX template for each reverse transcription primer; (b) digesting each of  
 XX the prepared aggregates of the double-stranded cDNAs with restriction  
 XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 XX separate lanes. The method can be used to analyse gene expression  
 XX rapidly and easily.  
 XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA...AAAAA 1100  
 DB 21 TAGGAAAAA...AAAAA 1  
 RESULT 145  
 AAQ75756/C  
 ID AAQ75756 standard; DNA; 21 BP.  
 AC AAQ75756;  
 DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.

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XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 146
AAQ75764/C
ID AAQ75764 standard; DNA; 21 BP.
AC AAQ75764;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 145
AAQ75764/C
ID AAQ75764 standard; DNA; 21 BP.
AC AAQ75764;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression

```

```

CC rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 147
AAQ75628/C
ID AAQ75628 standard; DNA; 21 BP.
XX AAQ75628;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-0112515.
XX PR 16-APR-1993; 93JP-0112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA
XX PT followed by digestion with restriction enzymes
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an
XX CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX CC and a plural type of labelled reverse transcription primers
XX CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
XX CC template for each reverse transcription primer; (b) digesting each of
XX CC the prepared aggregates of the double-stranded cDNAs with restriction
XX CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX CC separate lanes. The method can be used to analyse gene expression
XX CC rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAAAAA 1100
DB 21 TTTGAAAAA 1
RESULT 148
AAQ75636/C
ID AAQ75636 standard; DNA; 21 BP.
XX AAQ75636;
XX 04-AUG-1995 (first entry)

```

XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX JF06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA 1100  
 Db 21 TGTCAAAAAA 1  
 RESULT 149  
 AAQ75643/c  
 ID AAQ75643 standard; DNA; 21 BP.  
 AC AAQ75643;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX JF06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA 1100  
 Db 21 TGTCAAAAAA 1  
 RESULT 149  
 AAQ75643/c  
 ID AAQ75643 standard; DNA; 21 BP.  
 AC AAQ75643;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX JF06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 SQ

PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1079 CTATTAAAAA 1099  
 Db 21 CTCAAAAA 1  
 RESULT 150  
 AAQ75616/c  
 ID AAQ75616 standard; DNA; 21 BP.  
 XX  
 AC AAQ75616;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX JF06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 6; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1100  
 DB 21 TACCAAAAAA 1

RESULT 151  
 AAQ75624/c  
 ID AAQ75624 standard; DNA; 21 BP.  
 XX  
 AC AAQ75624;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DT WPI; 1995-018287/03.  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DT WPI; 1995-018287/03.  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.

QY 1080 TATTAAAAA 1100  
 DB 21 TCTCAAAAAA 1

RESULT 152  
 AAQ75664/c  
 ID AAQ75664 standard; DNA; 21 BP.  
 XX  
 AC AAQ75664;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.

QY 1080 TATTAAAAA 1100  
 DB 21 TCTCAAAAAA 1

RESULT 153  
 AAQ75648/c  
 ID AAQ75648 standard; DNA; 21 BP.  
 XX  
 AC AAQ75648;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DT WPI; 1995-018287/03.  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.

XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 7; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;  
 XX

Query Match 1.6%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA 1100  
 DB 21 TAGCAAAAAA 1

RESULT 153  
 AAQ75648/c  
 ID AAQ75648 standard; DNA; 21 BP.  
 XX  
 AC AAQ75648;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DT WPI; 1995-018287/03.  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.

CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AA075547-075798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA...AAAAA 1100  
DB 21 TAACAAAAA...AAAAA 1

RESULT 154  
AAF32494/c  
ID AAF32494 standard; DNA; 21 BP.  
XX  
AC AAF32494;  
XX  
DT 19-APR-2001 (first entry)  
XX  
DE Human CD38 exon 4 PCR primer SEQ ID NO:9.  
XX  
KW Human; CD38; diabetes mellitus; detection; cyclic ADP-ribose; CADPR;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2000316578-A.  
XX  
PD 21-NOV-2000.  
XX  
PF 12-MAY-1999; 99JP-0131955.  
XX  
PR 12-MAY-1999; 99JP-0131955.  
XX  
PA (BMLB-) BML KK.  
PA (KANE/) KANETSUKA A.  
PA (OKAM/) OKAMOTO H.  
XX  
DR WPI; 2001-128255/14.  
XX  
PT Detecting onset of diabetes mellitus comprises detecting specific gene  
PT mutations in the CD38 gene -  
XX  
PS Example; Page 6; 19pp; Japanese.  
XX

The present invention describes a method using a mutation in the CD38  
Gene (involved in the production of cyclic ADP-ribose (CADPR)), to  
CC detect the onset of diabetes mellitus. The method is useful for  
CC detecting the onset of diabetes mellitus. The present sequence  
CC represents a PCR primer for human CD38, which is used in an example  
CC from the present invention.  
XX  
SQ Sequence 21 BP; 2 A; 10 C; 2 G; 7 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 995 AAGTCGAGGCTGGAGATGG 1015  
DB 21 AAGACGAGGCTGGAGATGG 1

RESULT 155  
AAZ00877/c

ID AAZ00877 standard; DNA; 24 BP.

XX  
AC AAZ00877;

DT 27-SEP-1999 (first entry)

DE PCR primer PGRT32 for PGI coding sequence.

XX  
KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;  
KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;  
KW PSA; human; ss.

XX  
OS Synthetic.

OS Homo sapiens.

XX  
PN WO9932644-A2.

XX  
PD 01-JUL-1999.

XX  
PF 22-DEC-1998; 98WO-IB02133.

XX  
PR 09-SEP-1998; 98US-0099658.

XX  
PR 22-DEC-1997; 97US-0996306.

XX  
PA (GEST ) GENSET.

XX  
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;

XX  
WPI; 1999-405178/34.

XX  
PT Use of a prostate cancer associated gene and biallelic markers  
PT derived from it

XX  
PS Example 6; Page 42; 385pp; English.

XX  
CC The invention relates to a mammalian PGI gene and protein, and a set of  
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are  
CC used in a hybridisation assay, a sequencing assay, or in an  
CC allele-specific amplification assay for determining the identity of a  
CC nucleotide at a PGI-related biallelic marker. The methods can be used to  
CC detect and to assess the risk of developing cancer or prostate cancer.  
CC Early-stage diagnosis of prostate cancer relies on prostate specific  
CC antigen (PSA) dosage. However, the effectiveness of this is limited due  
CC to its inability to discriminate between malignant and non-malignant  
CC affections of the organ. A need exists for both a reliable diagnostic  
CC procedure which would enable early-stage diagnosis, and for preventative  
CC and curative treatments of the disease. The PGI gene can be used for  
CC detection of prostate cancer, and the risk of developing it in the  
CC future, and can also be used to determine therapies for the disease.

XX  
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;

Query Match 1.6%; Score 17.8; DB 1; Length 24;  
Best Local Similarity 90.5%; Pred. No. 1.9e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1080 TATTAAAAA...AAAAA 1100  
DB 23 TTTCAAAAA...AAAAA 3

RESULT 156  
AAH75510/c  
ID AAH75510 standard; DNA; 24 BP.

XX  
AC AAH75510;

XX  
DT 18-OCT-2001 (first entry)

XX  
DE Human CCR4 related protein 31 PCR primer 2.

XX  
KW Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;  
KW PCR primer; ss.



```

XX OS Homo sapiens.
XX PN CN1296960-A.
XX PD 30-MAY-2001.
XX PF 22-NOV-1999; 99CN-0124049.
XX PR 22-NOV-1999; 99CN-0124049.
XX PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX PI Mao Y, Xie Y;
XX WPI; 2001-489558/54.
XX DR Polypeptide-human CCR4 related protein 31 and polynucleotide for coding
XX PT polypeptide, useful for treating e.g. cancer and HIV infection, is
XX FT prepared by DNA recombination -
XX PS Example 3; Page 17 (Disclosure); 34pp; Chinese.
XX CC The invention relates to human CCR4 related protein 31, the
XX CC polynucleotide encoding it and the use of the protein in treating
XX CC e.g. cancer and HIV infection. The present sequence is that of a human
XX CC CCR4 PCR primer of the invention.
XX SQ Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1080 TATTAATAAAAAAAAAAAAAA 1100
DB 22 TAATAATAAGAAAAA 2
RESULT 157
ABS54833
ID ABS54833 standard; DNA; 24 BP.
AC ABS54833;
XX 07-JAN-2003 (first entry)
XX Human fkbp 12.87 specific RT-PCR primer #1.
XX Human; ss; fkbp; 12.87; malignant tumour; haemopathy;
XX human immunodeficiency virus; HIV; infection; immunological disease;
XX inflammation; RT-PCR; primer; reverse transcription.
XX OS Homo sapiens.
XX CN1352169-A.
XX 05-JUN-2002.
XX 10-NOV-2000; 2000CN-0127372.
XX 10-NOV-2000; 2000CN-0127372.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-714435/78.
XX New human fkbp protein 12.87 and encoding polynucleotide for treating
XX malignant tumors, hemopathy, human immunodeficiency virus infection,
XX immunological diseases and various inflammations -
XX
PS Example 2; Page 17 (disclosure); 33pp; Chinese.
XX This invention relates to the DNA and protein sequences of a novel human
XX fkbp protein 12.87. The invention also comprises a method for producing
XX the polypeptide by recombinant DNA technology. The polypeptide is
XX useful in treating malignant tumours, haemopathy, human immunodeficiency
XX virus infection, immunological diseases and various inflammations. Also
XX disclosed in the invention is an antagonist to the fkbp protein and
XX a method for its use. The present sequence represents a reverse
XX transcriptase (RT) PCR primer used to isolate the human fkbp 12.87
XX cDNA of the invention.
XX SQ Sequence 24 BP; 5 A; 0 C; 6 G; 13 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 TTCAGGTTTGTATTATGAGT 950
DB 4 TTAAGGTTTATTATGAGT 24
RESULT 158
AAC96082/c
ID AAC96082 standard; DNA; 25 BP.
XX AAC96082;
XX 26-FEB-2001 (first entry)
XX 16s rRNA gene PCR primer #49.
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX WO200065088-A2.
XX 02-NOV-2000.
XX 20-APR-2000; 2000WO-EP03636.
XX 26-APR-1999; 99EP-0303215.
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX Ulfendahl P, Wong K;
XX WPI; 2000-679677/66.
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences
XX of specific length -
XX Claim 14; Page 45; 66pp; English.
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular.
XX SQ Sequence 25 BP; 5 A; 1 C; 3 G; 16 T; 0 other;
Query Match 1.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1077 AACTATTAAAAA 1097
DB 21 ATCTCTTAAAAA 1

RESULT 159
AAT9286
ID AAT9286 standard; DNA; 24 BP.
XX
AC AAT9286;
XX
XX 15-APR-1998 (first entry)
XX
DE POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; probe; hybridisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5672479-A.
XX
PD 30-SEP-1997.
XX
XX 07-JUN-1995; 95US-0486421.
XX
PR 06-JUN-1995; 95US-0470911.
PR 28-AUG-1992; 92US-0938189.
PR 02-FEB-1993; 93US-0014943.
PR 07-JUN-1995; 95US-0486421.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
XX WPI; 1997-488859/45.
XX
XX Assays for PUR protein ligands or modulators - using immobilised PUR
PT protein or fragments, to treat hyper-proliferative diseases, e.g.
PT cancer
XX
PS Examples; Column 33; 64pp; English.
XX
CC The oligonucleotides AAT9279-T99286 were used as competitor
CC oligonucleotides for the binding of PUR protein to DNA. The PUR sequence
CC can be used to identify chemical or biological compounds that bind to
CC PUR or binding fragments of PUR. Inhibitors of PUR activity may be
CC used to treat hyperproliferative diseases such as cancer.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA 1100
DB 1 AAAAAA 24

RESULT 160
AAV31743
ID AAV31743 standard; DNA; 24 BP.
XX
AC AAV31743;
XX
XX 24-SEP-1998 (first entry)
XX
DE Nucleotide sequence of the oligonucleotide POLYA.
XX
KW PUR-alpha gene; inhibition; viral infection; cancer; PUR element;

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KW hyperproliferative disease; ss.
XX
OS Synthetic.
XX
PN US5756684-A.
XX
PD 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-0470911.
XX
PR 06-JUN-1995; 95US-0470911.
PR 28-AUG-1992; 92US-0938189.
PR 02-FEB-1993; 93US-0014943.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
PT PUR protein and its fragments - that inhibit PUR protein binding to
PT PUR element or other proteins
XX
PS Example 7.1.1; Column 33; 63pp; English.
XX
CC This is the nucleotide sequence of an oligonucleotide used as a
CC competitor with the PUR element in the method of the invention,
CC involving the use of the PUR protein and its fragments, which inhibit
CC PUR protein binding to PUR element or other proteins. Inhibitors of
CC PUR activity may be useful for treating viral infections and
CC hyperproliferative diseases such as cancer.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTAAAAA 1100
DB 1 AAAAAA 24

RESULT 161
AAX04086
ID AAX04086 standard; DNA; 24 BP.
XX
AC AAX04086;
XX
XX 12-APR-1999 (first entry)
XX
DE Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5869622-A.
XX
PD 09-FEB-1999.
XX
XX 07-JUN-1995; 95US-0486809.
XX
PR 06-JUN-1995; 95US-0470911.
PR 28-AUG-1992; 92US-0938189.
PR 02-FEB-1993; 93US-0014943.
PR 07-JUN-1995; 95US-0486809.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;

```

```
XX WPI; 1999-152891/13.
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer
XX
XX Example; Column 33; 64pp; English.
XX
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present invention represents an
XX oligonucleotide used in the cloning and sequencing of the PUR protein
XX and its sequence element PUR repeat, in an example from the present
XX invention.
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTATAAAAAAAAAAAAAAAAA 1100
XX ||| ||||| ||||| ||||| |||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24
XX
XX RESULT 162
XX AAA40353/c
XX ID AAA40353 standard; DNA; 24 BP.
XX
XX AC AAA40353;
XX
XX DT 10-NOV-2000 (first entry)
XX DE pBluescriptSK+ phagemid primer SEQ ID NO: 3.
XX KW Primer; cloning; ligation; ss.
XX OS Synthetic.
XX
XX PN WO200036088-A1.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US30277.
XX PR 17-DEC-1998; 98US-0213834.
XX
XX PA (ROMA/) ROMANTCHIKOV Y.
XX PI Romantchikov Y;
XX OS
XX
XX PN WO200036088-A1.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US30277.
XX PR 17-DEC-1998; 98US-0213834.
XX
XX PA (ROMA/) ROMANTCHIKOV Y.
XX PI Romantchikov Y;
XX
XX WPI; 2000-442381/38.
XX
XX Inserting a nucleic acid into a circular vector comprising joining
XX their ends, melting, and reannealing ends at two different
XX concentrations, useful for cloning small amounts of nucleic acids and
XX forming genomic libraries -
XX
XX Example 1; Page 66; 71pp; English.
XX
XX This invention describes a novel method (M1) for inserting a nucleic
XX acid (N1) into a circular vector (V1) comprising joining ends of N1 and
XX V1 under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second
XX concentration. The methods are useful for the cloning small amounts of
XX nucleic acids and forming genomic libraries of complex populations of
XX or cDNA. The methods allow the cloning of minute amounts of nucleic acids
XX efficiently and avoids the size selection problems of prior art systems.
XX Larger nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is
XX avoided using the methods. AAA40351-A40366 represents primers used to
XX illustrate the method of the invention.
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 other;
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XX representative libraries to be made. Vector to vector ligation is
XX avoided using the methods. AAA40351-A40366 represents primers used to
XX illustrate the method of the invention.
XX
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
XX
XX Query Match 1.6%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 2e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1077 AACTATTATAAAAAAAAAAAAAAAAA 1100
XX ||| ||||| ||||| ||||| |||||
XX Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 163
XX AAA40359/c
XX ID AAA40359 standard; RNA; 24 BP.
XX
XX AC AAA40359;
XX
XX DT 10-NOV-2000 (first entry)
XX DE pBluescriptSK+ phagemid primer SEQ ID NO: 9.
XX KW Primer; cloning; ligation; ss.
XX OS Synthetic.
XX
XX PN WO200036088-A1.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US30277.
XX PR 17-DEC-1998; 98US-0213834.
XX
XX PA (ROMA/) ROMANTCHIKOV Y.
XX PI Romantchikov Y;
XX OS
XX
XX WPI; 2000-442381/38.
XX
XX Inserting a nucleic acid into a circular vector comprising joining
XX their ends, melting, and reannealing ends at two different
XX concentrations, useful for cloning small amounts of nucleic acids and
XX forming genomic libraries -
XX
XX Example 3; Page 67; 71pp; English.
XX
XX This invention describes a novel method (M1) for inserting a nucleic
XX acid (N1) into a circular vector (V1) comprising joining ends of N1 and
XX V1 under a first nucleic acid concentration, melting hybridized cohesive
XX circularization ends, and reannealing the ends at a second
XX concentration. The methods are useful for the cloning small amounts of
XX nucleic acids and forming genomic libraries of complex populations of
XX or cDNA. The methods allow the cloning of minute amounts of nucleic acids
XX efficiently and avoids the size selection problems of prior art systems.
XX Larger nucleic acid fragments are just as easily cloned, allowing highly
XX representative libraries to be made. Vector to vector ligation is
XX avoided using the methods. AAA40351-A40366 represents primers used to
XX illustrate the method of the invention.
XX
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 other;
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RESULT 164
ID AAF99304/c
XX AAF99304 standard; DNA; 24 BP.
AC AAF99304;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #420.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
PS Claim 101; Page 46; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 165
ID AAF99756/c
XX AAF99756 standard; DNA; 24 BP.
AC AAF99756;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #873.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
PS Claim 101; Page 46; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1077 AACTATTATTAATAAAAAAAAAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 166
ID AAF99757
XX AAF99757 standard; DNA; 24 BP.
AC AAF99757;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #873.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX

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PA (COLE-) COLEY PHARM GROUP INC.
PI Bratzler RL;
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least
PT one antiangiogenic nucleic acid molecule to the subject
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.
CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC joints, angiofibroma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 169
ABS78477/c
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW macular degeneration; corneal graft rejection; neovascular glaucoma;
KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophiliac joint; angiofibroma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
FN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US48458.
XX
PR 14-DEC-2000; 2000US-255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least
one antiangiogenic nucleic acid molecule to the subject
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the
CC antiangiogenic nucleic acids, and instructions for administering them to
CC a subject having a condition characterised by unwanted angiogenesis.
CC The method is useful for inhibiting angiogenesis associated with solid
CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,
CC macular degeneration, corneal graft rejection, neovascular glaucoma,
CC retrolental fibroplasia, rubeosis, Osler-Weber Syndrome, myocardial
CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac
CC joints, angiofibroma, wound granulation, intestinal adhesions,
CC atherosclerosis, scleroderma and hypertrophic scars. The present
CC sequence is an antiangiogenic nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;
Query Match 1.6%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1077 AACTATTAAAAA 1100
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 170
ABS78478
ID ABS78478 standard; DNA; 24 BP.
XX
AC ABS78478;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #962.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis;
KW psoriasis; diabetic retinopathy; retinopathy of prematurity;
KW macular degeneration; corneal graft rejection; neovascular glaucoma;
KW retrolental fibroplasia; rubeosis; Osler-Weber Syndrome;
KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
KW haemophiliac joint; angiofibroma; wound granulation;
KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
FN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US48458.
XX
PR 14-DEC-2000; 2000US-255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least
one antiangiogenic nucleic acid molecule to the subject
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule.
CC Also included is a kit comprising a first container housing the

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CC the polynucleotide sequence with the first and second probes or the  
CC polynucleotide sequence with the first and third probes. The  
CC oligonucleotide probes have labels non-covalently bound to allow for  
CC their detection upon binding. The method of the invention is useful for  
CC detecting the presence of a single nucleotide polymorphism (SNP) in a  
CC fragment of genomic DNA. The method can be used for the direct detection  
CC of nucleic acid in very small quantities without amplification. In  
CC addition, the method may be carried out with amplification of the target  
CC and reference sequences. This sequence represents an oligonucleotide  
CC probe A24 used to create dotPCR chimiluminescer sensitizer particles in  
CC the method of the invention. Binding the nucleic acid to a suspendable  
CC particle acts as a support and provides a means of segregating the bound  
CC polynucleotide target from the bulk solution  
XX  
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. NO. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1077 AACTATTAAAAA 1100  
Db 1 AAAAAA 24

RESULT 173  
ABK15639/c  
ID ABK15639 standard; DNA; 24 BP.

AC ABK15639;

DT 08-MAY-2002 (first entry)

DE RNA-PCR procedure primer poly(dT)24.

XX RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;  
XX mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;  
XX high throughput screening; D-RNAi; DNA-RNA interference; RdRp;  
XX RNA dependent RNA polymerase; posttranscriptional gene silencing.

OS Synthetic.

XX WO200210374-A2.

XX 07-FEB-2002.

XX 02-AUG-2001; 2001WO-US24412.

XX 02-AUG-2000; 2000US-222479P.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Lin S, Chuong C, Widelitz RB;

XX WPI; 2002-188740/24.

XX Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or  
XX treating or preventing microbe related genes, comprises thermocycling  
XX steps of promoter-linked double-stranded cDNA or RNA synthesis -  
XX  
XX Example 5; Page 26; 53pp; English.

CC The invention relates to generating mRNA-cDNA hybrids, comprising  
CC (a) providing a solution containing a nucleic acid template, one or  
CC more primers complementary to the sense conformation of the nucleic  
CC acid template, and one or more promoter-linked primers complementary to  
CC the antisense conformation of the nucleic acid template, and with an  
CC RNA promoter, (b) treating the nucleic acid template with the one of more  
CC primers to synthesise a first cDNA strand, (c) treating the first cDNA  
CC strand with one or more promoter-linked primers to synthesise a promoter-  
CC linked double-stranded nucleic acid, (d) treating the promoter-linked  
CC double-stranded nucleic acid to synthesise amplified mRNA fragments and  
CC (e) treating the mRNA fragments with one or more primers to synthesise

CC mRNA-cDNA hybrids by reverse transcription of the amplified mRNA  
CC fragments. The method is useful for preparing high amounts of pure and  
CC specific mRNA-cDNA hybrids for transducing biological effects of  
CC interest in vitro as well as in vivo, for inhibiting gene function in  
CC prokaryotes and eukaryotes in vivo and in vitro, for suppressing  
CC cancer-related genes, in treating or preventing microbe related genes,  
CC in studying candidate molecular pathways with systematic knock out of  
CC involved molecules, in high throughput screening of gene functions  
CC based on microarray analysis, and as a tool in studying gene function  
CC in physiological conditions. The mRNA-cDNA hybrids may be used to  
CC screen for special gene functions, for manipulating gene expression in  
CC vitro, and for designing therapy for genetic diseases in vivo. The cDNA  
CC part of a D-RNAi (DNA-RNA interference) can be modified by nucleotide  
CC analogue incorporation to increase the stability and effectiveness of  
CC transcribed probe activities. The RdRp (RNA dependent RNA polymerase)  
CC enzyme may provide higher affinity of the mRNA template of a D-RNAi  
CC compared to ds-RNA due to lower binding interaction between DNA-RNA  
CC duplexes than RNA-RNA duplexes. The cDNA part of a D-RNAi provides  
CC further antisense gene knockout activity in addition to the  
CC posttranscriptional gene silencing (PTGS) mechanisms of the sense-RNA  
CC template, resulting in multiple specific gene interference effects with  
CC one probe. The present sequence is a poly(dT) PCR primer used in  
CC conjunction with oligo(dC)10N primers to reverse transcribe mRNA into  
CC first strand cDNA in the method of the invention.

XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. NO. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1077 AACTATTAAAAA 1100  
Db 24 AAAAAA 1

RESULT 174  
ABL39405/c

ID ABL39405 standard; DNA; 24 BP.

XX ABL39405;

XX 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 841.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1..24

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "phosphorothioate backbone"

XX WO200197843-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US20154.

XX 22-JUN-2000; 2000US-213346P.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Weiner G, Hartmann G;

XX WPI; 2002-154611/20.

XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
XX administering immunostimulatory nucleic acids that induce expression of



PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer -  
PS Disclosure; Page 309; 312pp; English.  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,  
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in  
CC the exemplification of the invention.  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;  
  
Query Match 1.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1077 AACTATTATAAAAAAAAAAAAA 1100  
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 175  
ID ACA58802/c  
XX ACA58802;  
XX  
XX 10-JUN-2003 (first entry)  
DE Gastric ulcer treatment immunostimulatory nucleic acid #148.  
XX Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;  
XX Helicobacter pylori.  
XX Synthetic.  
XX  
XX US2002198165-A1.  
XX  
XX 26-DEC-2002.  
XX  
XX 01-AUG-2001; 2001US-0920313.  
XX  
XX 01-AUG-2000; 2000US-222248P.  
XX  
XX (BRAT/) BRATZLER R L.  
XX (PETE/) PETERSEN D M.  
XX  
XX Bratzler RL, Petersen DM;  
XX  
XX WPI; 2003-370798/35.  
XX  
XX Prevention or treatment of gastric ulcer involves administering nucleic  
XX acid -  
XX  
XX Disclosure; Page 14; 45pp; English.  
XX  
XX The invention relates to a method of prevention or treatment of gastric  
XX ulcer comprising administering a nucleic acid to a subject in need for  
XX treatment of gastric ulcer. A nucleic acid sample comprising  
XX oligonucleotide 206 was administered to a mouse model by an oral route  
XX or a vehicle control. Colonisation of mice by Helicobacter pylori was  
XX assessed at time points from 1 day to 1 month after treatment. The  
XX ability of the nucleic acid to reduce H. pylori colonisation was

CC assessed. The method is useful for preventing or treating a gastric ulcer  
CC on a subject e.g. human or non-human vertebrate animal including dog,  
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,  
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively  
CC treats or prevents gastric ulcers. The present sequence represents an  
CC immunostimulatory nucleic acid for the treatment of gastric ulcers.  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;  
  
Query Match 1.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1077 AACTATTATAAAAAAAAAAAAA 1100  
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 176  
ID ABZ80181/c  
XX ABZ80181 standard; DNA; 24 BP.  
XX  
XX ABZ80181;  
XX  
XX 23-MAY-2003 (first entry)  
DE Immunostimulatory oligonucleotide SEQ ID NO:53.  
XX  
XX Immunostimulation; immune response; natural killer cell; interferon;  
XX type 1 interferon; IFN; cancer; infectious disease; allergic disorder;  
XX immune related disorder; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..24  
XX /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "optionally phosphorothioate backbone"  
XX  
XX WO2003015711-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 19-AUG-2002; 2002WO-US26468.  
XX  
XX 17-AUG-2001; 2001US-313273P.  
XX 03-JUL-2002; 2002US-393952P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
XX (COLE-) COLEY PHARM GMBH.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Krieg AM, Vollmer J, Uihman E;  
XX  
XX WPI; 2003-268241/26.  
XX  
XX New immunostimulatory nucleic acid, useful for preparing a composition  
XX for treating an allergic condition -  
XX  
XX Example 1; Page 44; 115pp; English.  
XX  
XX The present invention describes immunostimulatory nucleic acids of 14-100  
XX nucleotides in length comprising the formula 5' X1DCGHX2 3' (1), where X1  
XX or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other  
XX than C; C = cytosine; G = guanine; H = nucleotide other than G. The  
XX immunostimulatory nucleic acid further comprises a sequence consisting of  
XX P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell  
XX neutralising sequence, where N begins with a CGG trinucleotide and is at  
XX least 10 nucleotides long and P is GC-rich palindromic containing sequence  
XX at least 10 nucleotides long. Also described: (1) a pharmaceutical  
XX composition comprising the immunostimulatory nucleic acid and a carrier;  
XX and (2) treating an allergic condition. (1) has antiallergic activity and

CC can be used in gene therapy. (I) can be used for preparing a composition  
 CC for treating a variety of immune related disorders such as cancer,  
 CC infectious diseases and allergic disorders. (I) also stimulates the  
 CC activation of natural killer cells and the production of type 1  
 CC interferon (IFN). The present sequence represents an immunostimulatory  
 CC oligonucleotide, which is used in an example from the present invention.  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1077 AACTATTAAAAA 1100  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 177  
 AAQ95960/c  
 ID AAQ95960 standard; DNA; 25 BP.  
 XX  
 AC AAQ95960;  
 XX  
 DT 06-FEB-1996 (first entry)  
 XX  
 DE Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.  
 XX  
 KW Immobilisation; solid support; salt; cationic detergent; capture probe;  
 KW hybridisation; primer; template-dependent extension; target organism;  
 KW sequencing; genetic polymorphism; ss.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 misc\_feature 1  
 FT /\*tag= a  
 FT /note= "biotinylated"  
 FT  
 XX  
 PN WO9515970-A1.  
 XX  
 PD 15-JUN-1995.

PF 06-DEC-1994; 94WO-US14096.  
 XX  
 PR 16-NOV-1994; 94US-0341148.  
 PR 06-DEC-1993; 93US-0162397.  
 XX  
 PA (MOLE-) MOLECULAR TOOL INC.  
 XX  
 PI Knapp MR, Nikiforov T;  
 XX  
 DR WPI; 1995-224282/29.  
 XX  
 PT Immobilising synthetic nucleic acid on solid support - by incubation  
 PT in presence of salt or cationic detergent, for use in hybridisation  
 PT assays, sequencing and analysis of polymorphism  
 XX  
 PS Example 1; Page 18; 61pp; English.

CC Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a  
 CC novel method of immobilising oligonucleotides to a solid support by  
 CC incubating in the presence of a salt or cationic detergent e.g. NaCl  
 CC (50-250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3  
 CC carbodiimide hydrochloride (EDC). The oligonucleotides can be capture  
 CC probes for detection of specific nucleic acids by hybridisation or can  
 CC be primers for template-dependent extension from the immobilised primers  
 CC on nucleic acid from a target organism. The method can be used in  
 CC hybridisation assays, sequencing and analysis of genetic polymorphism.  
 XX  
 SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1077 AACTATTAAAAA 1100  
 DB 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 178  
 AAX84260/c  
 ID AAX84260 standard; DNA; 25 BP.  
 XX  
 AC AAX84260;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE PCR primer for human Nck associated protein 1 coding sequence.  
 XX  
 KW Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;  
 KW therapy; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9931239-A1.  
 XX  
 PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-JP05646.  
 XX  
 PR 15-DEC-1997; 97JP-0363183.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA (SAKA/) SAKAKI Y.  
 XX  
 PI Sakaki Y;  
 XX  
 DR WPI; 1999-395181/33.  
 XX  
 PT Protein inhibiting apoptosis, useful in the diagnosis and treatment  
 PT of Alzheimer's disease  
 XX  
 PS Disclosure; Page 77; 90pp; Japanese.

CC This sequence represents a PCR primer used to isolate DNA encoding the  
 CC human Nck associated protein 1 (Napi) of the invention. Napi inhibits  
 CC apoptosis. The protein can be used in the investigation, diagnosis and  
 CC treatment (e.g. by gene therapy) of Alzheimer's disease.  
 XX  
 SQ Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1077 AACTATTAAAAA 1100  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 179  
 AAC96201/c  
 ID AAC96201 standard; DNA; 25 BP.  
 XX  
 AC AAC96201;  
 XX  
 DT 26-FEB-2001 (first entry)  
 XX  
 DE 16s rRNA gene PCR primer #168.  
 XX  
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
 KW human leukocyte antigen; PCR primer; ss.

```

XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP03636.
XX PR 26-APR-1999; 99EP-0303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX PS WPI; 2000-679677/66.
XX PT Identifying extendible primers for use in identification, or
XX PT classification of a nucleic acid of an organism, allele or gene such as
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences
XX PT of specific length -
XX PS Claim 14; Page 47; 66pp; English.
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX CC particular.
XX SQ Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1075 GCAACTATTATAAAAAAAAAAAAA 1098
DB 24 GCAAGACTGAAAAAAAAAAAAAA 1

RESULT 180
AAC96858/c
ID AAC96858 standard; DNA; 25 BP.
XX AC AAC96858;
XX DT 26-FEB-2001 (first entry)
XX DE HLA HLA-C gene PCR primer #63.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP03636.
XX PR 26-APR-1999; 99EP-0303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX PS WPI; 2000-679677/66.
XX PT Identifying extendible primers for use in identification, or
XX PT classification of a nucleic acid of an organism, allele or gene such as
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences
XX PT of specific length -
XX PS Claim 14; Page 47; 66pp; English.
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX CC particular.
XX SQ Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 other;

Query Match 1.6%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1073 AAGCAACTATTATAAAAAAAAAAAAA 1096
DB 24 ACGGCGCTACTAAAAAAAAAAAAAA 1

RESULT 181
AAA39306/c
ID AAA39306 standard; RNA; 25 BP.
XX AC AAA39306;
XX DT 11-SEP-2000 (first entry)
XX DE Rapid capture probe designated Neu-probe SEQ ID NO:1.
XX KW Rapid detection; probe; target nucleic acid; enzymatic amplification;
XX KW isolation; detection; ss.
XX OS Synthetic.
XX PN US6060246-A.
XX PD 09-MAY-2000.
XX PF 13-NOV-1997; 97US-0969813.
XX PR 15-NOV-1996; 96US-0030963.
XX PA (AVIB-) AVI BIOPHARMA INC.
XX PI Wages JM, Summerton JE, Weller DD;
XX DR WPI; 2000-364413/31.
XX PT Reagent for rapidly detecting or isolating target nucleic acid
XX PT sequences in polynucleotide-containing sample, comprises capture
XX PT component and target-specific probe linked to solid substrate -
XX PS Example 3; Column 17; 24pp; English.
XX CC The present invention describes a rapid pairing reagent (I) for the
XX CC isolation or detection of a polynucleotide (PN) analyte molecule having
XX CC a selected target base sequence, in a sample containing the analyte
XX CC molecule and non-target polynucleotide, comprising a capture component
XX CC (A) and a target-specific probe (B) linked to a solid substrate. The
XX CC isolated sequences are useful for enzymatic amplification. (I) is
XX CC capable of rapidly binding nucleic acids in the sample and placing them
XX CC in close proximity to target probes on the reagent, thus enabling
XX CC binding under low stringency. Combination of rapid capture and
XX CC concentration of polynucleotides with selective targeting of analyte
XX CC molecules, greatly enhances the isolation process. Non-ionic morpholino
XX CC oligomers used as probes are not extended by polymerases and therefore

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```
Query Match      1.6%;      Score 17.6;  DB 1;      Length 25;
Best Local Similarity 83.3%;  Pred. No. 2.1e+02;
Matches 20: Conservative 0; Mismatches 4; Indels
```

AA  
AC  
AAQ75556;

DT 04-AUG-1995 (first entry)  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 KW Synthetic.  
 XX  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 DT 1082 TTAAAAA...AAAAA 1100  
 XX  
 XX 19 TGA...AAAAA 1  
 XX  
 RESULT 185  
 AAQ75548/c  
 ID AAQ75548 standard; DNA; 19 BP.  
 XX  
 AC AAQ75548;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTAAAAA...AAAAA 1100  
 DB 19 TC...AAAAA 1  
 DB  
 RESULT 186  
 AAQ75596/c  
 ID AAQ75596 standard; DNA; 20 BP.  
 XX  
 AC AAQ75596;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 DE  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-0112515.  
 PF  
 XX 16-APR-1993; 93JP-0112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 PT  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 CC  
 XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 other;  
 SQ  
 Query Match 1.6%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100  
 ID AAQ75598 standard; DNA; 20 BP.  
 DB 20 TTGAAAAA 2

RESULT 187  
 AAQ75598/c  
 ID AAQ75598 standard; DNA; 20 BP.  
 AC AAQ75598;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX  
 SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100  
 ID AAQ75598 standard; DNA; 20 BP.  
 DB 20 TTGAAAAA 1

RESULT 188  
 AAQ75598/c  
 ID AAQ75598 standard; DNA; 20 BP.  
 AC AAQ75598;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 XX  
 SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAAAAA 1100  
 ID AAQ75598 standard; DNA; 20 BP.  
 DB 20 TTGAAAAA 1

RESULT 189  
 AAQ75566/c  
 ID AAQ75566 standard; DNA; 20 BP.  
 AC AAQ75566;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an

PD 25-JAN-2001.

PF 19-JUL-2000; 2000WO-CA00853.  
 XX  
 PR 19-JUL-1999; 99US-0144495.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (MIYA/) MIYAKE H.  
 XX  
 PI Gleave M;  
 XX  
 DR WPI; 2001-168448/17.  
 XX  
 CC This sequence represents an antisense oligonucleotide targeted against  
 CC human insulin-like growth factor binding protein-5 (IGFBP-5). The  
 CC invention relates to a composition for treatment of hormone-regulated  
 CC cancer, comprising an antisense oligonucleotide (such as this sequence)  
 CC which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.  
 CC The compositions is useful for delaying progression of hormone-regulated  
 CC tumour cells such as prostatic cancer cells or breast cancer cells, to an  
 CC androgen-independent state, by treating hormone sensitive tumour cells  
 CC with the antisense sequence which inhibits expression of IGFBP-5 by the  
 CC tumour cells. The composition can also be used for treating a  
 CC hormone-responsive cancer in an individual, and administering the  
 CC composition to the individual after initiation of hormone-withdrawal to  
 CC induce apoptotic cell death of hormone-responsive tumour cells, and  
 CC therefore delaying the progression of hormone-responsive cancer cells to  
 CC a hormone-independent state in the individual. It can also be used for  
 CC inhibiting or delaying metastatic bone progression of an IGF-1  
 CC sensitive tumour in a mammal, by administering the composition to  
 CC inhibit the expression of IGFBP-5 by the hormone-responsive cancer  
 CC cells, and therefore inhibiting or delaying metastatic bone  
 CC progression of the tumour.  
 XX  
 SQ Sequence 20 BP; 3 A; 1 C; 0 G; 16 T; 0 other;  
 Query Match 1.6%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTAAAAAATAAAAAAAAAA 1100  
 Db 19 TCGAAAAAATAAAAAAAAAA 1  
 RESULT 193  
 AAQ75751/C  
 ID AAQ75751 standard; DNA; 21 BP.  
 XX  
 AC AAQ75751;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 JF06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
 Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTAAAAAATAAAAAAAAAA 1100  
 Db 19 TCGAAAAAATAAAAAAAAAA 1  
 RESULT 194  
 AAQ75753/C  
 ID AAQ75753 standard; DNA; 21 BP.  
 XX  
 AC AAQ75753;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 JF06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 XX  
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 PS Disclosure; Page 8; 11pp; Japanese.  
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 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
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 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
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 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
 Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTAAAAAATAAAAAAAAAA 1100  
 Db 19 TCGAAAAAATAAAAAAAAAA 1  
 RESULT 194  
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 PD 01-NOV-1994.  
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 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
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 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 DR WPI; 1995-018287/03.  
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 PS Disclosure; Page 8; 11pp; Japanese.  
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 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
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 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;



Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 195  
 AAQ75754/C  
 ID AAQ75754 standard; DNA; 21 BP.  
 AC AAQ75754;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 9; 11pp; Japanese.  
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 CC A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 196  
 AAQ75772/C  
 ID AAQ75772 standard; DNA; 21 BP.  
 AC AAQ75772;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis of cDNA and gene expression - by amplification of mRNA  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-0112515.  
 XX  
 PR 16-APR-1993; 93JP-0112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
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 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
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 CC (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
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 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 197  
 AAQ75755/C  
 ID AAQ75755 standard; DNA; 21 BP.  
 AC AAQ75755;  
 XX  
 XX 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
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 PF 16-APR-1993; 93JP-0112515.  
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 PR 16-APR-1993; 93JP-0112515.  
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 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 PT Analysis of cDNA and gene expression - by amplification of mRNA  
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 XX  
 PS Disclosure; Page 9; 11pp; Japanese.  
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 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
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 XX  
 SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
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PS Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
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CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAA...AAAAAAAAA 1100
DB 20 TTGAAAAA...AAAAAAAAA 2
RESULT 198
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
AC AAQ75758;
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
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PR
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XX Disclosure; Page 8; 11pp; Japanese.
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CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAAAAA...AAAAAAAAA 1100
DB 20 TTGAAAAA...AAAAAAAAA 2
RESULT 200
AAQ75765/c
ID AAQ75765 standard; DNA; 21 BP.
AC AAQ75765;
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
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DB 20 TTGAAAAA...AAAAAAAAA 2
RESULT 199
AAQ75763/c
ID AAQ75763 standard; DNA; 21 BP.
XX
XX AAQ75763;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-0112515.
PF
XX 16-APR-1993; 93JP-0112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
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XX WPI; 1995-018287/03.
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CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the
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CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;
SQ
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 19 TGA...AAAAAAAAA 1
RESULT 200
AAQ75765/c
ID AAQ75765 standard; DNA; 21 BP.
XX
XX AAQ75765;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
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PD 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
 XX 16-APR-1993; 93JP-0112515.  
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
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 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
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 XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 other;  
 SQ Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TGAATAAAAAAAAAAAAAA 1  
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 ID AAQ75766 standard; DNA; 21 BP.  
 AC AAQ75766;  
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 XX Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
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 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 other;  
 SQ Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TGAATAAAAAAAAAAAAAA 1  
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 ID AAQ75630 standard; DNA; 21 BP.  
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 DT 04-AUG-1995 (first entry)  
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 XX Analysis; Gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.  
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 XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-0112515.  
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 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
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 XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 other;  
 SQ Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. NO. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 20 TTCATAAAAAAAAAAAAAA 2  
 RESULT 203  
 AAQ75635/c  
 ID AAQ75635 standard; DNA; 21 BP.  
 XX

AC AAQ75635;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
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PD 01-NOV-1994.  
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PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
XX  
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Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1082 TTAAAAA AAAAAAAAAA 1100  
DB 19 TCAAAAA AAAAAAAAAA 1  
RESULT 204  
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ID AAQ75637 standard; DNA; 21 BP.  
AC AAQ75637;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;  
XX  
Query Match 1.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1082 TTAAAAA AAAAAAAAAA 1100  
DB 19 TCAAAAA AAAAAAAAAA 1  
RESULT 204  
AAQ75637/c  
ID AAQ75637 standard; DNA; 21 BP.  
AC AAQ75637;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;

XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 other;  
XX  
Query Match 1.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1082 TTAAAAA AAAAAAAAAA 1100  
DB 19 TCAAAAA AAAAAAAAAA 1  
RESULT 205  
AAQ75638/c  
ID AAQ75638 standard; DNA; 21 BP.  
AC AAQ75638;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-0112515.  
XX  
PR 16-APR-1993; 93JP-0112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA  
PT followed by digestion with restriction enzymes  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 other;

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 206  
 AAQ75623/C  
 ID AAQ75623 standard; DNA; 21 BP.  
 AC AAQ75623;  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 WPI; 1995-018287/03.  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX Disclosure; Page 6; 11pp; Japanese.  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESQ files AAQ75623-075798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 CC Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;  
 SQ WPI; 1995-018287/03.  
 DR Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 PT Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX Disclosure; Page 6; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESQ files AAQ75623-075798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 CC Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 other;  
 SQ

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 207  
 AAQ75625/C  
 ID AAQ75625 standard; DNA; 21 BP.  
 AC AAQ75625;  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 WPI; 1995-018287/03.  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX Disclosure; Page 6; 11pp; Japanese.

aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 WPI; 1995-018287/03.  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX Disclosure; Page 6; 11pp; Japanese.  
 CC A method for the analysis of cDNA comprises (a) preparing an  
 aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 and a plural type of labelled reverse transcription primers  
 (GENESQ files AAQ75623-075798) and using the aggregate of mRNAs as the  
 template for each reverse transcription primer; (b) digesting each of  
 the prepared aggregates of the double-stranded cDNAs with restriction  
 enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 separate lanes. The method can be used to analyse gene expression  
 rapidly and easily.  
 CC Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 other;  
 SQ

Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1100  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 208  
 AAQ75626/C  
 ID AAQ75626 standard; DNA; 21 BP.  
 AC AAQ75626;  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 XX 01-NOV-1994.  
 PF 16-APR-1993; 93JP-0112515.  
 PR 16-APR-1993; 93JP-0112515.  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 WPI; 1995-018287/03.  
 PT Analysis of cDNA and gene expression - by amplification of mRNA  
 followed by digestion with restriction enzymes  
 XX Disclosure; Page 6; 11pp; Japanese.

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XX A method for the analysis of cDNA comprises (a) preparing an
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs
CC and a plural type of labelled reverse transcription primers
CC (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
CC template for each reverse transcription primer; (b) digesting each of
CC the prepared aggregates of the double-stranded cDNAs with restriction
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
CC separate lanes. The method can be used to analyse gene expression
CC rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 19 TCAAAAAAATAAAAAA 1
RESULT 209
AAQ75627/c
ID AAQ75627 standard; DNA; 21 BP.
AC AAQ75627;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 20 TTAACAAAAAATAAAAAA 2
RESULT 209
AAQ75627/c
ID AAQ75627 standard; DNA; 21 BP.
AC AAQ75627;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 20 TTAACAAAAAATAAAAAA 2

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RESULT 210
AAQ75644/c
ID AAQ75644 standard; DNA; 21 BP.
XX
XX AAQ75644;
AC AAQ75644;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX 16-APR-1993; 93JP-0112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA
XX followed by digestion with restriction enzymes
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an
XX aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX and a plural type of labelled reverse transcription primers
XX (GENESEQ files AAQ7547-Q75798) and using the aggregate of mRNAs as the
XX template for each reverse transcription primer; (b) digesting each of
XX the prepared aggregates of the double-stranded cDNAs with restriction
XX enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX separate lanes. The method can be used to analyse gene expression
XX rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
XX
Query Match 1.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1082 TTAACAAAAAATAAAAAA 1100
Db 21 TTACAAAAAATAAAAAA 3
RESULT 211
AAQ26584
ID AAQ26584 standard; DNA; 21 BP.
XX
XX AAQ26584;
AC AAQ26584;
XX
XX 30-NOV-1999 (first entry)
XX
XX Human polymorphic region 773.
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX Homo sapiens.

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XX WO9841648-A2.  
 XX 24-SEP-1998.  
 XX 19-MAR-1998; 98WO-US05419.  
 XX 20-MAR-1997; 97US-0041057.  
 XX (VARI-) VARIAGENICS INC.  
 XX Housman D, Ledley FD, Stanton VP;  
 XX WPI; 1998-521232/44.  
 XX Identifying target genes for allele-specific drugs - used for  
 XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic  
 XX plaque, dysplastic lesions, endometriosis or graft versus host disease  
 XX Disclosure; Figure 7; 605pp; English.  
 XX This invention describes a novel method for identifying an inhibitor  
 XX potentially useful for treatment of cancer, where the inhibitor is  
 XX active on a gene vital for cell growth or viability, and where the gene  
 XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 XX used for preventing the development of cancer in a patient having a  
 XX precancerous condition, by administering to the patient a first allele  
 XX specific inhibitor (ASI) targeted to an allele of a first essential gene  
 XX present in cells of the precancerous condition, where the normal somatic  
 XX cells of the patient are heterozygous for the first gene, the inhibitor  
 XX is active on at least one but less than all allelic forms of the gene  
 XX present in a population and targets only one allelic form present in the  
 XX normal somatic cells, and the first gene. The products and methods can  
 XX be used in the diagnosis, prevention and treatment of LOH disorders,  
 XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or  
 XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney  
 XX disease, and graft versus host disease. The method can also be used to  
 XX remove malignant cells from bone marrow transplants. AA225812-226825  
 XX represent human polymorphic sites described in the method of the  
 XX invention.  
 XX Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 other;  
 Query Match 1.6%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1080 TATTAAAAA 1098  
 Db 3 TTTAAAAA 21  
 RESULT 212  
 AAI64873/c  
 ID AAI64873 standard; DNA; 24 BP.  
 XX AAI64873;  
 XX 04-DEC-2001 (first entry)  
 XX Human serine/threonine protein kinase 48 cDNA PCR primer #2.  
 XX Human; serine/threonine protein kinase 48; cancer; HIV infection;  
 XX gene therapy; PCR primer; ss.  
 XX Homo sapiens.  
 XX CN1300831-A.  
 XX 27-JUN-2001.  
 XX 22-DEC-1999; 99CN-0125686.

PR 22-DEC-1999; 99CN-0125686.  
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX Mao Y, Xie Y;  
 XX WPI; 2001-530471/59.  
 XX New human serine/threonine protein kinase 48 and its encoding  
 XX polynucleotide, useful for treating cancer and human immunodeficiency  
 XX virus infection -  
 XX Example 3; Page 17(Disclosure); 33pp; Chinese.  
 XX The present invention provides the protein and coding sequences of human  
 XX serine/threonine protein kinase 48. The sequences can be used in the  
 XX treatment of cancer and HIV infection. The present sequence is a PCR  
 XX primer for the coding sequence of the invention.  
 XX Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 other;  
 Query Match 1.6%; Score 17.4; DB 1; Length 24;  
 Best Local Similarity 94.7%; Pred. No. 2.2e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1082 TTTAAAAA 1100  
 Db 19 TTACAAAAA 1  
 RESULT 213  
 ABZ23536  
 ID ABZ23536 standard; DNA; 24 BP.  
 XX ABZ23536;  
 XX 07-APR-2003 (first entry)  
 XX fragment of a plasmid used to detect somatic instability.  
 XX Replication error; drug development; somatic instability; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX misc\_feature 4  
 XX /\*tag= a  
 XX /note= "this base represents an unspecified number of  
 XX bases"  
 XX misc\_feature 21  
 XX /\*tag= b  
 XX /note= "this base represents an unspecified number of  
 XX bases"  
 XX WO200295071-A2.  
 XX 28-NOV-2002.  
 XX 22-MAY-2002; 2002WO-NL00322.  
 XX 22-MAY-2001; 2001EP-0201936.  
 XX (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.  
 XX (TIJS/) TIJSTERMAN M.  
 XX Plasterk RHA;  
 XX WPI; 2003-129440/12.  
 XX Determining whether a product of a gene is involved in preventing a  
 XX replication error in a cell comprises providing a specific inhibitor  
 XX for the product and determining the level of expression of a marker  
 XX gene -

XX Example 1; Fig 3; 47pp; English.

CC The specification describes a method for determining whether a product  
 CC of a gene is involved in preventing a replication error in a cell. The  
 CC method comprises providing the cell with a specific inhibitor for the  
 CC product and determining the level of functional expression of a marker  
 CC gene in the cell, where the level of expression of the marker gene is  
 CC dependent on the occurrence of the replication error. The method is  
 CC used for determining whether a product of a gene is involved in  
 CC preventing a replication error in a cell. The identified genes are  
 CC useful for developing diagnostic tools, or as targets for drug  
 CC development to manipulate cells on the basis of the presence or absence  
 CC of function of the gene. ABZ23535-36 represents fragments of plasmids  
 CC used to detect somatic instability, in the course of the invention.

XX SQ Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 2 other;

Query Match 1.6%; Score 17.4; DB 1; Length 24;  
 Best Local Similarity 90.0%; Pred. No. 2.2e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1081 ATTAAAAA 1100  
 :|||||  
 Db 1 ATGNA 20

RESULT 214  
 AAT94431  
 ID AAT94431 standard; mRNA; 19 BP.  
 AC AAT94431;  
 XX  
 DT 02-MAR-1998 (first entry)  
 XX  
 DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.  
 XX  
 KW Primer: detection; characterisation; mRNA; restriction display PCR;  
 KW synthesis; cDNA; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9729211-A1.  
 XX  
 PD 14-AUG-1997.  
 XX  
 PF 07-FEB-1997; 97WO-US02009.  
 XX  
 PR 09-FEB-1996; 96US-0011379.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Boulamwini J, Weinstein JN;  
 XX  
 WI; 1997-415362/38.  
 XX  
 PT Detection and characterisation of mRNA by restriction display PCR -  
 PT comprising synthesis of cDNA, digestion with a restriction  
 FT endonuclease, ligation to an adaptor DNA and PCR amplification  
 XX  
 PS Disclosure; Page 24; 40pp; English.

CC A method has been improved for detecting and characterising mRNA  
 CC molecules which includes synthesising a double stranded (ds) cDNA from  
 CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to  
 CC produce cDNA fragments in which at least one end of the cDNA fragments  
 CC has a sequence capable of hybridising to an adaptor DNA sequence. The  
 CC improvement comprises: (a) hybridising adaptor DNA sequences to at least  
 CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences  
 CC to the cDNA fragments; (c) amplifying the cDNA fragments having ligated  
 CC adaptor DNA sequences by a PCR using primers that hybridise to the ends  
 CC of the cDNA fragments, where the primers have at least one nucleotide

CC at the 3' end that specifically hybridises to a subset of cDNA  
 CC molecules; and (d) detecting the presence of the resulting amplified  
 CC cDNA fragments. The present sequence represent a template poly-A tail  
 CC used in the present specification. The method designate restriction  
 CC display PCR can be used for characterising cells based on their mRNA  
 CC content, for representing expressed genes, and for discovery of  
 CC therapeutics that alter cellular gene expression. The method is also  
 CC useful for characterising cells of a variety of types and under a  
 CC variety of physiological conditions. The method is also useful for  
 CC identifying cells or tissue from particular individuals or species  
 CC based on the fingerprint obtained from the mRNA content of isolated  
 CC cells or tissue and comparing it to cells or tissue from a known source.

XX SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 U; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA 1100  
 :|||||  
 Db 2 BAAAAA 19

RESULT 215  
 AAX18390/c  
 ID AAX18390 standard; DNA; 19 BP.  
 XX  
 AC AAX18390;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE RT-PCR primer of the invention SEQ ID 31.  
 XX  
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JPI1032765-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 18-JUL-1997; 97JP-0208312.  
 XX  
 PR 18-JUL-1997; 97JP-0208312.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 WI; 1999-183822/16.  
 XX  
 PT Peptides having at least two new nucleotides - useful as primers in  
 FT RT-PCR  
 XX  
 PS Example 1; Page 12; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula:  
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where  
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;  
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition  
 CC of alpha; beta, delta = V or N; V = adenine, guanine or cytosine;  
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;  
 CC k = natural number of 3 or over indicating the repetition of gamma, in  
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,  
 CC guanine and/or cytosine. The new nucleotides are useful as primers for  
 CC RT-PCR and determination of base sequences. The new sequences allow for  
 CC reproductive and highly efficient analysis of gene sequences.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 1083 TAAAAA1100  
 :|||||  
 Db 18 BAAAAA1

RESULT 216  
 AAX06572/c  
 ID AAX06572 standard; DNA; 19 BP.

XX AC AAX06572;

DT 06-APR-1999 (first entry)

DE (-)-limonene-6-hydroxylase primer 3.B.

KW (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;  
 KW spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;  
 KW trans-isopiperitenol; pathogen defense mechanism; attractant;  
 KW environmental signal; monoterpene hydroxylase; PCR primer; ss.

XX Synthetic.

OS Mentha spicata.

XX WO9859042-A1.

XX 30-DEC-1998.

XX 15-JUN-1998; 98WO-US12581.

XX 24-JUN-1997; 97US-0881784.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

PI Croteau RB, Karp F, Lupien SL;

XX WPI; 1999-105618/09.

XX New isolated limonene hydroxylase nucleic acids - which encode  
 PT limonene-6-hydroxylase and limonene-3-hydroxylase, which can be used  
 PT to produce trans-carveol and trans-isopiperitenol

XX Example 4; Page 27; 80pp; English.

CC The invention relates to nucleotide sequences encoding spearmint  
 CC (-)-limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3-  
 CC hydroxylase (L3H). Host cells containing a vector comprising the  
 CC nucleotide sequences can be used for the recombinant production of  
 CC limonene hydroxylases or of primary enzyme products. The primary enzyme  
 CC products are trans-carveol in the case of (-)-L6H or  
 CC trans-isopiperitenol in the case of (-)-L3H, which are of subsequent use,  
 CC to obtain enhanced expression of limonene hydroxylase in plants to attain  
 CC enhanced trans-carveol or trans-isopiperitenol production as a predator  
 CC or pathogen defense mechanism, attractant or environmental signal. The  
 CC limonene hydroxylase cDNAs also provide a useful tool for isolating  
 CC other monoterpene hydroxylase genes and for examining the developmental  
 CC regulation of monoterpene biosynthesis. Sequences AAX06564-73 represent  
 CC primers for the PCR amplification of (-)-limonene-6-hydroxylase cDNA.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA1100  
 :|||||  
 Db 19 DAAAAA2

RESULT 217

AAX299489/c  
 ID AAX299489 standard; DNA; 19 BP.

XX AC AAZ99489;

DT 03-JUL-2000 (first entry)

DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.

XX Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;  
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;  
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;  
 KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.

XX Cucurbita maxima.

XX WO200009722-A2.

XX 24-FEB-2000.

XX 10-AUG-1999; 99WO-US18066.

XX 10-AUG-1998; 98US-0096111.

XX 07-JUN-1999; 99US-0137977.

XX (MONS) MONSANTO CO.

PI Brown SM, Eich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;  
 PI Pillar KJ, Rao S, Ream JE;

XX WPI; 2000-224351/19.

XX Obtaining transgenic plant useful for controlling seed germination and  
 PT seedling growth comprises transgene comprising a sequence expressing  
 PT altered levels of an essential hormone

XX Example 17; Page 262; 267pp; English.

XX The present primer was used to reverse transcribe cDNA encoding a C-20  
 CC oxidase. The amplification fragment is used in the method of the invention.  
 CC The specification describes methods for the inhibition and control of  
 CC gibberellic acid levels. Gibberellic acid levels may be inhibited or  
 CC controlled by use of a chimeric expression construct expressing a RNA or  
 CC protein which suppresses the gibberellin biosynthetic pathway sequence,  
 CC diverts substrate from the pathway, or degrades pathway substrates or  
 CC products. The methods uses copalyl diphosphate synthase,  
 CC 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a  
 CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is  
 CC used to control seed germination and seedling growth especially to  
 CC regulate gene products of gibberellin biosynthetic pathway and  
 CC restoration of normal seed germination, in transgenic plants. The  
 CC plants produced are gibberellin deficient, and have shortened hypocotyl  
 CC and/or epicotyl phenotypes compared to normal plants.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA1100  
 :|||||  
 Db 19 BAAAAA2

RESULT 218

AAD15201/c  
 ID AAD15201 standard; DNA; 19 BP.

XX AC AAD15201;

XX 01-NOV-2001 (first entry)

XX 3' sequencing primer #1 to identify and characterise polynucleotides.

KW Fatty lesion development; atherosclerosis; Alzheimer's disease;  
 KW nervous system disorder; Parkinson's disease; immune system disorder;  
 KW ischaemia; lymphopenia; leukocyte adhesion deficiency syndrome;  
 KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW coagulation disorder; blood platelet disorder; autoimmune disorder;  
 KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;  
 KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;  
 KW cardiovascular; antiviral; primer; ss.  
 XX Unidentified.  
 OS  
 XX WO200154651-A2.  
 PN  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US02439.  
 XX  
 XX 25-JAN-2000; 2000US-0177963.  
 XX  
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 PA  
 XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;  
 XX WPI; 2001-514526/56.  
 DR  
 XX New polynucleotides regulated by fatty lesion development and their  
 PT encoded polypeptides, useful for preventing, treating or ameliorating  
 PT atherosclerosis, as well as for immune or hyperproliferative disorders  
 PT -  
 PS  
 XX Example 1; Page 79; 189pp; English.  
 XX  
 CC The present invention relates to an isolated nucleic acid regulated by  
 CC fatty lesion development, which comprises any of 55 polynucleotide  
 CC sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or  
 CC antibody is useful for preventing, treating, modulating or ameliorating  
 CC a medical condition, particularly atherosclerosis. The invention is used  
 CC as a marker or detector of nervous system disorder or disease (e.g.  
 CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The  
 CC invention may also be useful for treating deficiencies or disorders of  
 CC the immune system (e.g. lymphopenia, leukocyte adhesion deficiency  
 CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders  
 CC (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),  
 CC coagulation disorders, blood platelet disorders and autoimmune disorders  
 CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).  
 CC The polynucleotide sequence is also used in gene therapy. The present  
 CC sequence is a 3' sequencing primer used in the identification and  
 CC characterisation of polynucleotides up-regulated by fatty lesion  
 CC development.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;  
 Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 Db :|||||  
 19 BAAAAAATAAAAAAAAAA 2  
 RESULT 219  
 AAS06525/c  
 ID AAS06525 standard; DNA; 19 BP.  
 XX  
 AC AAS06525;  
 XX  
 XX 07-SEP-2001 (first entry)  
 XX  
 DE Mouse microglia and macrophage regulatory gene primer #60.  
 KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag;  
 KW DST; PCR-based total gene expression analysis; TOGA; infectious disorder;

KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;  
 KW hyperproliferative disorder; autoimmune; inflammatory disorder;  
 KW primer; ss.  
 XX  
 OS Mus musculus.  
 XX WO200134770-A2.  
 PN  
 XX 17-MAY-2001.  
 PD  
 XX  
 XX 06-NOV-2000; 2000WO-US30585.  
 XX  
 XX 12-NOV-1999; 99WO-US26824.  
 PR 03-MAR-2000; 2000US-0186770.  
 PR 19-JUN-2000; 2000US-0212465.  
 XX  
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 PA  
 XX Carson MJ, Sutcliffe JG, Almazan MT, Tobal GM;  
 PI WPI; 2001-308782/32.  
 DR  
 XX New regulated genes of microglia and macrophages, useful for  
 PT diagnosing, preventing or treating neuroinflammatory pathology and  
 PT neurodegenerative disease -  
 PT  
 XX Example 1; Page 88; 244pp; English.  
 PS  
 XX The present sequence represents a primer used to isolate novel  
 CC mouse microglia and macrophage regulatory gene DST (digital sequence  
 CC tag) sequences. AAS06401-AAS06590 represent these novel sequences and  
 CC the primer sequences used to isolate them. The PCR-based total gene  
 CC expression analysis (TOGA) system is used to examine the expression  
 CC pattern of molecules corresponding to genes that are regulated in  
 CC unstimulated microglia, activated microglia, unstimulated macrophage and  
 CC activated macrophage. The polynucleotides of the invention, the  
 CC polypeptides encoded by them and antibodies that bind to these  
 CC polypeptides are useful for the diagnosis, prevention,  
 CC treatment or amelioration of a medical condition, preferably a  
 CC neuroinflammatory pathology or a neurodegenerative disease such as  
 CC Alzheimer's disease, senile dementia, Parkinson's disease, obsessive  
 CC compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,  
 CC depression and bipolar manic-depressive disorder. The sequences and  
 CC methods of the invention can also be used for detecting or treating  
 CC infectious disorders (e.g. AIDS), hyperproliferative disorders  
 CC (e.g. cancer), immune disorders (e.g. severe combined immunodeficiency,  
 CC SCID) autoimmune diseases (e.g. insulin dependent diabetes mellitus),  
 CC inflammatory disorders (e.g. arthritis). The polynucleotides can be used  
 CC for gene therapy.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;  
 Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAAAAAA 1100  
 Db :|||||  
 19 BAAAAAATAAAAAAAAAA 2  
 RESULT 220  
 AAH21968/c  
 ID AAH21968 standard; DNA; 19 BP.  
 XX  
 AC AAH21968;  
 XX  
 XX 16-AUG-2001 (first entry)  
 XX  
 DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.  
 XX Mouse; human; total gene expression analysis; TOGA; DST; EST;  
 KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;

central nervous system; antidepressant; gene therapy; diagnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addition-related behaviour; chromosome identification; immune response; PCR primer; probe; ss.

Mus musculus.

WO200130972-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29690.

26-OCT-1999; 99US-0161379.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Haseel KW; WPI; 2001-300499/31.

New neuroleptic-regulated polynucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior

Example 1; Page 87; 210pp; English.

The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (I), polypeptides (II) encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behaviour. (I) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned disorders, identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, diagnostic probes for the presence of specific mRNA in a particular cell type, as a probe to subtract-out known sequences in the process of discovering novel polynucleotides, for selection and making oligomers for attachment to a gene chip or other support, to raise anti-DNA antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100  
:|||||  
Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 221  
AAF76617/c  
ID AAF76617 standard; DNA; 19 BP.  
AC AAF76617;  
XX  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.

central nervous system; antidepressant; gene therapy; diagnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addition-related behaviour; chromosome identification; immune response; PCR primer; probe; ss.

Mus musculus.

WO200130972-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US29690.

26-OCT-1999; 99US-0161379.

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Haseel KW; WPI; 2001-300499/31.

New neuroleptic-regulated polynucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior

Example 1; Page 87; 210pp; English.

The present invention describes isolated neuroleptic-regulated nucleic acid molecules. (I) have neuroleptic, antimanic and antidepressant activities, and can be used in gene therapy. (I), polypeptides (II) encoded by (I), or a host cell (III) comprising (I), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (I) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behaviour. (I) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue sample. (I) can be used as probes and primers, for chromosome identification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned disorders, identifying individuals from minute biological samples, as an alternative to restriction fragment length polymorphism (RFLP) and as polymorphic markers for forensic purposes. (I) is also useful as molecular weight markers on Southern gels, diagnostic probes for the presence of specific mRNA in a particular cell type, as a probe to subtract-out known sequences in the process of discovering novel polynucleotides, for selection and making oligomers for attachment to a gene chip or other support, to raise anti-DNA antibodies using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in the exemplification of the present invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100  
:|||||  
Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 221  
AAF76617/c  
ID AAF76617 standard; DNA; 19 BP.  
AC AAF76617;  
XX  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.

XX  
KW Spearmint; peppermint; (-)-limonene-6-hydroxylase;  
XW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.  
XX  
OS Mentha spicata.  
XX  
PN US6194185-B1.  
XX  
PD 27-FEB-2001.  
XX  
PF 14-APR-1999; 99US-0292768.  
XX  
PR 24-JUN-1997; 97US-0881784.  
XX  
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Croteau RB, Lupien SL, Karp F;  
XX  
WPI; 2001-243405/25.  
XX  
PT Novel isolated limonene hydroxylase encoding nucleic acid molecule,  
PT useful for altering production of limonene-6-hydroxylase or  
PT limonene-3-hydroxylase in suitable host cell -  
XX  
PS Example 4; Column 55; 57pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint  
CC (-)-limonene-6-hydroxylase. Also provided are a number of probes and PCR  
CC primers which were used to isolate the sequences. These are useful in the  
CC production of transgenic plants with altered flavour and aroma.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAAATAAAAAAAAAA 1100  
:|||||  
Db 19 DAAAAAATAAAAAAAAAA 2

RESULT 222  
AAD40279/c  
ID AAD40279 standard; DNA; 19 BP.  
XX  
AC AAD40279;  
XX  
DT 22-OCT-2002 (first entry)  
XX  
DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.  
XX  
KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;  
KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.  
OS Cucurbita pepo.  
XX  
PN US2002053095-A1.  
XX  
PD 02-MAY-2002.  
XX  
PF 10-AUG-1999; 99US-0371307.  
XX  
PR 10-AUG-1999; 99US-0371307.  
XX  
PA (BROW/) BROWN S M.  
XX  
PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;  
PI Piller KU, Rao S, Ream JE;  
XX  
WPI; 2002-489107/52.  
XX

PT Control of gibberellin levels in plants useful to avoid unfavorable  
 PT conditions in crops to increase yields, using transgenic plants having  
 PT reduced seed germination and early seedling growth then treatment to  
 PT restore these properties -  
 XX  
 PS Example 19; Page 104; 155pp; English.

XX The invention relates to control of gibberellin (GA) levels in plants.  
 CC The method involves producing transgenic plants having a phenotype  
 CC of reduced seed germination and reduced early seedling growth, then  
 CC restoring seed germination and early seedling growth by treating  
 CC plants with an appropriate compound when conditions are favorable.  
 CC The method is useful to control seed germination and/or early seedling  
 CC growth in agricultural production so that unfavorable environmental  
 CC conditions normally reducing agronomic output can be avoided and  
 CC yields increased. Plants also demonstrate increased uniformity of  
 CC germination, emergence and seedling vigor, so increasing yields at  
 CC harvest. The method is especially useful in crop plants such as e.g.  
 CC canola, soybean, cotton, etc., and is also useful in storage and  
 CC transport of seeds to reduce premature germination which may affect  
 CC agronomic or food quality of the seeds. The present sequence is a  
 CC PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.  
 CC This primer is used in the exemplification of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100  
 :|||||  
 Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 223

ABQ73231/c

ID ABQ73231 standard; DNA; 19 BP.

XX AC ABQ73231;

XX 27-SEP-2002 (first entry)

XX Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.

XX Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;  
 KW TOGA primer; ss.  
 KW Oryctolagus cuniculus.  
 OS Synthetic.

XX WO200242420-A2.

XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-US44072.

XX 21-NOV-2000; 2000US-252216P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Leonardi A, Sartani A, Glass JR, Hasel KW;

XX WPI; 2002-575233/61.

XX New polynucleotides related to regulated genes characteristic of  
 PT atherosclerosis, useful for diagnosing, preventing, treating,  
 PT modulating or ameliorating atherosclerosis in a mammalian subject -  
 XX Disclosure; Page 28; 130pp; English.

XX The present invention describes an isolated polynucleotide (I) and its  
 CC complements, and degenerate variants, comprising a sequence selected

CC from those given in ABQ73206 to ABQ73222 (NS), which is a digital  
 CC sequence tag (DST) corresponding to mRNAs whose expression is regulated  
 CC by proliferative lesion development caused by mechanically induced  
 CC intimal hyperplasia, or by lercanidipine treatment, or by proliferative  
 CC lesions and reversed by lercanidipine treatment. (I) has  
 CC antiatherosclerotic activity and can be used in gene therapy. (I) can be  
 CC used for diagnosing a medical condition (e.g. atherosclerosis) in a  
 CC subject which involves determining the presence or absence of a mutation  
 CC in (I) and diagnosing the medical condition based on the presence or  
 CC absence of the mutation. (I) is also useful for diagnosing  
 CC atherosclerosis, or the susceptibility to atherosclerosis in a subject  
 CC which involves detecting an alteration (an increase or decrease) in  
 CC amount of expression of (I). (I) is also useful for diagnosing or  
 CC monitoring the effects of treating a subject with dihydropyridine  
 CC calcium antagonist e.g., lercanidipine. (I) can also be used for  
 CC preventing, treating, modulating, or ameliorating a medical condition  
 CC such as atherosclerosis in a mammalian subject. The present sequence  
 CC represents a TOGA primer which is used in the exemplification of the  
 CC present invention.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100  
 :|||||  
 Db 19 BAAAAAATAAAAAAAAAA 2

RESULT 224

ABK71509/c

ID ABK71509 standard; DNA; 19 BP.

XX AC ABK71509;

XX 30-JUL-2002 (first entry)

XX CNS related 3' sequencing primer.

XX Central nervous system; CNS; neuroleptic; mouse; human; psychoses;  
 KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;  
 KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;  
 KW Parkinson's disease; obsessive compulsive disorder; epilepsy;  
 KW ischaemia; addiction; multiple sclerosis; depression;  
 KW manic-depressive disorder; primer; ss.

XX OS Synthetic.

XX WO200226936-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-US30695.

XX 29-SEP-2000; 2000US-236790P.

XX 18-JAN-2001; 2001US-263084P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;

XX WPI; 2002-383271/41.

XX New polynucleotide useful in gene therapy for preventing, treating  
 PT modulating or ameliorating a medical condition such as psychoses or a  
 PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in  
 PT a mammal -  
 XX Example 1; Page 40; 254pp; English.

XX This invention relates to the cDNA sequences of novel isolated

CC polynucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D<sub>2</sub> receptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the manufacture of a medicament useful for preventing, treating, modulating or ameliorating a medical condition e.g. a neuropsychiatric disorder. An antibody that binds the proteins of the invention is useful for preventing, treating, modulating or ameliorating neurological disorders such as psychoses or other neuropsychiatric disorders in a subject. The sequences are also useful for diagnosing neurological disorders or a susceptibility to a neurological disorder such as psychoses and other neuropsychiatric disorders in a subject by determining the presence or absence of mutation in the nucleotide sequence of apolipoprotein D or by determining the alteration (increase or decrease) in the expression of apolipoprotein D. The sequences of the invention are useful in treating deficiencies or disorders of the central nervous system or peripheral nervous system by activating or inhibiting the proliferation, differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells or glial cells. The sequences are useful as a marker or detector of a particular nervous system disease or disorder such as Alzheimer's disease, Pick's disease, Binswanger's disease, other senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosis, depression and manic-depressive disorder. The present sequence represents an oligonucleotide primer used in the identification of the cDNA sequences of the invention.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100  
Db 19 BAAAAA...AAAAA 2

RESULT 225  
AAD34663/C  
ID AAD34663 standard; DNA; 19 BP.  
XX  
AC AAD34663;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.  
XX  
KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;  
KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;  
KW TOGA; Total Gene expression Analysis; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200222783-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 17-SEP-2001; 2001WO-US29123.  
XX  
PR 15-SEP-2000; 2000US-233176P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;  
XX  
DR WPI; 2002-339865/37.  
XX

Preventing and treating hepatitis viral infection in a mammal, comprises administering nucleic acid molecules that up- or down-regulate in hepatitis B virus infection or polypeptides encoded by the nucleic acid molecules -

PS Disclosure; Page 28; 125pp; English.

XX The present invention relates to a method for preventing, treating, modulating or ameliorating a medical condition. The method involves administering one or more nucleic acid molecules up- or down-regulated in hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic acid molecules or antibodies that bind to the polypeptide. The method is useful for preventing, treating, modulating or ameliorating a medical condition. It is also useful for determining the presence or absence of a mutation in the nucleic acid molecules or detecting an alteration in expression of the polypeptide which is useful for the diagnosis of hepatitis viral infection. The method is useful for assessing the stage of hepatitis viral infection (e.g., acute hepatitis versus chronic hepatitis) or assessing the efficacy or toxicity of therapeutic treatment for hepatitis viral infection and a gene expression profile is useful for identifying polypeptides and polynucleotides which are associated with hepatitis viral infection. Sequences of the invention are used in gene therapy and as vaccines. Nucleic acid sequences are useful as a diagnostic marker for HBV infection and for treating infectious diseases. The present DNA sequence is a PCR primer which is used for direct sequencing of TOGA (Total Gene expression Analysis) generated PCR products.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 TAAAAA...AAAAA 1100  
Db 19 BAAAAA...AAAAA 2

RESULT 226  
ABZ68389/C  
ID ABZ68389 standard; DNA; 19 BP.  
XX  
AC ABZ68389;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Reverse transcription primer used to produce yeast cDNA.  
XX  
KW Histone acetyltransferase; histone deacetylase; gene expression profile;  
KW chromatin-associated protein; gene expression; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003000715-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-US19750.  
XX  
PR 22-JUN-2001; 2001US-300135P.  
XX  
PA (CERE-) CERES INC.  
XX  
PI Dang V, Okamura J;  
XX  
DR WPI; 2003-175280/17.  
XX

New chimeric polypeptide comprising a histone acetyltransferase polypeptide segment and a segment comprising a histone deacetylase chromatin-associated protein complex subunit, useful for modulating gene expression in cells -

Example 10; Page 54; 85pp; English.

The specification describes chimeric histone acetyltransferase polypeptides. The chimeric polypeptides comprise a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide

CC segment having 40% or greater sequence identity to a subunit of a  
 CC histone deacetylase chromatin-associated protein complex. The chimeric  
 CC polypeptides are useful for determining gene expression profiles in  
 CC specific cells, for modulating gene expression in specific cells, and  
 CC for making genetically modified eukaryotes. The present sequence  
 CC represents a reverse transcription primer used in the method of the  
 CC invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
 :|||||  
 Db 19 BAAAAA...AAAAA 2

RESULT 227  
 AAD50267/c  
 ID AAD50267 standard; DNA; 19 BP.  
 XX AC AAD50267;  
 XX AC

DT 24-MAR-2003 (first entry)

DE 3' sequencing primer #1 used to illustrate the method of the invention.  
 XX Gene expression; drug interaction mechanism; drug screening; primer;  
 KW genomic mapping; ss.

XX Unidentified.

XX WO200261045-A2.

XX 08-AUG-2002.

PF 01-FEB-2002; 2002WO-US02666.

XX 01-FEB-2001; 2001US-0775217.

PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 (QUAN/) QUAN J.

PI Quan J, Hilbush BS, Hasel KW, Sutcliffe GJ, Chang HW;  
 PI Callahan MA;

XX WPI; 2003-092784/08.

XX Simplified TOGA method for simultaneous sequence-specific  
 PT identification of multiple mRNA molecules in RNA population, useful  
 PT for determining tissue-specific patterns of gene expression or  
 PT mechanisms of drug interaction -

PS Disclosure; Page 39; 93pp; English.

XX The present invention relates to a novel simplified TOGA (RTM) method for  
 CC simultaneous sequence-specific identification of multiple mRNA molecules  
 CC in a RNA population. The method involves characterising each of the  
 CC sequence-specific polymerase chain reaction (PCR) products by partial  
 CC sequence and length. The method is useful for determining tissue-specific  
 CC patterns of gene expression or mechanisms of drug interaction. It is  
 CC also useful for drug screening, studying physiological processes, genomic  
 CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.  
 CC The present sequence is a primer used to illustrate the method of the  
 CC invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100  
 :|||||  
 Db 19 BAAAAA...AAAAA 2

RESULT 228  
 AAD49149/c  
 ID AAD49149 standard; DNA; 19 BP.

XX AC AAD49149;

DT 07-MAR-2003 (first entry)

DE 3' sequencing primer #1 used in the invention.

XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;  
 KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;  
 KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;  
 KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;  
 KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;  
 KW food additive; food preservative; primer; ss.

XX Unidentified.

XX WO200281726-A2.

XX 17-OCT-2002.

XX 15-NOV-2001; 2001WO-US43741.

XX 15-NOV-2000; 2000US-248992P.

XX 28-NOV-2000; 2000US-253623P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;

XX WPI; 2003-058561/05.

XX New polypeptide associated with atherosclerosis, useful for treating  
 PT atherosclerosis, nervous system disorders, immune disorders,  
 PT hyperproliferative disorders and infectious diseases -

PS Disclosure; Page 139; 146pp; English.

XX The invention relates to polynucleotides and polypeptides associated  
 CC with atherosclerosis. Polynucleotides of the invention are useful  
 CC for delivery of genes, DNA vaccines, diagnostic reagents, peptides,  
 CC proteins or macromolecules. Sequences of the invention are useful  
 CC for treating nervous system disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease, multiple sclerosis, epilepsy), immune disorders  
 CC (e.g., autoimmune disorders such as rheumatoid arthritis, Addison's  
 CC disease, haemolytic anaemia, graft-versus-host disease, inflammation),  
 CC hyperproliferative disorders (e.g., neoplasms) and infectious diseases  
 CC (e.g., viral, bacterial, fungal or parasite infection). They are used  
 CC for regeneration of tissues, to repair, replace or protect damage  
 CC tissues, for increasing chemotaxis activity of cells, for increasing  
 CC or decreasing the differentiation or proliferation of embryonic stem  
 CC cells from a lineage, for modulating mammalian characteristics, (such  
 CC as body weight or height), for modulating mammalian metabolism  
 CC affecting catabolism, anabolism, processing utilisation and storage  
 CC of energy, to change a mammal's mental or physical state, or as a food  
 CC additive or preservative. The invention is useful in gene therapy. The  
 CC present sequence is a sequencing primer used in the invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;

Query Match 1.6%; Score 17.2; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAA...AAAAA 1100



CC acid with the exact sequence as GenBank Accession No: AJ012376.1.  
CC The present sequence represents a polymorphic site of the human ABC1  
CC gene.  
XX

SQ Sequence 22 BP; 6 A; 2 C; 11 G; 3 T; 0 other;  
Query Match 1.6%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 991 TTGGAGTCTGAGGCTGGAGAA 1012  
1 TTGGAGGCTGAGGAGGAGAA 22

RESULT 231  
AAL50570/C  
ID AAL50570 standard; DNA; 22 BP.

XX AC AAL50570;

DT 12-DEC-2002 (first entry)

DE Molecular array production method-related PCR primer.

XX Molecular array; ss; target molecule identification; genetic analysis;  
KW gene expression; SNP detection; haplotyping; sequencing; PCR; primer.  
XX

OS Unidentified.

XX WO200274988-A2.

XX 26-SEP-2002.

PF 18-MAR-2002; 2002WO-GB01245.

PR 16-MAR-2001; 2001GB-0006635.

PR 02-AUG-2001; 2001GB-0018879.

PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.

PI Mir K;

XX WPI; 2002-732872/79.

XX Producing a molecular array with a plurality of molecules immobilized  
PT to a solid substrate, useful in genetic analysis, gene expression  
PT studies or the detection or typing of single nucleotide polymorphisms  
PT in a sample of nucleic acids -

XX Example 15; Page 122; 166pp; English.

XX The invention comprises a method for producing a molecular array, the  
CC method involves immobilising molecules to a solid phase at a density  
CC which allows individual immobilised molecules to be individually  
CC resolved. The molecular array produced by the method of the invention is  
CC useful for identifying one or more target molecules in a sample. The  
CC molecular array is also useful in genetic analysis, gene expression  
CC studies, identifying molecules which interact with a target molecule,  
CC detection/typing of single nucleotide polymorphisms, haplotyping and  
CC sequencing. The present DNA sequence represents a PCR primer that was  
CC used in an example of the invention.

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;  
Query Match 1.6%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 94.4%; Pred. No. 2.2e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100  
21 BAAAAAATAAAAAAAAAA 4

RESULT 233  
ABX74887/C  
ID ABX74887 standard; DNA; 22 BP.  
XX

RESULT 232  
AAD51324/C

ID AAD51324 standard; DNA; 22 BP.

XX AC AAD51324;

DT 16-APR-2003 (first entry)

XX Anchored oligo dT primer used to illustrate the method of the invention.  
DE Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;  
KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;  
KW musculoskeletal damage; ss.

XX Unidentified.

PN WO200290579-A1.

XX 14-NOV-2002.

PF 03-MAY-2002; 2002WO-AU00553.

PR 04-MAY-2001; 2001AU-0004809.

PR 29-JUN-2001; 2001US-0896941.

PA (GENO-) GENOMICS RES PARTNERS PTY LTD.

XX Brandon RB;

XX WPI; 2003-120558/11.

XX Assessing condition e.g. athletic ability, stage of disease, presence  
PT of drugs, response to exercise, response to vaccines, therapies,  
PT nutritional states, of performance animal involves analyzing nucleic  
PT acid expression -

PS Disclosure; Page 46; 87pp; English.

XX The invention relates to a method for assessing a condition of a  
CC performance animal. The method involves determining in sample abundance  
CC of expressed target nucleic acid; transmitting digital sample signal to  
CC remote diagnostic server; processing digital sample signal at remotely  
CC located database to correlate digital signal with digital information  
CC and returning report of particular condition of animal. The method is  
CC useful for assessing a condition of a performance animal preferably  
CC human, dog or camel. The condition can be an athletic ability and a  
CC condition that enhances, hinders, impedes or does not change an expected  
CC ability of the performance animal; and also normal, pre-clinical, overt  
CC progress and/or stage of disease, undiagnosed or unclassified conditions,  
CC presence of drugs, response to exercise, response to vaccines, therapies,  
CC nutritional states and response to environmental conditions. Diseases  
CC assessed by the invention include laminitis, lameness, viral or bacterial  
CC disease, gastritis, gastric ulcers, respiratory ailments, fractures.  
CC epistaxis, musculoskeletal damage or disorders and joint diseases. The  
CC present sequence is a primer used to illustrate the method of the  
CC invention.

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;  
Query Match 1.6%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 94.4%; Pred. No. 2.2e+02;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100  
21 BAAAAAATAAAAAAAAAA 4



```

AC ABX74887;
DT 21-MAR-2003 (first entry)
DE Oligo-dT primer used in human CC-RCC invention.
XX Microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
XX OS Synthetic.
XX WO200279411-A2.
XX 10-OCT-2002.
XX 29-MAR-2002; 2002WO-US09576.
XX 29-MAR-2001; 2001US-279411P.
XX (VAND-) VAN ANDEL INST.
XX Haab B, Rhodes D, Teh BT, Takashi M;
XX WPI; 2003-040679/03.
XX New microarray, comprising a matrix of cDNA probe from a set of probes
PT immobilised to a solid surface in predetermined order, useful in the
PT prognosis of patients with clear cell renal carcinoma -
XX Example 2; Page 30; 179pp; English.
XX The present invention relates to a microarray comprising a matrix of
CC at least one cDNA probe from a set of probes immobilised to a solid
CC surface in a predetermined order, where a row of pixels corresponds
CC to replicates of one distinct probe from the set. The probes are
CC complementary to nucleic acid sequences that are expressed
CC differentially in aggressive as compared to non-aggressive types of
CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
CC under high stringency conditions. The microarray is useful for the
CC prognosis of patients with CC-RCC, wherein aggressive and
CC non-aggressive CC-RCC tumour types are characterised by differential
CC expression profiles of genes that hybridise with one or more probes
CC immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present
CC sequence represents an oligo-dT primer used in the examples of the
XX present invention.
XX SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 2 other;

Query Match 1.6%; Score 17.2; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db :|||||
21 BAAAAAATAAAAAAAAAA 4

RESULT 234
ABK13916/c
ID ABK13916 standard; DNA; 23 BP.
XX AC ABK13916;
XX 21-MAY-2002 (first entry)
XX 3'-PCR primer used in method of identifying transcribed genes.
XX Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.

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XX OS Synthetic.
XX WO200208461-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-IB01539.
XX 21-JUL-2000; 2000GB-0018016.
XX 21-JUL-2000; 2000US-219925P.
XX (GLOB-) GLOBAL GENOMICS AB.
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.
XX Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analysing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes -
XX Example 2; Page 45; 67pp; English.
XX The present invention relates to a method for providing a profile of
CC mRNA molecules present in a sample. The method comprises generating
CC two independent patterns characteristic of the population of mRNA
CC molecules expressed in the sample and analysing the patterns using a
CC combinatorial algorithm, comparing gene expression by different or
CC same cell types under different conditions, and identifying genes
CC having a role in various cellular processes. The method is useful
CC for the analysis and identification of transcribed genes, and
CC fingerprinting. The method can be used to identify genes which play a
CC role in determining various cellular processes, including susceptibility
CC to external factors, development, and disease. The present sequence for
CC a PCR primer is used in the methods of the present invention.
XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 3 other;

Query Match 1.6%; Score 17.2; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1083 TAAAAAATAAAAAAAAAA 1100
Db :|||||
21 BAAAAAATAAAAAAAAAA 4

RESULT 235
ABS55943
ID ABS55943 standard; DNA; 24 BP.
XX AC ABS55943;
XX 22-JAN-2003 (first entry)
XX DNA topoisomerase II (TOP2) 21.34 cDNA RT-PCR primer #2.
XX DNA topoisomerase II 21.34; TOP2; primer; ss; DNA recombination; cancer;
KW malignant tumour; haemopathy; human immunodeficiency virus; HIV; RT-PCR;
KW immunological disease; inflammation; development disturbance;
KW reverse transcriptase.
XX OS Unidentified.
XX CN1345941-A.
XX 24-APR-2002.
XX 29-SEP-2000; 2000CN-0125577.
XX 29-SEP-2000; 2000CN-0125577.

```

XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-539340/58.  
 XX XX  
 PT New polypeptide-DNA topoisomerase II (Top2) 21.34 for treating  
 PT malignant tumour, haemopathy, development disturbance, human  
 PT immunodeficiency virus infection, immunological disease and various  
 PT inflammations -  
 XX XX  
 PS Example 2; Page 18 (Disclosure); 34pp; Chinese.  
 XX XX  
 CC The invention relates to the polypeptide DNA topoisomerase II (TOP2)  
 CC 21.34, a polynucleotide encoding the polypeptide and a method for  
 CC producing the polypeptide by DNA recombination technology. The  
 CC polypeptide is used for curing several diseases, such as malignant  
 CC tumours, haemopathy, development disturbance, human immunodeficiency  
 CC virus (HIV) infection, immunological diseases and various inflammations.  
 CC This sequence represents a reverse transcriptase PCR (RT-PCR) primer used  
 CC in isolation of cDNA encoding DNA topoisomerase II (TOP2) 21.34.  
 XX XX  
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;  
 Query Match 1.6%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 323 CAGAGACGCTGCGAGCACTT 344  
 DB ||||| ||||| ||||| ||||| |||||  
 2 CAGAGCAGCTCGGAGCGACTT 23  
 RESULT 236  
 ABK91269/C  
 ID ABK91269 standard; DNA; 24 BP.  
 XX AC  
 XX ABK91269;  
 XX DT  
 XX 05-NOV-2002 (first entry)  
 XX DE  
 XX Leukaemia related protein 24.09 specific RT-PCR primer #2.  
 XX KW  
 XX Leukaemia related protein; leukaemia; lymphoma; primer; ss;  
 XX KW haemopathy; growth development disturbance disease;  
 XX KW reverse transcription; RT-PCR.  
 XX OS  
 XX Unidentified.  
 XX PN  
 XX CN1341647-A.  
 XX PD  
 XX 27-MAR-2002.  
 XX PF  
 XX 07-SEP-2000; 2000CN-0125055.  
 XX PR  
 XX 07-SEP-2000; 2000CN-0125055.  
 XX PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-520722/56.  
 XX XX  
 PT Novel leukemia related protein 24.09 -  
 XX PS  
 XX Example 3; Page 17 (disclosure); 32pp; Chinese.  
 XX XX  
 CC This invention relates to the DNA and protein sequences of leukemia  
 CC related protein 24.09. The invention also comprises methods for  
 CC producing the protein using recombinant DNA technology and  
 CC antagonists of the protein which may be used for inhibiting the  
 CC action of the protein. The sequences of the invention may be used

CC for treating several diseases such as leukaemia, lymphoma, other  
 CC haemopathy and growth development disturbance disease. The present  
 CC sequence represents a reverse transcription (RT) PCR primer used to  
 CC isolate the leukaemia related protein cDNA 24.09 of the invention.  
 XX SQ Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 other;  
 Query Match 1.6%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1079 CTATTAAAAA 1100  
 DB ||||| ||||| ||||| ||||| |||||  
 23 CAATTGAAAAA 2  
 RESULT 237  
 ABQ76045/C  
 ID ABQ76045 standard; DNA; 24 BP.  
 XX AC  
 XX ABQ76045;  
 XX DT  
 XX 30-SEP-2002 (first entry)  
 XX DE  
 XX Human actin similar protein 56.43 RT-PCR primer #2.  
 XX KW  
 XX Human; actin similar protein 56.43; palsy; arrhythmia; bronchial asthma;  
 XX KW peptic ulcer; diabetes; tumour; PCR; primer; ss.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 XX CN1339501-A.  
 XX PD  
 XX 13-MAR-2002.  
 XX PF  
 XX 23-AUG-2000; 2000CN-0119737.  
 XX PR  
 XX 23-AUG-2000; 2000CN-0119737.  
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-472210/51.  
 XX XX  
 PT New polypeptide-human actin similar protein 56.43 for treating periodic  
 PT palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes,  
 PT tumours, etc. The present invention also discloses the antagonist  
 CC resisting the polypeptide and its treatment effect. This sequence  
 CC represents a RT-PCR primer used in the amplification of the human actin  
 CC similar protein 56.43 described in the disclosure of the invention.  
 XX SQ Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 other;  
 Query Match 1.6%; Score 17.2; DB 1; Length 24;  
 Best Local Similarity 86.4%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1079 CTATTAAAAA 1100  
 DB ||||| ||||| ||||| ||||| |||||  
 23 CTCTTCAAAAAA 2  
 RESULT 238

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ABK48140/c
ID  ABK48140 standard; DNA; 24 BP.
XX  AC
XX  ABK48140;
XX  DT
XX  18-JUN-2002 (first entry)
XX  DE
XX  Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX  KW
XX  Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
XX  KW  baked product; cheese; poly-T; reverse transcriptase PCR.
XX  OS
XX  Synthetic.
XX  FN
XX  WO200216618-A1.
XX  PD
XX  28-FEB-2002.
XX  PF
XX  22-AUG-2001; 2001WO-EP09925.
XX  PR
XX  23-AUG-2000; 2000EP-0202995.
XX  PA
XX  (STAM ) DSM NV.
XX  PI
XX  Basten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;
XX  DR
XX  WPI; 2002-257917/30.
XX  CC
XX  An isolated polypeptide with aminopeptidase activity, for preparing
XX  PT  food compositions, such as bread and cheese, with enhanced flavouring -
XX  PT  Example 5; Page 40; 94pp; English.
XX  CC
XX  The invention relates to an isolated polypeptide with aminopeptidase
XX  CC  activity and the gene encoding it (including sequences complementary to
XX  CC  the gene and which hybridise to it at high stringency), from Aspergillus
XX  CC  niger. Also included are a nucleic acid construct comprising the above
XX  CC  polynucleotide operably linked to one or more control sequences that
XX  CC  direct the production of the polypeptide in a suitable expression host,
XX  CC  a recombinant expression vector comprising the above nucleic acid
XX  CC  construct, a recombinant host cell comprising the above nucleic acid
XX  CC  vector, and producing the protein comprising the above construct or
XX  CC  recombinant host cell to produce a supernatant and/or cells comprising
XX  CC  the polypeptide and recovering the polypeptide. The aminopeptidase is
XX  CC  used to prepare a food composition such as dough to enhance the flavour
XX  CC  of a baked product from the dough and for preparing a cheese to enhance
XX  CC  the flavour. The invention provides a bacterial enzyme for protein
XX  CC  hydrolysis i.e. with aminopeptidase activity, to produce flavouring
XX  CC  agents, and the enzyme has been isolated and characterised, compared to
XX  CC  a previously observed weak aminopeptidase activity which was detected
XX  CC  in an Aspergillus niger culture filtrate but the source was never
XX  CC  isolated or identified. The use of enzymes to produce flavouring agents
XX  CC  from proteinaceous material is better than use of strong acids which
XX  CC  can severely degrade the amino acids obtained. The present sequence
XX  CC  is a reverse transcriptase (RT)-PCR primer used to investigate the
XX  CC  intron-exon structure of the aminopeptidase gene.
XX  SQ  Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 1 other;

Query Match      1.6%; Score 17.2; DB 1; Length 24;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1083 TAAAAAATAAAAAA 1100
Db  24 BAAAAAATAAAAAA 7

RESULT 239
ABA04737/c
ID  ABA04737 standard; DNA; 24 BP.
XX  XX
XX  AC  ABA04737;

22-FEB-2002 (first entry)
Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.
Human; alkylation DNA protein cysteine methyltransferase 11; cytostatic;
haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;
tumour; haemopathy; HIV infection; immunological disease; inflammation;
PCR primer; ss.
Homo sapiens.
WO200188146-A1.
22-NOV-2001.
26-MAR-2001; 2001WO-CN00464.
28-MAR-2000; 2000CN-0115226.
(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Mao Y, Xie Y;
WPI; 2002-055701/07.
Human alkylation-DNA-protein cysteine methyltransferase and encoding
polynucleotide, used in diagnosis and treatment of malignant tumors,
hemopathy, human immunodeficiency virus infection, immunological
diseases and inflammation -
Example 2; Page 19; 40pp; Chinese.
The present invention relates to human alkylation-DNA-protein cysteine
methyltransferase (see AAM47739). The protein and its coding sequence
are useful in the diagnosis and treatment of malignant tumors,
haemopathy, HIV infection, immunological diseases and various
inflammations. The present sequence is a PCR primer, which was used in an
example from the present invention.
Sequence 24 BP; 4 A; 0 C; 4 G; 16 T; 0 other;

Query Match      1.6%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1078 ACTATTAAAAAATAAAAAA 1099
Db  22 ACTATAAAAAATACAAAAA 1

RESULT 240
AAAX18370/c
ID  AAAX18370 standard; DNA; 17 BP.
XX  AC
XX  AAAX18370;
XX  DT
XX  11-MAY-1999 (first entry)
XX  DE
XX  RT-PCR primer of the invention SEQ ID 11.
XX  KW
XX  RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX  OS
XX  Synthetic.
XX  PN
XX  JPI1032765-A.
XX  PD
XX  09-FEB-1999.
XX  PF
XX  18-JUL-1997; 97JP-0208312.
XX  PR
XX  18-JUL-1997; 97JP-0208312.

```

PA (TAKI ) TAKARA SHUZO CO LTD.  
XX WPI; 1999-183822/16.  
XX Peptides having at least two new nucleotides - useful as primers in  
XX RT-PCR  
PS Disclosure; Page 11; 19pp; Japanese.  
XX  
XX This sequence represents a primer of the invention. The invention relates  
XX to sequences of at least two nucleotides of formula:  
XX (X)ms'-(alpha)n-beta-N3'; or (X)ms'-(gamma)k-delta-N3'; where  
XX X = a labelled compound and/or a nucleotide with voluntary sequence;  
XX m = 0 or 1; alpha = thymine; n = natural number indicating the repetition  
XX of alpha; beta; delta = V or N; V = adenine, guanine or cytosine;  
XX N = adenine, guanine, cytosine or thymine; gamma = thymine;  
XX k = natural number of 3' or over indicating the repetition of gamma, in  
XX which thymine expressed by gamma is composed of 1/3 or less of adenine,  
XX guanine and/or cytosine. The new nucleotides are useful as primers for  
XX RT-PCR and determination of base sequences. The new sequences allow for  
XX reproductive and highly efficient analysis of gene sequences.  
XX  
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1082 TTAATAAAAAAAAAAAAAA 1098  
Db 17 TTAATAAAAAAAAAAAAAA 1  
RESULT 241  
ID AAA98232/C  
XX AAA98232 standard; DNA; 17 BP.  
AC AAA98232;  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Human retrovirus HERV LTR PCR primer #31.  
XX  
KW Cell-specific expression; tissue-specific expression; gene therapy; LTR;  
KW U3-R segment; long terminal repeat; retroviral expression vector;  
KW PCR primer; ss.  
XX  
OS Human retrovirus.  
XX  
PN WO200053789-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-EP02064.  
XX  
PR 10-MAR-1999; 99DE-1010650.  
XX  
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.  
XX  
PI Leib-Moesch C, Schoen U, Baust C;  
XX  
DR WPI; 2000-587442/55.  
XX  
PT Retroviral expression vector, useful in gene therapy, contains a  
PT promoter from a human endogenous retrovirus to provide cell-specific  
PT expression -  
XX  
PS Disclosure; Page 27; 67pp; German.  
XX  
XX This invention describes a novel retroviral expression vector (A)  
XX containing DNA sequences (I) for packaging vector RNA and for  
XX cell-specific expression of proteins or peptides encoding by heterologous  
XX DNA (II). The sequences controlling cell-specific expression contain a

cell-specifically regulatable promoter region (P) from a human endogenous  
retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and  
RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)  
eukaryotic cells containing (A) in integrated form; (d) virions  
containing a retroviral expression vector RNA derived from (A); (e) a  
method for producing the virions of (d); (f) a method for incorporating  
protein-encoding nucleic acid sequences into a eukaryotic cell by  
infection with the virions of (d); and (g) a retroviral vector system  
containing (A) and a packaging cell line, that contains at least one  
(recombinant) retrovirus construct that encodes for the packaging  
proteins of (A). (A) are used for cell- or tissue-specific expression of  
foreign genes for gene therapy and to produce virions for introducing  
(II) into the chromosomal DNA of eukaryotic cells, preferably mammalian  
and specifically human. (A) retain the advantages of usual retroviral  
promoters with all the signal structures required for transcription in a  
small region within the U3-R segment, but without their disadvantages  
(excessive strength and limited cell specificity). Since (A) are derived  
from endogenous (harmless) viral sequences, they do not introduce any new  
viral sequences into the genome and recombination will not create new  
types of retrovirus. The promoters provide cell or tissue specific  
expression, according to which HERV they are derived from.  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 242  
ID AAA50197/C  
XX AAA50197 standard; DNA; 17 BP.  
AC AAA50197;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.  
XX  
KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..19  
FT /\*tag= a  
FT /\*note= "2'-methoxyethoxy modified thymidine"  
FT modified\_base 1..17  
FT /\*tag= b  
FT /\*note= "phosphorothioate internucleoside linkages"  
XX  
PN WO200047593-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US03543.  
XX  
PR 12-FEB-1999; 99US-0250075.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Maier MA;  
XX  
DR WPI; 2000-558188/51.  
XX  
XX Preparation of mixed backbone oligomeric compounds useful as e.g.  
PT primers for diagnostic tests, involves oxidation of H-phosphonate  
PT internucleoside linkages to phosphodiester internucleoside linkages -

```

PS Example 12; Page 34; 49pp; English.
XX
CC The present sequence is that of a phosphorothioate oligonucleotide
CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group
CC on its 5' ribosyl sugar moiety. It is an example of an oligomeric
CC compound produced according to the methods of the invention. The
CC invention provides compounds and methods for the preparation of
CC mixed backbone oligomeric, or chimeric, compounds having
CC phosphodiester internucleoside linkages in addition to
CC phosphorothioate and/or phosphoramidate internucleoside linkages.
CC The methods also include incorporation of boranophosphate
CC internucleoside linkages. The methods utilize H-phosphonate
CC intermediates that are coupled together forming contiguous regions
CC of 1 or more H-phosphonate internucleoside linkages. Each
CC contiguous region is subsequently oxidized to phosphodiester,
CC phosphorothioate, phosphoramidate or boranophosphate
CC internucleoside linkages prior to further elongation. Mixed
CC backbone oligomeric compounds are prepared in this manner by
CC oxidizing adjacent regions with different reagents. Oligomeric
CC compounds of the invention are prepared using novel oxidation steps
CC that oxidize a region of 1 or more H-phosphonate internucleoside
CC linkages without degrading existing linkages that have been
CC previously oxidized. The oligonucleotides obtained are useful as
CC primers in PCR, probes, linkers, gene fragments and for other
CC diagnostic tests on e.g. biological tissue, fluid, cells etc., as
CC research reagents, and as antiviral agents.
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 243
AAA25450/C
ID AAA25450 standard; DNA; 17 BP.
XX AC AAA25450;
XX
XX 19-JUL-2000 (first entry)
DT
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
XX
KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US08547.
PF
XX
XX 20-APR-1998; 98US-0082404.
PR
XX 23-JUN-1998; 98US-0103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target
PT

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PT sequences, used to treat cancer -
XX
XX Claim 77; Page 79; 148pp; English.
XX

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CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX

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SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 other;

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Query Match 1.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 17 AAAAAAAAAAAAAAAAAA 1

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RESULT 244
AAQ34110
ID AAQ34110 standard; DNA; 18 BP.
XX AC AAQ34110;
XX
XX 25-MAR-2003 (updated)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA60B.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX
XX WO9213102-A1.
PN
XX
XX 06-AUG-1992.
PD
XX
XX 15-JAN-1992; 92WO-US00340.
PF
XX
XX 15-JAN-1991; 91US-0642342.
PR
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
XX Table 7; Page 375; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obtd.
CC by screening a library of bovine MboI DNA fragments of between

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Db      17 AAAAAAAAAAAAAAAAAA 1
RESULT 247
AAT94669/c
ID AAT94669 standard; DNA; 18 BP.
XX
AC AAT94669;
XX
DT 27-MAR-1998 (first entry)
XX
DE Anchored poly(T) oligonucleotide polyT-Anch3.
XX
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour;
KW transgenic plant; snapdragon; primer; ss.
XX
OS Synthetic.
XX
PN WO9732023-A1.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-AU00124.
XX
PR 01-MAR-1996; 96AU-0008386.
XX
PA (FLOR-) FLORIGENE LTD.
XX
PI Brugniera F, Holton TA, Michael MZ;
XX
WPI; 1997-448691/41.
XX
PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT corresponding DNA, used in the manipulation of pigmentation in
PT plants
XX
PS Example 15; Page 59; 234pp; English.
XX
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA,
CC and were also utilised in the PCR amplification of plant
CC cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see
CC AAT94657) encoding flavonoid 3'-hydroxylase (see AAW35704) was isolated
CC using a differential display approach. This can be used to
CC manipulate the pigmentation of transgenic plants.
XX
SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 248
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX

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OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP00905.
XX
PR 05-MAR-1997; 97JP-0050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis,
PT preventing or treating diseases associated with apoptosis
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method
CC of the invention, involving the use of novel apoptosis-related DNAs
CC and proteins. The inventions can be used as diagnostic reagents for
CC apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent
CC in immunohistological staining, as apoptosis inhibitors. It can also
CC be used for treatment of apoptosis-related diseases.
XX
SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 TTAATAAAAAAAAAAAAAA 1098
DB 18 TTAATAAAAAAAAAAAAAA 2

RESULT 249
AAV07750
ID AAV07750 standard; DNA; 18 BP.
XX
AC AAV07750;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphorothioate oligodeoxynucleotide.
XX
KW phosphorothioate; electrospray ionisation-Fourier transform;
KW mass spectrometry; off-resonance excitation; ss.
XX
OS Synthetic.
XX
PI Key Location/Qualifiers
XX misc_difference 1..18
XX /*tag= a
XX /note= "phosphorothioate internucleotide linkages"

WPI; 1998-520830/44.
XX

```

PT Determining the nucleotide sequence of a nucleic acid analyte -  
 XX using electro-spray ionisation  
 PS Example 1; Figure 3A; 25pp; English.  
 XX  
 CC The invention relates to an analytical method for determining the  
 CC nucleotide sequence of nucleic acid analytes, including chemically  
 CC modified oligonucleotides. This new method utilises electrospray  
 CC ionisation-Fourier transform mass spectrometry. The ions are excited by  
 CC sustained off-resonance excitation with single shot excitation, and the  
 CC target fragmented by collisionally activated dissociation by a neutral  
 CC gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation  
 CC can be nozzle skimmer dissociation. The method is used in molecular  
 CC biology and biomedical applications. The method, utilising electrospray  
 CC ionisation-Fourier transform ion cyclotron resonance mass spectrometry,  
 CC is extremely rapid and acts directly on the oligonucleotide. The method  
 CC is effective for a variety of nucleic acid analytes, particularly  
 CC chemically modified oligonucleotides which have not previously been  
 CC successfully sequenced. The present sequence represents a  
 CC phosphorothioate oligodeoxynucleotide.  
 XX  
 SQ Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 250  
 AAV37712  
 ID AAV37712 standard; cDNA; 18 BP.  
 AC AAV37712;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 07-SEP-1998 (first entry)  
 XX  
 DE Human protein Aq2\_li 3'-portion and polyA tail.  
 XX  
 KW Human; secreted protein; murine adult spleen; human foetal kidney; ovary;  
 KW bone marrow; thymus; AE648\_li; AE693\_li; AK438\_li; AK609\_li; AM1060\_li;  
 KW Aq2\_li; K433\_li; L256\_li; prevent; treat; ameliorate; medical; ds.  
 XX  
 OS Homo sapiens.  
 PN WO9820130-A2.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 31-OCT-1997; 97WO-US19857.  
 XX  
 PR 01-NOV-1996; 96US-0742973.  
 PR 29-OCT-1997; 97US-0960024.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;  
 PI Racie LA, Spaulding V, Treacy M;  
 XX  
 DR WPI; 1998-286946/25.  
 XX  
 CC New secreted proteins and associated polynucleotides - obtained from  
 PT murine adult spleen, human foetal kidney, human ovary, murine bone  
 PT marrow and murine adult thymus  
 XX  
 PS Disclosure; Page 58; 75pp; English.  
 XX  
 CC The present invention describes novel proteins isolated from cDNA  
 CC clones: AE648\_li; AE693\_li; AK438\_li; AK609\_li; AM1060\_li; Aq2\_li;

CC K433\_li; or L256\_li, deposited as ATCC 98237. The present sequence  
 CC represents the 3'-portion of Aq2\_li isolated from a human ovary cDNA  
 CC library. The proteins from the present invention may be administered  
 CC in a composition to prevent, treat or ameliorate a medical condition.  
 CC The proteins may exhibit biological activities such as nutritional  
 CC activity, cytokine and cell proliferation/differentiation activity,  
 CC immune stimulating or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombotic activity,  
 CC receptor/ligand activity, anti-inflammatory activity, cachectin/tumour  
 CC invasion suppressor activity, tumour inhibition activity and other  
 CC activities.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 2 AAAAAAAAAAAAAAAAAA 18  
 RESULT 251  
 AAV21970/c  
 ID AAV21970 standard; DNA; 18 BP.  
 XX  
 AC AAV21970;  
 XX  
 DT 14-JUL-1998 (first entry)  
 XX  
 DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.  
 XX  
 KW Nuclease resistant; bacterial infection; antibiotic; target;  
 KW veterinary medicine; treatment; human; industrial process;  
 KW bacterial control; ss.  
 XX  
 OS Synthetic.  
 PN WO9803533-A1.  
 XX  
 PD 29-JAN-1998.  
 XX  
 PF 23-JUL-1997; 97WO-US12961.  
 XX  
 PR 24-JUL-1996; 96US-0685575.  
 XX  
 PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.  
 XX  
 PI Arrow A, Pale RMK, Thompson TL;  
 XX  
 DR WPI; 1998-120687/11.  
 XX  
 PT Treating bacterial infections in humans or animals with  
 PT oligo:nucleotide(s) - resistant to nuclease and targeted to  
 PT bacterial nucleic acid or proteins, also conjugates of these  
 PT oligo:nucleotide(s) with antibiotics  
 XX  
 PS Claim 49; Page 87; 163pp; English.  
 XX  
 CC This antisense oligonucleotide is nuclease resistant and can be used in  
 CC the treatment of animals, including humans, having a bacterial infection.  
 CC The treatment comprises administration of such nuclease resistant  
 CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,  
 CC and formulated with a carrier. A compound comprising this nucleic  
 CC resistant oligonucleotide can be covalently linked to an antibiotic. The  
 CC method is used to treat infections by a wide variety of Gram-positive and  
 CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.  
 CC The methods are particularly used in immuno-compromised individuals  
 CC (e.g. patients with acquired immunodeficiency syndrome or those receiving  
 CC chemotherapy or radiation therapy), optionally in combination with, or



CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from  
 CC therapeutic use, the oligonucleotides can be used to control bacteria  
 CC in laboratory cultures, foods, beverages and industrial processes. The  
 CC oligonucleotides are specific for bacteria, without affecting metabolism  
 CC in mammalian cells. They may also activate RNase H and have a general,  
 CC non-specific immune-stimulating effect. The oligonucleotides can be  
 CC administered orally, intranasally, rectally, topically or by injection,  
 CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that  
 CC enhances cellular uptake.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred.No.1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2

## RESULT 252

AAAX19942  
 ID AAX19942 standard; DNA; 18 BP.

XX AC AAX19942;

XX DT 14-JUN-1999 (first entry)

XX DE Primer SEQ ID NO:2 from JP11075880.

XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX OS Synthetic.

XX FN JP11075880-A.

XX PD 23-MAR-1999.

XX PF 10-JUL-1998; 98JP-0195719.

XX PR 14-JUL-1997; 97JP-0205378.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX DR WPI; 1999-257710/22.

XX PT Labelling of an oligonucleotide - useful for detecting genes

XX PS Example 1; Page 7; 10pp; Japanese.

XX CC A method has been developed for labelling an oligonucleotide having a  
 CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
 CC adenine and thymine or uracil or guanine and cytosine, and n is an  
 CC integer of 1 or more) at the 3'-terminal side in which the repeated  
 CC sequence is added and extended using a labelled body of the nucleotide  
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to  
 CC 3' exonuclease activity. The method can be used for detecting a gene.  
 CC The method can detect a gene in a sensitivity up to ten times higher  
 CC than prior art methods. The present sequence represents a primer used  
 CC in an example from the present invention.

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred.No.1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 253  
 AAAX19943/c  
 ID AAX19943 standard; DNA; 18 BP.  
 XX AC AAX19943;  
 XX DT 14-JUN-1999 (first entry)  
 XX DE Primer SEQ ID NO:3 from JP11075880.

XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX OS Synthetic.

XX FN JP11075880-A.

XX PD 23-MAR-1999.

XX PF 10-JUL-1998; 98JP-0195719.

XX PR 14-JUL-1997; 97JP-0205378.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX DR WPI; 1999-257710/22.

XX PT Labelling of an oligonucleotide - useful for detecting genes

XX PS Example 1; Page 7; 10pp; Japanese.

XX CC A method has been developed for labelling an oligonucleotide having a  
 CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
 CC adenine and thymine or uracil or guanine and cytosine, and n is an  
 CC integer of 1 or more) at the 3'-terminal side in which the repeated  
 CC sequence is added and extended using a labelled body of the nucleotide  
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to  
 CC 3' exonuclease activity. The method can be used for detecting a gene.  
 CC The method can detect a gene in a sensitivity up to ten times higher  
 CC than prior art methods. The present sequence represents a primer used  
 CC in an example from the present invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred.No.1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2

## RESULT 254

AAAX18373/c  
 ID AAX18373 standard; DNA; 18 BP.

XX AC AAX18373;

XX DT 11-MAY-1999 (first entry)

XX DE RT-PCR primer of the invention SEQ ID 14.

XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX OS Synthetic.

XX FN JP11032765-A.

XX PD 09-FEB-1999.

XX PF 18-JUL-1997; 97JP-0208312.

XX PR 18-JUL-1997; 97JP-0208312.

XX PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX WPI; 1999-183822/16.  
 DR PT Peptides having at least two new nucleotides - useful as primers in  
 PT RT-PCR  
 XX PS Disclosure; Page 11; 19pp; Japanese.  
 XX CC This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula:  
 CC (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where  
 CC X = a labelled compound and/or a nucleotide with voluntary sequence;  
 CC m = 0 or 1; alpha = thymine; n = natural number indicating the repetition  
 CC of alpha; beta; delta = V or N; V = adenine, guanine or cytosine;  
 CC N = adenine, guanine, cytosine or thymine; gamma = thymine;  
 CC k = natural number of 3 or over indicating the repetition of gamma, in  
 CC which thymine expressed by gamma is composed of 1/3 or less of adenine,  
 CC guanine and/or cytosine. The new nucleotides are useful as primers for  
 CC RT-PCR and determination of base sequences. The new sequences allow for  
 CC reproductive and highly efficient analysis of gene sequences.  
 XX CC Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1083 TAAAAAATAAAAAA 1099  
 DB 17 TAAAAAATAAAAAA 1  
 RESULT 255  
 ID AAA40563  
 AC AAA40563 standard; cDNA; 18 BP.  
 XX AC AAA40563;  
 DT 16-NOV-2000 (first entry)  
 XX DE Human adult ovary cDNA fragment AQ2\_11 #2.  
 XX KW Secreted protein; cytosolic; immunostimulatory; antimicrobial;  
 KW antiviral; immunosuppressive; antiinflammatory; vulnary; cytokine;  
 KW cell proliferation; differentiation; regulator; treatment; tumor;  
 KW autoimmune disease; inflammatory disorder; wound; microbial infection;  
 KW viral disease; graft versus host reaction suppression; ss.  
 XX OS Homo sapiens.  
 XX PN WO200037630-A1.  
 XX PD 29-JUN-2000.  
 XX PF 22-DEC-1999; 99WO-US31005.  
 XX PR 23-DEC-1998; 98US-0220876.  
 XX PA (GEMV ) GENETICS INST INC.  
 XX PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Bowman MR;  
 XX WPI; 2000-442661/38.  
 DR P-PSDB; AAB10274.  
 XX PT Secreted human proteins AS296-1i and AS34-1i, useful for treating  
 PT tumors, autoimmune diseases, inflammatory disorders, wounds, microbial  
 PT infections and viral diseases -  
 XX PS Disclosure; Page 269; 293pp; English.

XX CC This invention describes novel secreted human proteins (I) which have  
 CC cytostatic, immunostimulatory, antimicrobial, antiviral,  
 CC immunosuppressive, antiinflammatory and vulnerary activity and which act  
 CC as cytokine, cell proliferation or differentiation regulators. (I)  
 CC is useful for treating tumors, autoimmune diseases, inflammatory  
 CC disorders, wounds, microbial infections and viral diseases. (I) is also  
 CC useful for suppressing graft versus host reaction. AAA40490-A40580  
 CC represent cDNA fragments that encode the secreted proteins  
 CC AAB10226-B10288 described in the method of the invention.  
 XX CC Sequence 18 BP; 17 A; 0 C; 1 G; 0 U; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAATAAAAAA 1100  
 DB 2 AAAAAAATAAAAAA 18  
 RESULT 256  
 ID AAZ90646/c  
 XX ID AAZ90646 standard; DNA; 18 BP.  
 XX AC AAZ90646;  
 XX DT 13-JUN-2000 (first entry)  
 XX DE Human adipose tissue gene amplifying primer #7.  
 XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
 XX OS Homo sapiens.  
 XX PN JP2000037190-A.  
 XX PD 08-FEB-2000.  
 XX PF 23-JUL-1998; 98JP-0225228.  
 XX PR 23-JUL-1998; 98JP-0225228.  
 XX PA (NTSB ) JAPAN TOBACCO INC.  
 XX WPI; 2000-306578/27.  
 XX PT A physiologically active protein specifically derived from mammal  
 PT tissue -  
 XX PS Example 2; Page 18; 50pp; Japanese.  
 XX CC The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension,  
 CC arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes  
 CC (AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic  
 CC diagnosis, prevention and treatment of adipose tissue related diseases.  
 CC Sequences AAZ90640-51 represent PCR primers amplifying the human adipose  
 CC tissue genes.  
 XX CC Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1082 TTAATAAATAAAAAA 1098  
 DB 18 TTAATAAATAAAAAA 2

```
RESULT 257
AAZ87161
ID AAZ87161 standard; RNA; 18 BP.
XX
XX AAZ87161;
XX
XX 08-MAY-2000 (first entry)
XX
XX Oligoarabinonucleotide SEQ ID NO:2.
XX
XX Beta-D-arabinose; antisense; inhibition;
KW transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
XX W09967378-A1.
XX
XX 29-DEC-1999.
XX
XX 17-JUN-1999; 99WO-CA00571.
XX
XX 19-JUN-1998; 98CA-2241361.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
XX Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication
XX
XX Example 1; Page 29; 91pp; English.
XX
XX The invention relates to a new composition for selective, sequence-
XX specific inhibition of gene transcription and expression in a host. The
XX composition comprises oligonucleotides containing arabinose sugars that
XX can hybridize to either a single-stranded (ss) RNA to induce RNase H
XX cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX helix, thereby inhibiting DNA replication and/or transcription. The
XX oligoarabinonucleotides are used for antisense inhibition of gene
XX expression or to prevent DNA replication, or reverse transcription of
XX RNA by retroviruses. The compositions are therefore particularly used to
XX inhibit retroviral replication. The oligoarabinonucleotides can also be
XX used, in combination with RNase H, as reagents for sequence-specific
XX cleavage or RNA mapping, and additionally for the study and control of
XX gene expression in cells. The oligoarabinonucleotides have excellent
XX affinity for RNA, increased resistance to nucleases and show little if
XX any non-specific binding to cellular or serum proteins. They target ss
XX retroviral genomic RNA to inhibit the early stages of viral replication.
XX Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX with significantly higher thermal stability than those produced by
XX normal oligonucleotides. Sequences AAZ87160-287164 represent
XX oligoarabinonucleotides containing beta-D-arabinose used in an
XX exemplification of the present invention.
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1084 AAAAAAAAAAAAAAAAAA 1100
XX ||||||||||||||||
```

```
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 258
AAZ87162/c
ID AAZ87162 standard; RNA; 18 BP.
XX
XX AAZ87162;
XX
XX 08-MAY-2000 (first entry)
XX
XX Oligoarabinonucleotide SEQ ID NO:3.
XX
XX Beta-D-arabinose; antisense; inhibition;
KW transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
XX W09967378-A1.
XX
XX 29-DEC-1999.
XX
XX 17-JUN-1999; 99WO-CA00571.
XX
XX 19-JUN-1998; 98CA-2241361.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
XX Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication
XX
XX Example 1; Page 29; 91pp; English.
XX
XX The invention relates to a new composition for selective, sequence-
XX specific inhibition of gene transcription and expression in a host. The
XX composition comprises oligonucleotides containing arabinose sugars that
XX can hybridize to either a single-stranded (ss) RNA to induce RNase H
XX cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX helix, thereby inhibiting DNA replication and/or transcription. The
XX oligoarabinonucleotides are used for antisense inhibition of gene
XX expression or to prevent DNA replication, or reverse transcription of
XX RNA by retroviruses. The compositions are therefore particularly used to
XX inhibit retroviral replication. The oligoarabinonucleotides can also be
XX used, in combination with RNase H, as reagents for sequence-specific
XX cleavage or RNA mapping, and additionally for the study and control of
XX gene expression in cells. The oligoarabinonucleotides have excellent
XX affinity for RNA, increased resistance to nucleases and show little if
XX any non-specific binding to cellular or serum proteins. They target ss
XX retroviral genomic RNA to inhibit the early stages of viral replication.
XX Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX with significantly higher thermal stability than those produced by
XX normal oligonucleotides. Sequences AAZ87160-287164 represent
XX oligoarabinonucleotides containing beta-D-arabinose used in an
XX exemplification of the present invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 U; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1084 AAAAAAAAAAAAAAAA 1100
    |||||
Db 18 AAAAAAAAAAAAAAAA 2

RESULT 259
AAZ87166/c
ID AAZ87166 standard; DNA; 18 BP.
XX
AC AAZ87166;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:7.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00571.
XX
PR 19-JUN-1998; 98CA-2241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication
XX
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonucleotides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
helix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonucleotides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
RNA by retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonucleotides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonucleotides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins. They target ss
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonucleotides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
normal oligonucleotides. Sequences AAZ87165-287169 represent
oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
arabinose used in an exemplification of the present invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;
1.5%; Score 17; DB 1; Length 18;
Query Match
```

```
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100
    |||||
Db 18 AAAAAAAAAAAAAAAA 2

RESULT 260
AAZ87167
ID AAZ87167 standard; DNA; 18 BP.
XX
AC AAZ87167;
XX
DT 08-MAY-2000 (first entry)
XX
DE Deoxyarabinonucleotide SEQ ID NO:8.
XX
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription;
KW viral replication; RNase H cleavage; triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
fluoro-beta-D-arabinose"
XX
PN WO9967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00571.
XX
PR 19-JUN-1998; 98CA-2241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication
XX
PS Example 2; Page 31; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonucleotides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNase H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
helix, thereby inhibiting DNA replication and/or transcription. The
oligoarabinonucleotides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of
RNA by retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonucleotides can also be
used, in combination with RNase H, as reagents for sequence-specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinonucleotides have excellent
affinity for RNA, increased resistance to nucleases and show little if
any non-specific binding to cellular or serum proteins. They target ss
retroviral genomic RNA to inhibit the early stages of viral replication.
Oligoarabinonucleotides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by
normal oligonucleotides. Sequences AAZ87165-287169 represent
oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
arabinose used in an exemplification of the present invention.
XX
```

SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 261  
 AAD20091  
 ID AAD20091 standard; mRNA; 18 BP.  
 XX  
 AC AAD20091;  
 XX  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE mRNA fragment used in 3' end PCR/IVT method of the invention.  
 XX  
 KW RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US6271002-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 04-OCT-1999; 99US-0411074.  
 XX  
 PR 04-OCT-1999; 99US-0411074.  
 XX  
 PA (ROSE-) ROSETTA INPHARMATICS INC.  
 XX  
 PI Linsley PS, Schelter JM;  
 XX  
 DR WPI; 2001-624273/72.  
 XX  
 PT Amplifying and detecting RNA derived from a population of cells by  
 PT employing a primer that contains an RNA polymerase promoter in a  
 PT polymerase chain reaction -  
 XX  
 XX Example 3; Fig 1; 29pp; English.  
 CC The invention relates to methods and kits for amplification of mRNA  
 CC using a primer in PCR that contains an RNA polymerase (RNAP) promoter.  
 CC The invention provides methods for amplification and detection of RNA  
 CC derived from a population of cells, preferably eukaryotic cells and  
 CC most preferably mammalian cells, which methods preserve fidelity with  
 CC respect to sequence and transcript representation and additionally  
 CC enable amplification of extremely small amounts of mRNA. The method  
 CC and kit are useful for amplifying and detecting RNA derived from a  
 CC population of cells, especially eukaryotic cells like mammals. The  
 CC RNAs generated are useful for profiling gene expression in different  
 CC populations of cells. The present sequence is a mRNA fragment used  
 CC in 3' end PCR/IVT (in vitro transcription) method of the invention.  
 XX  
 SQ Sequence 18 BP; 17 A; 0 C; 0 G; 0 U; 1 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 262  
 AAF82472/c  
 ID AAF82472 standard; DNA; 18 BP.  
 XX

AC AAF82472;  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Phagemid vector PCR2.1 polylinker oligonucleotide #6.  
 XX  
 KW Phagemid vector; PCR2.1; rat; secreted factor; P00210D09; cardiant;  
 KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;  
 KW renal disease; inflammatory disease; polylinker; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200123419-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 27-SEP-2000; 2000WO-US26582.  
 XX  
 PR 27-SEP-1999; 99US-0156277.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Stanton LW, Kapoun AM;  
 XX  
 DR WPI; 2001-328177/34.  
 XX  
 PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,  
 PT treating and/or preventing various cardiac, renal and inflammatory  
 PT diseases -  
 XX  
 XX Example 1; Page 41; 69pp; English.  
 CC The present sequence corresponds to polylinker DNA of the phagemid  
 CC vector PCR2.1. It was used in the construction of a normalised rat cDNA  
 CC library, which was used in an example demonstrating differential  
 CC expression of a rat gene referred to as clone P00210D09. The invention  
 CC relates to a polypeptide comprising a sequence of at least 80% identity  
 CC to residues 22-122 of the present sequence, or a sequence encoded by a  
 CC nucleic acid hybridising under stringent conditions to the complement of  
 CC the coding region comprising 1031 nucleotides, and having at least one  
 CC biological activity of the polypeptide encoded by clone P00210D09. The  
 CC polypeptides and polynucleotides of the invention are useful for the  
 CC treatment of cardiac, renal and inflammatory diseases. The  
 CC polynucleotides are useful in antisense mediated gene inhibition and in  
 CC gene therapy. The polypeptides are useful in assays for identifying lead  
 CC compounds that may be used as therapeutic agents in the treatment of  
 CC cardiac, kidney or inflammatory diseases.  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 |||||  
 Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 263  
 AAD03565/c  
 ID AAD03565 standard; DNA; 18 BP.  
 XX  
 AC AAD03565;  
 XX  
 DT 19-JUN-2001 (first entry)  
 XX  
 DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.  
 XX  
 KW Rat; secreted factor; clone P00188 Di2; cardiant; antiinflammatory;  
 KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;  
 KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;  
 KW antibacterial; osteopathic; cerebroprotective; vasotropic; antitumor;

KW nootropic; neuroprotective; congestive heart failure; myocarditis;  
 KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;  
 KW kidney disease; acute renal failure; renal glucosuria; renal infarction;  
 KW polycystic kidney disease; hereditary nephritis; inflammatory disease;  
 KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;  
 KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;  
 KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.  
 OS  
 XX Rattus norvegicus.  
 XX  
 FN WO200123564-A1.  
 XX  
 XX PD 05-APR-2001.  
 XX  
 XX PF 27-SEP-2000; 2000WO-US26544.  
 XX  
 XX PR 27-SEP-1999; 99US-0156280.  
 XX  
 XX PA (SCIO-) SCIOS INC.  
 XX  
 XX PI Stanton LW, Kapoun AM;  
 XX  
 XX DR WPI; 2001-266159/27.  
 XX  
 XX PT Novel secreted factor encoded by clone P00188D12 which is  
 PT differentially expressed in certain disease states, useful in  
 PT diagnosing and treating cardiac, renal or inflammatory diseases -  
 XX  
 XX PS Example 1; Page 42; 71pp; English.  
 XX

CC The patent discloses novel secreted factor protein encoded by clone  
 CC P00188 D12. The secreted factor is differentially expressed in certain  
 CC disease states. Secreted protein, its antibodies, antagonists or  
 CC compositions comprising them are useful in the diagnosis and treatment  
 CC of cardiac diseases such as congestive heart failure, myocarditis,  
 CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,  
 CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute  
 CC renal failure, renal glucosuria, renal infarction, nephrogenic  
 CC diabetes insipidus, polycystic kidney disease, hereditary nephritis  
 CC and inflammatory diseases such as asthma, autoimmune diabetes, tumour  
 CC syndrome, aschma, stroke, neural trauma, psoriasis, cerebral malaria,  
 CC osteoporosis, Crohn's disease, ulcerative colitis, Alzheimer's disease.  
 CC Secreted protein DNA is useful in antisense-mediated gene inhibition  
 CC and in gene therapy. An array comprising one or more oligonucleotides  
 CC complementary to reference RNA or DNA encoding the secreted factor is  
 CC useful for detecting cardiac, kidney and inflammatory disease.  
 CC The present DNA sequence is an oligonucleotide which is used in the  
 CC preparation of a normalised cDNA library containing secreted factor  
 CC DNAs. The normalised cDNA libraries are used in the identification  
 CC of differentially expressed rat secreted factor P00188\_D12 gene.  
 XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 264  
 AAF99708/C

ID AAF99708 standard; DNA; 18 BP.

XX AAF99708;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #824.

XX

KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS  
 XX Synthetic.  
 XX  
 FN WO200122972-A2.  
 XX  
 XX PD 05-APR-2001.  
 XX  
 XX PF 25-SEP-2000; 2000WO-US26383.  
 XX  
 XX PR 25-SEP-1999; 99US-0156113.  
 XX  
 XX PR 27-SEP-1999; 99US-0156135.  
 XX  
 XX PR 23-AUG-2000; 2000US-0227436.  
 XX  
 XX PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 XX PA (COLE-) COLEY PHARM GMBH.  
 XX  
 XX PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 XX DR WPI; 2001-273485/28.  
 XX  
 XX PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids -  
 XX  
 XX PS Claim 101; Page 56; 338pp; English.  
 XX

CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells.  
 CC Note: the present sequence may have a phosphorothioate backbone.

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 265  
 AAF99734/C

ID AAF99734 standard; DNA; 18 BP.

XX AAF99734;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #850.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS  
 XX Synthetic.  
 OS  
 XX WO200122972-A2.

FN

XX PD 05-APR-2001.  
 XX PF 25-SEP-2000; 2000WO-US26383.  
 XX XX 25-SEP-1999; 99US-0156113.  
 PR 27-SEP-1999; 99US-0156135.  
 PR 23-AUG-2000; 2000US-0227436.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids -  
 XX Claim 101; Page 56; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-todent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells.  
 CC Note: the present sequence may have a phosphorothioate backbone.  
 XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 18 AAAAAAAAAAAAAAAAAA 2  
 RESULT 266  
 AAD17014  
 ID AAD17014 standard; DNA; 18 BP.  
 XX AAD17014;  
 AC 29-NOV-2001 (first entry)  
 DT Oligonucleotide A18-2PEG linker.  
 DE Scaffold protein; antibody mimic; fibronectin type III domain;  
 KW randomised loop; randomised beta-sheet; diagnostic purpose;  
 KW protein designing; ss.  
 XX Unidentified.  
 OS Key Location/Qualifiers  
 XX misc\_feature 18  
 FT /\*tag= a  
 FT /note= "Linked to (PEG)2CCPuromycin"  
 XX WO200164942-A1.  
 PN 07-SEP-2001.  
 XX 28-FEB-2001; 2001WO-US06414.

XX 29-FEB-2000; 2000US-0515260.  
 XX (PHYL-) PHYLOS INC.  
 XX Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2001-557782/62.  
 XX Fibronectin scaffold protein array for obtaining a protein/compound  
 PT which binds to a compound/protein, comprises a fibronectin type III  
 PT domain having a randomised loop, a randomised beta-sheet or their  
 PT combination -  
 XX Disclosure; Page 25; 67pp; English.  
 XX The present invention relates to an array of proteins (antibody mimics)  
 CC comprising a fibronectin type III domain having a randomised loop, a  
 CC randomised beta-sheet, or their combination, and has the capacity to  
 CC bind to a compound that is not bound by a corresponding naturally-  
 CC occurring fibronectin, immobilised onto a solid support. The antibody  
 CC mimics is useful for detecting a compound preferably a protein, in a  
 CC biological sample. It is also useful to detect one or more different  
 CC analytes simultaneously in a sample. Hence is useful for diagnostic  
 CC purposes. It is also useful for the purpose of designing proteins  
 CC capable of binding to virtually any compound of interest. The present  
 CC sequence is an oligonucleotide A18-2PEG linker used in an  
 CC exemplification of the invention.  
 XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 U; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 1 AAAAAAAAAAAAAAAAAA 17  
 RESULT 267  
 ABS78429/C  
 ID ABS78429 standard; DNA; 18 BP.  
 XX ABS78429;  
 AC 13-DEC-2002 (first entry)  
 DT Angiogenesis inhibitory oligonucleotide #913.  
 DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis;  
 KW psoriasis; diabetic retinopathy; retinopathy of prematurity;  
 KW macular degeneration; corneal graft rejection; neovascular glaucoma;  
 KW retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;  
 KW haemophilic joint; angiofibroma; wound granulation;  
 KW intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.  
 XX Synthetic.  
 OS WO200253141-A2.  
 PN 11-JUL-2002.  
 PD 14-DEC-2001; 2001WO-US48458.  
 XX 14-DEC-2000; 2000US-255534P.  
 PR (COLE-) COLEY PHARM GROUP INC.  
 PA Bratzler RL;  
 XX

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least

PT one antiangiogenic nucleic acid molecule to the subject -

XX PS

XX Claim 2; Page 35; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the

CC antiangiogenic nucleic acids, and instructions for administering them to

CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid

CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid

CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,

CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial

CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac

CC joints, angiofibroma, wound granulation, intestinal adhesions,

CC atherosclerosis, scleroderma and hypertrophic scars. The present

CC sequence is an antiangiogenic nucleic acid of the invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAA 2

RESULT 268

ABS78455/C

ID ABS78455 standard; DNA; 18 BP.

XX ABS78455;

XX 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #939.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

XX tumour metastasis; precancerous lesion; rheumatoid arthritis;

XX psoriasis; diabetic retinopathy; retinopathy of prematurity;

XX macular degeneration; corneal graft rejection; neovascular glaucoma;

XX retrolental fibroplasia; rubeosis; Osler-Webber Syndrome;

XX myocardial angiogenesis; plaque neovascularisation; telangiectasia;

XX haemophiliac joint; angiofibroma; wound granulation;

XX intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US48458.

XX 14-DEC-2000; 2000US-255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

XX WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least

PT one antiangiogenic nucleic acid molecule to the subject -

XX PS

XX Claim 2; Page 36; 276pp; English.

CC The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule.

CC Also included is a kit comprising a first container housing the

CC antiangiogenic nucleic acids, and instructions for administering them to

CC a subject having a condition characterised by unwanted angiogenesis.

CC The method is useful for inhibiting angiogenesis associated with solid

CC tumour growth, tumour metastasis, precancerous lesion, rheumatoid

CC arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity,

CC macular degeneration, corneal graft rejection, neovascular glaucoma,

CC retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial

CC angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac

CC joints, angiofibroma, wound granulation, intestinal adhesions,

CC atherosclerosis, scleroderma and hypertrophic scars. The present

CC sequence is an antiangiogenic nucleic acid of the invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100

DB 18 AAAAAAAAAAAAAA 2

RESULT 269

ABS53437/C

ID ABS53437 standard; DNA; 18 BP.

XX ABS53437;

XX 29-NOV-2002 (first entry)

XX Poly d(T) primer.

XX Terminal continuation; TC; ss; second strand cDNA synthesis;

XX primer; poly d(T).

XX Synthetic.

XX WO200265093-A2.

XX 22-AUG-2002.

XX 14-FEB-2002; 2002WO-US05713.

XX 14-FEB-2001; 2001US-268645P.

XX 14-FEB-2001; 2001US-268664P.

XX 18-JUL-2001; 2001US-306216P.

XX 07-NOV-2001; 2001US-344557P.

XX 07-NOV-2001; 2001US-348242P.

XX 09-NOV-2001; 2001US-350176P.

XX (BAY ) BAYLOR COLLEGE MEDICINE.

XX (REMB-) RES FOUND MENTAL HYGIENE INC.

XX Ginsberg SD, Che S;

XX WPI; 2002-567050/60.

XX Increasing efficiency of second strand cDNA synthesis using terminal

PT continuation model before performing further RNA amplification by RNA

PT transcription -

XX Example 7; Page 80; 128pp; English.

XX This invention relates to a novel method for increasing the efficiency

CC of second strand cDNA synthesis through a mechanism of terminal

CC continuation. In the method an RNA molecule is obtained and a first

CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added

CC comprising at least one riboguanine at the 3' end of the primer. A first





CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus  
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's  
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode  
CC the secreted factor polypeptides of the invention, and oligonucleotide  
CC probes and PCR primers.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | |  
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 272  
ABA93239/C  
ID ABA93239 standard; DNA; 18 BP.  
XX AC ABA93239;  
XX DT 18-APR-2002 (first entry)  
XX AD Adaptor oligonucleotide SEQ ID NO:2.

XX DE Detection; comparative detection; adaptor; ss.  
XX KW Synthetic.  
XX OS

XX PN JP2001333800-A.

XX PD 04-DEC-2001.

XX PF 30-MAY-2000; 2000JP-0160324.

XX PR 30-MAY-2000; 2000JP-0160324.

XX PA (UNIT-) UNITECH CO LTD.

XX DR WPI; 2002-135950/18.

XX PT Comparative detection of the amounts of RNA and DNA -

XX PS Disclosure; Page 9; 9pp; Japanese.

XX CC The present invention describes a method for the comparative detection  
XX of the amount of an RNA. The method comprises: (a) cDNAs obtained by  
XX transcribing respectively from at least two tissue RNAs are respectively  
XX fragmented by using a same restriction enzyme; (b) each different adaptor  
XX and a common adaptor are added to each of the cDNA fragments derived from  
XX the same or different tissues by the step (a); (c) the resultant adaptor-  
XX added cDNAs are mixed together; (d) an adaptor primer having the common  
XX sequence to said different adaptor and a gene-specific adaptor are used  
XX to amplify said adaptor-added cDNAs containing no region derived from  
XX polyadenylic acid of the mRNA before the addition of the adaptor among  
XX the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
XX cDNA amounts are measured between the tissues; (f) the RNA is detected  
XX from the measured result; (g) each different adaptor and a common adaptor  
XX are added to each of the genomic DNA fragments derived from a same or  
XX different individuals; (h) the resultant adaptor-added genomic DNAs are  
XX mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
XX an adaptor primer having the common sequence to the different adaptor and  
XX a sequence-specific adaptor; and (j) the ratios of the amplified amounts  
XX of the genomic DNAs are measured between the individuals. The method is  
XX used for the detection of the amounts of RNA and DNA. The present  
XX sequence represents an oligonucleotide which is used in the  
XX exemplification of the present invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | |  
DB 18 AAAAAAAAAAAAAAAAAA 2

RESULT 273  
ABL39401/C  
ID ABL39401 standard; DNA; 18 BP.

XX AC ABL39401;

XX DT 16-APR-2002 (first entry)

XX IM Immunostimulatory nucleic acid SEQ ID NO: 837.

XX AB Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
XX AN angiogenesis; metastasis; cytostatic; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified\_base 1..18

XX FT /tag= a

XX FT /mod\_base= OTHER

XX FT /note= "phosphorothioate backbone"

XX PN WO200197843-A2.

XX PD 27-DEC-2001.

XX PF 22-JUN-2001; 2001WO-US20154.

XX PR 22-JUN-2000; 2000US-213346P.

XX PA (IOWA ) UNIV IOWA RES FOUND.

XX PI Weiner G, Hartmann G;

XX DR WPI; 2002-154611/20.

XX PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
XX administering immunostimulatory nucleic acids that induce expression of  
XX cell surface antigens and antibodies to a subject having or at risk of  
XX developing cancer -

XX PS Disclosure; Page 308; 312pp; English.

XX CC The present invention relates to methods for treating or preventing  
XX cancer, involving administering to a subject having or at risk of  
XX developing cancer immunostimulatory nucleic acids that induce expression  
XX of cell surface antigens and antibodies. The methods are useful for  
XX treating or preventing cancer such as basal cell carcinoma, bladder  
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,  
XX breast cancer, cervical cancer, colon and rectum cancer, connective  
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,  
XX non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The  
XX present sequence is an immunostimulatory oligonucleotide described in  
XX the exemplification of the invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | |



CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 277

AAQ75549/c

ID AAQ75549 standard; DNA; 19 BP.

XX AC AAQ75549;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX FN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 other;

Query Match

Best Local Similarity 1.5%; Score 17; DB 1; Length 19;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 278

AAQ75550/c

ID AAQ75550 standard; DNA; 19 BP.

XX

AC AAQ75550;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX FN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA  
XX followed by digestion with restriction enzymes

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an  
CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
CC and a plural type of labelled reverse transcription primers  
CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
CC template for each reverse transcription primer; (b) digesting each of  
CC the prepared aggregates of the double-stranded cDNAs with restriction  
CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
CC separate lanes. The method can be used to analyse gene expression  
CC rapidly and easily.

XX Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 other;

Query Match

Best Local Similarity 1.5%; Score 17; DB 1; Length 19;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 279

AAQ75547/c

ID AAQ75547 standard; DNA; 19 BP.

XX AC AAQ75547;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX FN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-0112515.

XX PR 16-APR-1993; 93JP-0112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA  
 PT followed by digestion with restriction enzymes  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an  
 CC aggregate of double-stranded cDNAs by using an aggregate of mRNAs  
 CC and a plural type of labelled reverse transcription primers  
 CC (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the  
 CC template for each reverse transcription primer; (b) digesting each of  
 CC the prepared aggregates of the double-stranded cDNAs with restriction  
 CC enzyme and; (c) electrophoresing the digested aggregate of cDNAs in  
 CC separate lanes. The method can be used to analyse gene expression  
 CC rapidly and easily.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 280  
 AAT10757/c  
 ID AAT10757 standard; RNA; 19 BP.  
 AC AAT10757;  
 XX  
 DT 09-SEP-1996 (first entry)  
 XX  
 DE Oligonucleotide probe, T-2.  
 XX  
 KW Electronically self-addressable device; ED; electrode;  
 KW current source; attachment layer; permeable; counterion;  
 KW genetic typing; probe; detection; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "5'-amino terminus"  
 XX  
 PN WO9601836-A1.  
 XX  
 PD 25-JAN-1996.  
 XX  
 PF 05-JUL-1995; 95WO-US08570.  
 XX  
 PR 07-JUL-1994; 94US-0271882.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX  
 PI Evans GA, Heller MJ, Sosnowski RG, Tu E;  
 XX  
 DR WPI; 1996-097582/10.  
 XX  
 XX Electronically self-addressable device - used for electronic control  
 PT of, e.g. nucleic acid hybridisation  
 XX  
 PS Example 1; Page 61; 155pp; English.  
 XX  
 CC The sequences given in AAT10742-67 are synthetic oligonucleotides  
 CC which are used in the construction of the electronically self-  
 CC addressable device (ED) of the invention. The ED comprises a  
 CC substrate, an electrode or opt. a number of electrodes supported by

CC the substrate, a current source operatively connected to the  
 CC electrode and an attachment layer adjacent to the electrode which is  
 CC permeable to a counterion but not permeable to a molecule capable of  
 CC insulating or binding to the electrode. The attachment layer is  
 CC capable of attaching a macromolecule. The ED is used for genetic  
 CC typing and comprises a number of electronically addressable  
 CC locations each comprising an electrode, and a binding entity, such  
 CC as one of these probes, attached to each of the locations capable  
 CC of detecting the presence of a genetic sequence.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
 Query Match 1.5%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 Db 19 AAAAAAAAAAAAAAAAAA 3  
 RESULT 281  
 AAV07878/c  
 ID AAV07878 standard; DNA; 19 BP.  
 AC AAV07878;  
 XX  
 DT 14-DEC-1998 (first entry)  
 XX  
 DE Aminoxy-modified oligonucleotide.  
 XX  
 KW phosphorothioate; ras gene; malignant cell growth; aminoxy-modified;  
 KW nuclease resistance; reporter group; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 15..18  
 FT /\*tag= a  
 FT /note= "5-methyl, 2'-aminoxyethoxy-thymidine"  
 XX  
 PN WO9835978-A1.  
 XX  
 PD 20-AUG-1998.  
 XX  
 PF 13-FEB-1998; 98WO-US02405.  
 XX  
 PR 30-JAN-1998; 98US-0016520.  
 PR 14-FEB-1997; 97US-0037143.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Cook PD, Kawasaki AM, Manoharan M;  
 FI WPI; 1998-568232/48.  
 DR  
 XX New aminoxy-modified oligonucleotides - which can show improved  
 PT binding to complementary strands and improved resistance to nuclease  
 XX  
 PS Disclosure; Page 84; 131pp; English.  
 XX  
 CC The invention relates to aminoxy-modified(oligo)nucleotides or  
 CC nucleosides which are useful as therapeutics, diagnostics, and research  
 CC reagents. They may be used, e.g., for modulation of the ras gene and may  
 CC be able to modulate the process of transformation from normal to  
 CC malignant cell growth. They may be prepared using known methods.  
 CC Inclusion of the aminoxy moieties can improve binding of  
 CC oligonucleotides to complementary strands. The moieties can also provide  
 CC conjugation sites useful for conjugation of useful ligands (e.g. reporter  
 CC groups and groups for modifying uptake, distribution or other  
 CC pharmacodynamic properties) to oligonucleotides. The present sequence  
 CC represents an example of an aminoxy-modified oligonucleotide disclosed  
 CC in the specification.

XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 19 AAAAAAAAAAAAAAAAAA 3  
RESULT 282  
AAV06820/c  
ID AAV06820 standard; DNA; 19 BP.  
XX  
AC AAV06820;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE Oligonucleotide containing modified internucleotide linkage.  
XX  
KW oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16..18  
FT /\*tag= a  
FT /note= "these T residues are formed as part of a  
FT conventional phosphoramidite oligonucleotide synthesis  
FT process but using as the reactant a thymosine nucleoside  
FT having at the 3'-position a group of formula  
FT -CH2-P(OCH2CH2CN)-N(ipr)2"  
XX  
PN WO9747636-A2.  
XX  
PD 18-DEC-1997.  
XX  
PF 03-JUN-1997; 97WO-GB01490.  
XX  
PR 13-JUN-1996; 96GB-0012600.  
XX  
PA (NOVS) NOVARTIS AG.  
XX  
PI Altmann K, Collingwood SP, Douglas ME, Moser HE;  
XX  
DR WPI; 1998-052233/05.  
XX  
PT New tetrahydrofuran derivatives - useful in the synthesis of  
PT oligonucleotides  
XX  
PS Example 12; Page 29; 37pp; English.  
XX  
CC The invention relates, inter alia, to a method of preparing an  
CC oligonucleotide by coupling (1) a new nucleoside having a protected  
CC 5'-hydroxy group and at the 3'-position a group of formula  
CC -CH2-P(OR3)-NR4R5, with (2) a nucleoside or oligonucleotide having a  
CC free 5'-hydroxy group, to give (3) a precursor having an  
CC internucleoside linkage of formula -CH2-P(OR3)-O-; and converting this  
CC to a linkage of formula -CH2-P(OR3) (=X)-O- (where X = S or O).  
CC The present sequence is a specific example of an oligonucleotide so  
CC prepared.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 19 AAAAAAAAAAAAAAAAAA 3  
RESULT 283  
AAZ01358/c  
ID AAZ01358 standard; DNA; 19 BP.  
XX  
AC AAZ01358;  
XX  
DT 27-SEP-1999 (first entry)  
XX  
DE PCR primer for PGI biallelic marker 4-4-187.  
XX  
KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;  
KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;  
KW PSA; human; ss.  
XX  
OS Synthetic.  
XX  
FH Homo sapiens.  
XX  
PN WO9932644-A2.  
XX  
PD 01-JUL-1999.  
XX  
PF 22-DEC-1998; 98WO-IB02133.  
XX  
PR 09-SEP-1998; 98US-0099658.  
PR 22-DEC-1997; 97US-0996306.  
XX  
PA (GEST) GENSET.  
XX  
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;  
XX  
DR WPI; 1999-405178/34.  
XX  
PT Use of a prostate cancer associated gene and biallelic markers  
PT derived from it  
XX  
PS Claim 4; Page 374; 385pp; English.  
XX  
CC The invention relates to a mammalian PGI gene and protein, and a set of  
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are  
CC used in a hybridisation assay, a sequencing assay, or in an  
CC allele-specific amplification assay for determining the identity of a  
CC nucleotide at a PGI-related biallelic marker. The methods can be used to  
CC detect and to assess the risk of developing cancer or prostate cancer.  
CC Early-stage diagnosis of prostate cancer relies on prostate specific  
CC antigen (PSA) dosage. However, the effectiveness of this is limited due  
CC to its inability to discriminate between malignant and non-malignant  
CC affections of the organ. A need exists for both a reliable diagnostic  
CC procedure which would enable early-stage diagnosis, and for preventative  
CC and curative treatments of the disease. The PGI gene can be used for  
CC detection of prostate cancer, and the risk of developing it in the  
CC future, and can also be used to determine therapies for the disease.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 19 AAAAAAAAAAAAAAAAAA 3  
RESULT 284  
AAZ01927/c  
ID AAZ01927 standard; DNA; 19 BP.  
XX  
AC AAZ01927;  
XX  
DT 07-SEP-1999 (first entry)  
XX

```
DE Polynucleotide strand with amino groups.
XX
KW Enzyme-specific cleavable polynucleotide substrate;
KW quenched fluorescent moiety; biological assay; detection;
KW identification; microorganism; sterilization assurance; nuclease; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 7 /*tag= a
FT /*note= "amine-modified C6 derivative of
FT deoxythymidine (dtr)"
FT modified_base 9 /*tag= b
FT /*note= "amine-modified C6 derivative of
FT deoxythymidine (dtr)"
FT modified_base 11 /*tag= c
FT /*note= "amine-modified C6 derivative of
FT deoxythymidine (dtr)"
FT modified_base 13 /*tag= d
FT /*note= "amine-modified C6 derivative of
FT deoxythymidine (dtr)"
XX
PN WO9935288-A1.
XX
PD 15-JUL-1999.
XX
PF 20-AUG-1998; 98WO-US17311.
XX
PR 09-JAN-1998; 98US-0005260.
XX
PA (MINN ) MINNESOTA MINING & MFG CO.
XX
PI Mach PA, Wei A;
XX
DR WPI; 1999-419356/35.
XX
PT An enzyme-specific cleavable polynucleotide substrate bearing
PT quenched fluorescent moieties
XX
PS Example 2; Page 20; 34pp; English.
XX
CC The specification describes an enzyme-specific cleavable polynucleotide
CC substrate bearing quenched fluorescent moieties. The enzyme-specific
CC cleavable polynucleotide substrate is useful in biological assays for
CC detection and identification of microorganisms, sterilization assurance,
CC pharmaceutical discovery, enzyme assays, immunoassays and other
CC biological assays. The method provides a rapid and convenient approach
CC for detection and identification of microorganisms. It can be adapted to
CC sequence-dependent or sequence-independent tests. The invention provides
CC improved accuracy, faster detection, and overall lower cost in detection
CC and identification of microorganisms. The presence of nuclease is
CC measured more accurately and sensitively by red-shifting the emission
CC wavelength from far UV region (350-400 nm) to the 500-600 nm region of
CC the electromagnetic spectrum and reducing the effect of background signal
CC levels of intact reagents. The present sequence is used in the
CC course of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3
RESULT 285
```

```
ANX81316/c
ID AAX81316 standard; DNA; 19 BP.
XX
AC AAX81316;
XX
DT 20-AUG-1999 (first entry)
XX
DE 5' amino oligonucleotide probe T-2.
XX
KW Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control;
KW transport; attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1 /*tag= a
FT /*note= "amino group attached at 5' terminal"
XX
PN WO9929711-A1.
XX
PD 17-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US25475.
XX
PR 05-DEC-1997; 97US-0986065.
XX
PA (NANO-) NANODGEN INC.
XX
PI Butler WF, Edman CF, Heller MJ, Nerenberg MI, Sosnowski RG;
PI Tu E;
XX
DR WPI; 1999-385567/32.
XX
PT New microelectronic device designed to carry out and control
PT multi-step and multiplex molecular biological reactions in
PT microscopic format
XX
PS Example 1; Page 90; 179pp; English.
XX
CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the
CC ion-permeable permeation layer which overlies the electrode. This
CC permeation layer allows attachment of nucleic acids to permit
CC immobilization but also separates the attached oligonucleotides and
CC hybridized target DNA sequences from the highly reactive electrochemical
CC environment generated immediately at the electrode surface. The
CC microelectronic device is designed and fabricated to actively carry
CC out and control reactions such as nucleic acid hybridizations,
CC antibody/antigen reactions, sample preparation, diagnostics and
CC biopolymer synthesis. The device can electronically control the
CC transport and attachment of specific binding entities, such as nucleic
CC acids and polypeptides, to specific micro-locations. The device can
CC subsequently control the transport and reaction of analytes or reactants
CC at the addressed specific micro-locations. The device is able to
CC concentrate analytes and reactants, remove non-specifically bound
CC molecules, provide stringency control for DNA hybridization reactions
CC and improve the detection of analytes. The present sequence
CC represents a probe used to exemplify the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3
```

```
RESULT 286
AA88947/c
ID AAA88947 standard; DNA; 19 BP.
XX
XX AAA88947;
XX
XX
XX 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22110.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22110 contains a phosphodiester backbone and
XX has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments
XX to determine the effects of snake venom phosphodiesterase and
XX liver homogenate on the stability of oligonucleotides. Novel
XX oligonucleotides of the invention have both A- and B-form
XX conformational geometries. The A-form geometry modulates the binding
XX affinity and nuclease resistance of the oligonucleotide. The B-form
XX geometry allows the oligonucleotide to serve as substrate for
XX RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other
XX inflammatory skin conditions, skin cancers and viral, bacterial and
XX fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
XX
XX
XX RESULT 287
XX AA88948/c
XX ID AAA88948 standard; DNA; 19 BP.
XX
XX AC AAA88948;
XX
XX 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22111.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; DNA-RNA hybrid; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)uridine"
XX
XX misc_RNA 19
XX /tag= e
XX /label= RNA
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22111 contains a phosphodiester backbone and
XX has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments
XX to determine the effects of snake venom phosphodiesterase and
XX liver homogenate on the stability of oligonucleotides. Novel
XX oligonucleotides of the invention have both A- and B-form
XX conformational geometries. The A-form geometry modulates the binding
XX affinity and nuclease resistance of the oligonucleotide. The B-form
XX geometry allows the oligonucleotide to serve as substrate for
XX RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other
```



CC inflammatory skin conditions, skin cancers and viral, bacterial and  
 CC fungal infections, and in various diagnostic applications.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1100  
 |||||  
 Db 19 AAAAAAAAAAAAAA 3

RESULT 288

AAA88949/c

ID AAA88949 standard; DNA; 19 BP.

XX AC AAA88949;

XX DT 05-MAR-2001 (first entry)

XX DE Oligonucleotide ISIS 22112.

XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
 KW dermatological; cytostatic; virucide; antibacterial; fungicide;  
 KW therapy; diagnosis; ss.  
 XX Synthetic.

XX Key

FT modified\_base 16 Location/Qualifiers

FT /tag= a

FT /mod\_base= OTHER

FT /note= "3'-O-(2-methoxyethyl)thymidine"

FT modified\_base 17

FT /tag= b

FT /mod\_base= OTHER

FT /note= "3'-O-(2-methoxyethyl)thymidine"

FT modified\_base 18

FT /tag= c

FT /mod\_base= OTHER

FT /note= "3'-O-(2-methoxyethyl)thymidine"

FT modified\_base 19

FT /tag= d

FT /mod\_base= OTHER

FT /note= "3'-O-(2-methoxyethyl)thymidine"

FT modified\_base 1.19

FT /tag= e

FT /note= "phosphorothioate linkage"

XX WO200066609-A1.

XX PN

XX PD

XX PF

XX PR 03-MAY-2000; 2000WO-US11913.

XX PP 03-MAY-1999; 99US-0303586.

XX PS (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Mohan V;

XX PI WPI; 2000-672833/65.

XX DR

XX FT

XX New oligonucleotides containing sequences with A and B geometry, used  
 to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal  
 and bacterial infections, bind to single stranded RNA or DNA -  
 Example 54; Page 69; 132pp; English.

XX Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and

CC has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments

CC to determine the effects of snake venom phosphodiesterase and  
 CC liver homogenate on the stability of oligonucleotides. Novel  
 CC oligonucleotides of the invention have both A- and B-form  
 CC conformational geometry. The A-form geometry modulates the binding  
 CC affinity and nuclease resistance of the oligonucleotide. The B-form  
 CC geometry allows the oligonucleotide to serve as substrate for  
 CC RNase-H when bound to a target nucleic acid strand. The  
 CC oligonucleotides can be used to treat psoriasis and other  
 CC inflammatory skin conditions, skin cancers and viral, bacterial and  
 CC fungal infections, and in various diagnostic applications.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02; 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 AAAAAAAAAAAAAA 1100  
 |||||  
 Db 19 AAAAAAAAAAAAAA 3

RESULT 289

AAA88950/c

ID AAA88950 standard; DNA; 19 BP.

XX AC AAA88950;

XX DT 05-MAR-2001 (first entry)

XX DE Oligonucleotide ISIS 22113.

XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
 KW dermatological; cytostatic; virucide; antibacterial; fungicide;  
 KW therapy; diagnosis; DNA-RNA hybrid; ss.  
 XX Synthetic.

XX Key

FT modified\_base 16 Location/Qualifiers

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-O-(2-methoxyethyl)thymidine"

FT modified\_base 17

FT /tag= b

FT /mod\_base= OTHER

FT /note= "2'-O-(2-methoxyethyl)thymidine"

FT modified\_base 18

FT /tag= c

FT /mod\_base= OTHER

FT /note= "2'-O-(2-methoxyethyl)thymidine"

FT modified\_base 19

FT /tag= d

FT /mod\_base= OTHER

FT /note= "2'-O-(2-methoxyethyl)uridine"

FT misc\_RNA 19

FT /tag= e

FT /label= RNA

FT modified\_base 1.19

FT /tag= f

FT /note= "phosphorothioate linkage"

XX WO200066609-A1.

XX PN

XX PD

XX PF 09-NOV-2000.

XX PR 03-MAY-2000; 2000WO-US11913.

XX PP 03-MAY-1999; 99US-0303586.

XX PS (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Mohan V;

XX PI PI

```
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and
XX has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments
XX to determine the effects of snake venom phosphodiesterase and
XX liver homogenate on the stability of oligonucleotides. Novel
XX oligonucleotides of the invention have both A- and B-form
XX conformational geometry. The A-form geometry modulates the binding
XX affinity and nuclease resistance of the oligonucleotide. The B-form
XX geometry allows the oligonucleotide to serve as substrate for
XX RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other
XX inflammatory skin conditions, skin cancers and viral, bacterial and
XX fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 290
XX AAA88951/c
XX ID AAA88951 standard; DNA; 19 BP.
XX
XX AC AAA88951;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22114.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
XX /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 1.15
XX /tag= e
XX /note= "phosphorothioate linkage"
XX
XX PN W0200066609-A1.
XX
XX PD 09-NOV-2000.
```

```
XX 03-MAY-2000; 2000WO-US11913.
XX
XX 03-MAY-1999; 99US-0303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used
XX to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal
XX and bacterial infections, bind to single stranded RNA or DNA -
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
XX phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry.
XX It was used in experiments to determine the effects of snake venom
XX phosphodiesterase and liver homogenate on the stability of
XX oligonucleotides. Novel oligonucleotides of the invention have
XX both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to
XX serve as substrate for RNase-H when bound to a target nucleic acid
XX strand. The oligonucleotides can be used to treat psoriasis and other
XX inflammatory skin conditions, skin cancers and viral, bacterial and
XX fungal infections, and in various diagnostic applications.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 291
XX AAA88952/c
XX ID AAA88952 standard; DNA; 19 BP.
XX
XX AC AAA88952;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22115.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide;
XX therapy; diagnosis; DNA-RNA hybrid; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 16
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-(2-methoxyethyl)thymidine"
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
```



OS Synthetic.  
PN US6127124-A.  
XX  
PD 03-OCT-2000.  
XX  
PF 20-JAN-1999; 99US-0234237.  
XX  
PR 20-JAN-1999; 99US-0234237.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Leeds JM, Cummins LJ;  
XX  
DR WPI; 2000-637737/61.  
XX  
XX Determining the nuclease stability and relative binding affinity of an  
PT oligomeric compound comprises capillary gel electrophoresis using  
PT laser-induced fluorescence -  
XX  
PS Example 3; column 19-20; 14pp; English.  
XX  
CC The present invention is concerned with methods of determining the  
CC nuclease stability of oligomeric compounds using capillary-gel  
CC electrophoresis and laser-induced fluorescence. The methods are useful in  
CC the polymerase chain reaction (PCR), molecular cloning and disease  
CC diagnosis and treatment. The present sequence was used in a demonstration  
CC of the methods of the invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
XX  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 19 AAAAAAAAAAAAAAAAAA 3  
RESULT 294  
AAC62454/c  
ID AAC62454 standard; DNA; 19 BP.  
XX  
AC AAC62454;  
XX  
DT 07-FEB-2001 (first entry)  
XX  
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.  
XX  
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;  
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;  
KW nucleic acid purification; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 10  
FT /\*tag= a  
XX  
PN WO200058329-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 28-MAR-2000; 2000WO-GH01190.  
XX  
PR 29-MAR-1999; 99GB-0007245.  
XX  
PA (GOLD/) GOLDSBOROUGH A.  
XX  
DR WPI; 2000-664908/64.  
XX  
PT Detaching nucleic acid molecule comprising unconventional nucleotide

PT incorporated at predetermined site from a solid support involves  
PT cleaving the nucleic acid molecule at the site of unconventional  
XX nucleotide -  
PS Example 3; Page 34; 47pp; English.  
XX  
CC The present invention is concerned with the cleavage of nucleic acids  
CC from solid supports. This is carried out by adding a non-conventional  
CC nucleotide into the nucleic acid attached to the support, so that it is  
CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
CC released. This is useful in many molecular biological procedures such as  
CC sequencing, in vitro amplifications, cDNA and template preparation,  
CC DNA-based assays, mutagenesis procedures, nucleic acid purification and  
CC affinity chromatography. The present sequence is an oligonucleotide used  
CC in assays to demonstrate the methods of the invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;  
XX  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
DB 19 AAAAAAAAAAAAAAAAAA 3  
RESULT 295  
AAA71630/c  
ID AAA71630 standard; DNA; 19 BP.  
XX  
AC AAA71630;  
XX  
DT 14-DEC-2000 (first entry)  
XX  
DE Phosphorothioate 20-mer primer DNA #1.  
XX  
KW Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkage"  
XX  
PN EP1028124-A2.  
XX  
PD 16-AUG-2000.  
XX  
PF 06-SEP-1999; 99EP-0307066.  
XX  
PR 04-FEB-1999; 99US-0118564.  
PR 09-APR-1999; 99US-0288679.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL, Guzaev A;  
PI WPI; 2000-500332/45.  
XX  
DR Novel method for the production of oligomers with reduced exocyclic  
XX adducts comprises treatment with deprotecting and cleaving reagents -  
PT  
PS Example 2; Page 17; 33pp; English.  
XX  
CC This invention describes a novel synthetic method (M) comprising: (a)  
CC providing a sample comprising a number of oligomers of formula (1); (b)  
CC contacting the sample with a deprotecting agent to remove R t groups from  
CC the oligomers; and (c) reacting the oligomer with a cleaving reagent.  
CC The method is used to produce oligomeric compounds for use in antisense  
CC and oligonucleotide therapies. The method enables the synthesis of

CC oligomers with a reduction in the number acrylonitrile groups attached.  
CC Acrylonitrile has been demonstrated to be a potent carcinogen in rats.  
CC This sequence represents a phosphorothioate 20-mer primer which is used  
CC in the method of the invention.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100  
|||||  
Db 19 AAAAAAAAAAAAAAAA 3

RESULT 296  
AA06839/C  
ID AAA06839 standard; DNA; 19 BP.  
XX  
AC AAA06839;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Modified T-containing oligonucleotide, SEQ ID NO:14.  
XX  
KW Modified nucleoside; aminoxy group;  
KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;  
KW hybridisation; binding affinity; ss.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FH modified\_base 16..19  
FT /tag= a  
FT /note= "These nucleotides are substituted with 2'-O-(2-[N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group"

XX WO200008042-A1.  
XX 17-FEB-2000.  
XX  
XX 09-AUG-1999; 99WO-US17988.  
XX  
XX 07-AUG-1998; 98US-0130973.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Manoharan M, Cook PD, Prakash TP, Kawasaki AM;  
XX WPI; 2000-224020/19.

XX Aminoxy-modified nucleosides and oligonucleotides useful in  
XX diagnostic, therapeutic and research reagents and for modulating the  
XX expression of protein in organisms -  
XX  
XX Example 99; Page 120; 195pp; English.

XX The invention relates to aminoxy-modified nucleosides and  
XX oligonucleotides and to oligonucleotides that elicit RNase H for cleavage  
XX in a complementary nucleic acid strand. It also relates to  
XX oligonucleotides wherein at least some of the nucleotides are  
XX functionalised to be nuclease resistant, at least some of the nucleotides  
XX include a substituent that potentiates hybridisation of the  
XX oligonucleotide to a complementary strand, and at least some of the  
XX nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The  
XX inclusion of one or more aminoxy moieties in such oligonucleotides  
XX provides for improved binding of such oligonucleotides to a complementary  
XX strand. The oligonucleotides of the invention are used as diagnostic,  
XX therapeutic or research reagents, and can be used to modulate gene  
XX expression in organisms. The oligonucleotides containing the modified  
XX nucleosides have increased nuclease resistance and increased binding

CC affinity to a complementary strand. The present sequence represents  
CC an oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group.  
XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAA 1100  
|||||  
Db 19 AAAAAAAAAAAAAAAA 3

RESULT 297  
AAZ61390/C  
ID AAZ61390 standard; DNA; 19 BP.  
XX  
AC AAZ61390;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Uniform phosphodiester oligonucleotide.  
XX  
KW Oligomeric compound; 2'-O-modified ribosyl nucleoside;  
KW 3' endo geometry; nuclease resistance; phosphodiester; ss.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FH modified\_base 16  
FT /tag= a  
FT /note= "2'-modified T"  
FT modified\_base 17  
FT /tag= b  
FT /note= "2'-modified T"  
FT modified\_base 18  
FT /tag= c  
FT /note= "2'-modified T"  
FT modified\_base 19  
FT /tag= d  
FT /note= "2'-modified T"

XX WO200008044-A1.  
XX 17-FEB-2000.  
XX  
XX 06-AUG-1999; 99WO-US17895.  
XX  
XX 07-AUG-1998; 98US-0130566.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Manoharan M, Cook PD;  
XX WPI; 2000-205668/18.

XX Novel 2'-O-aminoethylloxethyl modified nucleosides and oligonucleotides  
XX used in diagnostic, therapeutic and research reagents -  
XX  
XX Disclosure; Page 44; 60pp; English.

XX The present sequence represents an uniform phosphodiester  
XX oligonucleotide. The specification describes oligomeric compounds  
XX containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified  
XX nucleosides include ring structures that position the sugar moiety of  
XX the nucleosides preferentially in 3' endo geometries. The modified  
XX oligomeric compounds have increased binding affinity and increased  
XX nuclease resistance. The oligomeric compounds can be used in diagnostic,  
XX therapeutic and research reagents.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | | | | |  
DB 19 AAAAAAAAAAAAAA 3

RESULT 298  
AAZ61404/C  
ID AAZ61404 standard; DNA; 19 BP.

XX AC AAZ61404;  
XX DT 19-JUN-2000 (first entry)  
XX DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.  
XX KW Oligomeric compound; 2'-O-modified ribosyl nucleoside;  
XX KW 3' endo geometry; nuclease resistance; phosphorothioate; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT misc\_feature 1..19  
XX FT /\*tag= a  
XX FT /note= "nucleosides linked by phosphodiester  
XX FT linkages"  
XX FT modified\_base 16..19  
XX FT /\*tag= b  
XX FT /note= "2'-O-[2-N-dimethylaminoethyl]oxyethyl-5-  
XX FT methyl uridine"  
XX FN WO200008044-A1.  
XX PD 17-FEB-2000.  
XX PF 06-AUG-1999; 99WO-US17895.  
XX PR 07-AUG-1998; 98US-0130566.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Manoharan M, Cook PD;  
XX DR WPI; 2000-205668/18.  
XX PT Novel 2'-O-aminothioxyethyl modified nucleosides and oligonucleotides  
XX used in diagnostic, therapeutic and research reagents -  
XX PS Disclosure; Page 51; 60pp; English.  
XX CC The present sequence represents an oligomeric compound containing  
XX CC 2'-O-modified ribosyl nucleosides. The oligomeric compound contains  
XX CC phosphodiester linkages. The 2'-O-modified nucleosides include  
XX CC ring structures that position the sugar moiety of the nucleosides  
XX CC preferentially in 3' endo geometries. The modified oligomeric  
XX CC compounds have increased binding affinity and increased  
XX CC nuclease resistance. The oligomeric compounds can be used in  
XX CC diagnostic, therapeutic and research reagents.  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | | | | |  
DB 19 AAAAAAAAAAAAAA 3

RESULT 299  
AAZ95240/C  
ID AAZ95240 standard; DNA; 19 BP.

XX AC AAZ95240;  
XX DT 05-JUN-2000 (first entry)  
XX DE Modified oligonucleotide #3 ISIS # 22110.  
XX KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;  
XX KW research reagent; therapeutic; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT misc\_feature 1..15  
XX FT /\*tag= a  
XX FT /note= "Phosphorothioate internucleotide linkage"  
XX FT misc\_feature 15..19  
XX FT /\*tag= d  
XX FT /note= "Optionally all phosphorothioate internucleotide  
XX FT linkages"  
XX FT modified\_base 16..19  
XX FT /\*tag= c  
XX FT /mod\_base= OTHER  
XX FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all  
XX FT 2'-O-(2-methoxyethyl)"  
XX PN WO200004189-A1.  
XX PD 27-JAN-2000.  
XX PF 13-JUL-1999; 99WO-US15886.  
XX PR 14-JUL-1998; 98US-0115043.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Manoharan M, Cook PD;  
XX DR WPI; 2000-182445/16.  
XX PT Novel modified oligonucleotides, useful in antisense methodologies,  
XX PT diagnostics, therapeutics and as research reagents -  
XX PS Example 54; Page 59; 75pp; English.  
XX CC This sequence represents a modified oligonucleotide used in the course of  
XX CC the invention. The invention relates to oligonucleotides comprising  
XX CC nucleotides covalently linked together by internucleotide linkages where  
XX CC at least 1 nucleotide is linked to adjacent nucleotide by a  
XX CC 2',5'-internucleotide linkage and bears a 3'-substituent. The  
XX CC oligonucleotides can be used in gene therapy and are also useful in  
XX CC antisense methodologies, diagnostics, therapeutics and as research  
XX CC reagents.  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAA 1100  
| | | | | | | | | | | | | | | | | | | | |  
DB 19 AAAAAAAAAAAAAA 3

RESULT 300  
AAZ95241/C  
ID AAZ95241 standard; DNA; 19 BP.

XX

```
AC AAZ95241;
XX
DT 05-JUN-2000 (first entry)
XX
DE Modified oligonucleotide #3 ISIS # 22111.
XX
KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
XX research reagent; therapeutic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15..19
FT /tag= d
FT /note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT modified_base 16..19
FT /tag= c
FT /mod_base= OTHER
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all
FT 2'-O-(2-methoxyethyl)"
FT misc_RNA 19
FT /tag= d
XX
XX WO200004189-A1.
XX
XX 27-JAN-2000.
XX
XX 13-JUL-1999; 99WO-US15886.
XX
XX 14-JUL-1998; 98US-0115043.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX
XX WPI; 2000-182445/16.
XX
XX Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents -
XX
XX Example 54; Page 59; 75pp; English.
XX
XX This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a
XX 2',5'-internucleotide linkage and bears a 3'-substituent. The
XX oligonucleotides can be used in gene therapy and are also useful in
XX antisense methodologies, diagnostics, therapeutics and as research
XX reagents.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 301
AAH46460/c
ID AAH46460 standard; DNA; 19 BP.
XX
XX AAH46460;
XX
XX 14-SEP-2001 (first entry)
XX
```

```
XX Oligonucleotide #8.
XX
XX Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..19
XX /tag= a
XX /mod_base= "OTHER"
XX /note= "All bases are phosphorothioate"
XX modified_base 1
XX /tag= b
XX /mod_base= "OTHER"
XX /note= "Modified with 2'-O-methoxyethyl"
XX
XX US6242591-B1.
XX
XX 05-JUN-2001.
XX
XX 11-JAN-2000; 2000US-0481486.
XX
XX 15-OCT-1997; 97US-0950779.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cole DL, Ravikumar VT, Cheruvallath ZS;
XX WPI; 2001-407218/43.
XX
XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the
XX 5'-hydroxyl of a nucleic acid having a nucleoside with a 2'
XX modification -
XX
XX Example 12; Column 7; 7pp; English.
XX
XX The present invention relates to a method for preparing phosphorothioate
XX oligonucleotides having at least one nucleoside with a 2' modification.
XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX group having at least one nucleoside with a 2' modification in an
XX acetonitrile. The present sequence was used to illustrate the method of
XX the present invention. The method is useful for synthesizing sulphurised
XX 2' substituted phosphorothioate oligonucleotides, which may be used in
XX molecular biological research, in applications such as anti-viral
XX therapy, and for determining the stereochemical pathways of certain
XX enzymes which recognise nucleic acids.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 302
AAH25737/c
ID AAH25737 standard; DNA; 19 BP.
XX
XX AAH25737;
XX
XX 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #4.
XX
XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
XX gene therapy; primer; phosphorothioate backbone; ss.
XX
```

```

OS XX Synthetic.
PH Key Location/Qualifiers
FT modified_base 1..19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "optionally 3'-O-(2-methoxyethyl) or
FT 2'-O-(2-methoxyethyl)"
XX WO200123613-A1.
PN 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26729.
XX 30-SEP-1999; 99US-0409926.
XX (ISIS-) ISIS PHARM INC.
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies
XX
XX Example 54; Page 88; 178pp; English.
XX
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase H1 (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 303
AAH25738/c
ID AAH25738 standard; DNA; 19 BP.
XX
XX AAH25738;
XX
XX 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #5.
XX
XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
XX gene therapy; primer; phosphorothioate backbone; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "optionally 3'-O-(2-methoxyethyl) or
FT 2'-O-(2-methoxyethyl)"
XX WO200123613-A1.
PN 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26729.
XX 30-SEP-1999; 99US-0409926.
XX (ISIS-) ISIS PHARM INC.
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies
XX
XX Example 54; Page 88; 178pp; English.
XX
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase H1 (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 303
AAH25738/c
ID AAH25738 standard; DNA; 19 BP.
XX
XX AAH25738;
XX
XX 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #5.
XX
XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
XX gene therapy; primer; phosphorothioate backbone; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "optionally 3'-O-(2-methoxyethyl) or
FT 2'-O-(2-methoxyethyl)"
XX WO200123613-A1.
PN 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26729.
XX 30-SEP-1999; 99US-0409926.
XX (ISIS-) ISIS PHARM INC.
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies
XX
XX Example 54; Page 88; 178pp; English.
XX
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase H1 (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 304
AAF31458/c
ID AAF31458 standard; DNA; 19 BP.
XX
XX AAF31458;
XX
XX 10-APR-2001 (first entry)
XX
XX Oligonucleotide ISIS 109989.
XX
XX Gene expression; gene therapy; diagnosis; ss.
XX
XX Synthetic.
XX
XX WO200102423-A2.
XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US18609.
XX
XX 07-JUL-1999; 99US-0349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2001-138119/14.

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FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "optionally 3'-O-(2-methoxyethyl) or
FT 2'-O-(2-methoxyethyl)"
FT 19
FT FT /*tag= c
XX WO200123613-A1.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26729.
XX 30-SEP-1999; 99US-0409926.
XX (ISIS-) ISIS PHARM INC.
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies
XX
XX Example 54; Page 88; 178pp; English.
XX
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase H1 (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
XX
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 304
AAF31458/c
ID AAF31458 standard; DNA; 19 BP.
XX
XX AAF31458;
XX
XX 10-APR-2001 (first entry)
XX
XX Oligonucleotide ISIS 109989.
XX
XX Gene expression; gene therapy; diagnosis; ss.
XX
XX Synthetic.
XX
XX WO200102423-A2.
XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US18609.
XX
XX 07-JUL-1999; 99US-0349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2001-138119/14.

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```
XX PT Guanidinium functionalized oligomers prepared from corresponding
PT monomer units, are hybridizable with a specific RNA or DNA sequence,
PT useful for diagnostic and therapeutic purposes -
XX PS Example 26; Page 54; 108pp; English.
XX CC The present invention relates to nucleotide oligomers comprising
CC monomer units. Oligomers modulate gene expression when hybridized by a
CC single- or double-stranded nucleic acid. They are useful for
CC gene therapy, diagnostic and investigative purposes.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
RESULT 305
AAF31564/c
ID AAF31564 standard; DNA; 19 BP.
XX AC AAF31564;
XX DT 09-APR-2001 (first entry)
XX DE ISIS sequence 32327.
XX KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate;
XX KW AIDS; atherosclerosis; ss.
XX OS Synthetic.
XX PN WO200102419-A1.
XX PR 11-JAN-2001.
XX PF 05-JUL-2000; 2000WO-US40304.
XX PR 07-JUL-1999; 99US-0349033.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cook PD, Manoharan M, Maier M, An H;
XX DR WPI; 2001-138117/14.
XX CC New oligomers for use as research reagent, for treating disease caused
XX PT by undesired production of proteins, and for diagnosing and treating
XX PT AIDS, atherosclerosis -
XX PS Example 46; Page 74; 110pp; English.
XX CC The present invention relates to C3' methylene hydrogen phosphate
XX CC oligomers. The oligomers may be used as research reagents, for
XX CC treating disease caused by undesired production of proteins
XX CC and for diagnosing and treating AIDS and atherosclerosis.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
```

```
RESULT 306
AAC83664/c
ID AAC83664 standard; DNA; 19 BP.
XX AC AAC83664;
XX DT 02-MAR-2001 (first entry)
XX DE 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
XX KW 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
XX KW tumour formation; cancer; protein kinase C expression;
XX KW cell adhesion molecule expression; multidrug resistance; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
XX PN US6147200-A.
XX PD 14-NOV-2000.
XX PF 19-AUG-1999; 99US-0378568.
XX PR 19-AUG-1999; 99US-0378568.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD, Fraser AS, Prakash TP, Kawasaki AM;
XX DR WPI; 2001-069824/08.
XX CC New 2'-O-acetamido modified nucleosides (I) used to produce
XX PT oligonucleotides which have enhanced nuclease resistance and superior
XX PT hybridization properties than prior art.
XX PS Example 12; Column 28; 29pp; English.
XX CC The present sequence is a modified oligonucleotide.
XX CC 2'-O-acetamido-modified nucleosides were used to produce oligonucleotides
XX CC which have enhanced nuclease resistance and superior hybridisation
XX CC properties than prior art. The oligomeric compounds are useful for
XX CC identification or quantification of ribonucleic acid and deoxyribonucleic
XX CC acid or for modulating the activity of an ribonucleic acid or
XX CC deoxyribonucleic acid molecule. They have a modified nucleoside monomer
XX CC and are specifically hybridisable with a preselected nucleotide sequence
XX CC of a single-stranded or double-stranded target deoxyribonucleic acid or
XX CC ribonucleic acid molecule. The oligomers are further useful in a
XX CC ras-luciferase fusion system using ras-luciferase transactivation. They
XX CC are useful in abnormal cell proliferation and tumour formation and
XX CC modulation of expression of protein kinase C and cell adhesion
XX CC molecules such as ICAM. They are useful in the modulation of proteins
XX CC related to multidrug resistance and viral genomic nucleic acids such as
XX CC HIV, herpes viruses, Epstein-Barr virus, cytomegalovirus, papillomavirus,
XX CC hepatitis C virus and influenza virus.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
```

RESULT 307

```

AAD41998/c
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #1 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 308
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
XX AAD41999;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 308
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
XX AAD41999;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a

```

```

KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxyethoxy
XX (2'-DMAOE) residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
SQ
Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 309
AAD42000/c
ID AAD42000 standard; DNA; 19 BP.
XX
XX AAD42000;
XX
DT 04-NOV-2002 (first entry)
DE
DE Oligonucleotide #3 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a

```

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FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy (MOE) residues"
FN
XX
XX US6403779-B1.
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1084 AAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAA 3
XX
XX RESULT 310
XX AAD42001/c
XX ID AAD42001 standard; DNA; 19 BP.
XX
XX AC AAD42001;
XX
XX DT 04-NOV-2002 (first entry)
XX
XX DE Oligonucleotide #4 used to illustrate the method of the invention.
XX
XX KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside

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PR 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX
XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1084 AAAAAAAAAAAAAA 1100
XX | | | | | | | | | | | | | | | |
XX Db 19 AAAAAAAAAAAAAA 3
XX
XX RESULT 311
XX AAD42002/c
XX ID AAD42002 standard; DNA; 19 BP.
XX
XX AC AAD42002;
XX
XX DT 04-NOV-2002 (first entry)
XX
XX DE Oligonucleotide #5 used to illustrate the method of the invention.
XX
XX KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "5-methyl, 2'-methoxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-0227782.
XX
XX 08-JAN-1999; 99US-0227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside

```

PT used for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester -  
PS Example 46; Column 33; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 19 AAAAAAAAAAAAAAAAAA 3  
  
RESULT 312  
AAD42003/c  
ID AAD42003 standard; DNA; 19 BP.  
XX  
AC AAD42003;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #6 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16..19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-O-propyl residues"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-0227782.  
XX  
PR 08-JAN-1999; 99US-0227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside  
PT used for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester -  
XX  
PS Example 46; Column 33; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention.

CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
  
Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1084 AAAAAAAAAAAAAAAAAA 1100  
Db 19 AAAAAAAAAAAAAAAAAA 3  
  
RESULT 313  
AAD42004/c  
ID AAD42004 standard; DNA; 19 BP.  
XX  
AC AAD42004;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #7 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-dimethylaminoxyethyl residue"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-0227782.  
XX  
PR 08-JAN-1999; 99US-0227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside  
PT used for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester -  
XX  
PS Example 46; Column 33; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

```

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 314
AAD42005/c
ID AAD42005 standard; DNA; 19 BP.
XX
AC AAD42005;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #8 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 18
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "5-methyl, 2'-methoxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-0227782.
XX
PR 08-JAN-1999; 99US-0227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 33; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

```

```

RESULT 315
AAD42009/c
ID AAD42009 standard; DNA; 19 BP.
XX
AC AAD42009;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-0227782.
XX
PR 08-JAN-1999; 99US-0227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
XX used for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester -
XX
XX Example 46; Column 35; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match      1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 316
AAD42010/c
ID AAD42010 standard; DNA; 19 BP.
XX
AC AAD42010;
XX
DT 04-NOV-2002 (first entry)
XX

```

Oligonucleotide #13 used to illustrate the method of the invention.

Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.

Unidentified.

Key Location/Qualifiers  
modified\_base 16..19  
/tag= a  
/mod\_base= OTHER  
modified\_base 18..19  
/tag= b  
/mod\_base= OTHER  
/note= "Phosphorothioate backbone"

US6403779-B1.

11-JUN-2002.

08-JAN-1999; 99US-0227782.

08-JAN-1999; 99US-0227782.

(ISIS-) ISIS PHARM INC.

Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
WPI; 2002-546338/58.

Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -

Example 46; Column 35; 24pp; English.

The present invention relates to a novel method of selective alkylation of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
|||||  
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 317  
AAD42011/c  
ID AAD42011 standard; DNA; 19 BP.

AC AAD42011;

04-NOV-2002 (first entry)

Oligonucleotide #14 used to illustrate the method of the invention.

Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.

Unidentified.

Key Location/Qualifiers  
modified\_base 16..19  
/tag= a  
/mod\_base= OTHER  
/note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"

US6403779-B1.

11-JUN-2002.

08-JAN-1999; 99US-0227782.

08-JAN-1999; 99US-0227782.

(ISIS-) ISIS PHARM INC.

Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
WPI; 2002-546338/58.

Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester -

Example 46; Column 37; 24pp; English.

The present invention relates to a novel method of selective alkylation of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention.

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100  
|||||  
Db 19 AAAAAAAAAAAAAAAAAA 3

RESULT 318  
AAD42020/c  
ID AAD42020 standard; DNA; 19 BP.

AC AAD42020;

04-NOV-2002 (first entry)

Oligonucleotide #23 used to illustrate the method of the invention.

Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.

Unidentified.

Key Location/Qualifiers  
modified\_base 15..18  
/tag= a  
/mod\_base= OTHER  
/note= "2'-O-methyleneiminoxyethyl thymidine"

US6403779-B1.

```

XX PD 11-JUN-2002.
XX PF 08-JAN-1999; 99US-0227782.
XX PR 08-JAN-1999; 99US-0227782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX ALkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside
PT used for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester -
XX Example 46; Column 41; 24pp; English.
XX PS The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 319
ABK94423/C
ID ABK94423 standard; DNA; 19 BP.
XX AC ABK94423;
XX DT 27-AUG-2002 (first entry)
XX DE Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
XX hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
XX breast and ovarian cancer susceptibility gene; TGDS; human;
XX two-dimensional DNA electrophoresis; tumour suppressor gene;
XX breast cancer; ovarian cancer; tumour.
XX OS Homo sapiens.
XX WO200236819-A1.
XX 10-MAY-2002.
XX 06-NOV-2000; 2000WO-IB01607.
XX 06-NOV-2000; 2000WO-IB01607.
XX (SCSC-) ACAD APPLIED SCI.
XX Viig J;
XX WPI; 2002-471507/50.
XX

PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce
PT a characteristic spot pattern for a specific mutation in either the
PT BRCA1 or the hMLH1 gene -
XX Claim 6; Page 21; 57pp; English.
XX The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
XX comprising subjecting a set of amplification products to two-dimensional
XX DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
XX specific mutation in either the BRCA1 or the hMLH1 gene.
XX Also included are test kits for enabling BRCA1 or hMLH1 gene testing
XX comprising short PCR primers given in the specification, mixed in 20 mM
XX of Tris-HCl, 50 mM KCl, 25 micro M of dNTP, and 5 % formamide.
XX The method is useful for detecting mutations in the BRCA1 (breast
XX and ovarian cancer susceptibility gene, a tumour suppressor gene) and
XX hMLH1 gene (a DNA mismatch repair gene). The present sequence is a
XX PCR primer specific to hMLH1 used in the method of the invention.
XX SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1080 TATTAATAAAAAAAAAA 1096
DB 17 TATTAATAAAAAAAAAA 1

RESULT 320
ABL51520/C
ID ABL51520 standard; DNA; 19 BP.
XX AC ABL51520;
XX DT 01-JUL-2002 (first entry)
XX DE Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
XX Tailing reaction; tailed primer; primer; probe; identification;
XX detection; linear amplification scheme; chain extending enzyme;
XX telomerase; ss.
XX OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /*mod_base= OTHER
XX /*note= "biotinylated"
XX misc_RNA 19 /*tag= b
XX US2002031776-A1.
XX 14-MAR-2002.
XX 26-JUL-2001; 2001US-0917138.
XX 28-MAY-1999; 99US-136545P.
XX 25-MAY-2000; 2000US-0580358.
XX (TULL/) TULLIS R H.
XX (STRE/) STREIFEL J A.
XX Tullis RH, Streifel JA;
XX WPI; 2002-361176/39.
XX Identifying and detecting nucleic acids, particularly DNA hybridization
XX probes, involves employing chain extending enzymes (e.g. telomerase) to
XX elongate probes to render them readily detectable -

```

```
XX PS
XX CC Example 1; Page 5; 10pp; English.
XX CC
XX CC The present invention describes a method for detecting a nucleic acid
XX CC probe, which comprises using chain extending enzymes to elongate probes.
XX CC The method comprises: (a) treating the sample with a chain terminating
XX CC reagent to prevent polynucleotide chain growth from the nucleic acid in
XX CC the sample; (b) contacting the sample with the probe containing a
XX CC terminus capable of elongation by a chain extending enzyme, where the
XX CC probe hybridises to the nucleic acid in the sample; (c) contacting the
XX CC sample with a chain extending enzyme and its substrates, which elongates
XX CC the probe; and (d) detecting the elongated hybridised probe. Also
XX CC described is a method comprising: (a) treating nucleic acid molecules or
XX CC modified nucleic acids in a sample with a reagent or reagents that render
XX CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
XX CC (b) hybridising the treated molecules with a nucleic acid probe that
XX CC includes an extendable terminus, under conditions where hybrids form;
XX CC and (c) treating any hybrids formed with a non-template dependent chain
XX CC elongating enzyme and its substrates, where any hybridised probe is
XX CC extended. The method is useful for identifying and detecting nucleic
XX CC acids, particularly DNA hybridisation probes. The present sequence
XX CC represents a tailing reaction exemplary primer, which is used in an
XX CC example from the present invention.
XX CC Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 other;
XX SQ Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 19 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 321
XX ABL51521
XX ID ABL51521 standard; DNA; 19 BP.
XX AC ABL51521;
XX DT 01-JUL-2002 (first entry)
XX DE Tailing reaction related exemplary primer dA18U SEQ ID NO:2.
XX KW Tailing reaction; tailed primer; primer; probe; identification;
XX KW detection; linear amplification scheme; chain extending enzyme;
XX KW telomerase; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_RNA 19
XX FT /*tag= a
XX PN US2002031776-A1.
XX XX
XX PD 14-MAR-2002.
XX XX
XX PF 26-JUL-2001; 2001US-0917138.
XX PR 28-MAY-1999; 99US-136545P.
XX PR 25-MAY-2000; 2000US-0580358.
XX XX
XX PA (TULLIS R H.
XX PA (STREIFEL J A.
XX XX
XX PI Tullis RH, Streifel JA;
XX XX
XX WP1; 2002-361176/39.
XX XX
XX PT Identifying and detecting nucleic acids, particularly DNA hybridization
XX PT probes, involves employing chain extending enzymes (e.g. telomerase) to
```

```
PT XX
XX PS Example 1; Page 5; 10pp; English.
XX CC
XX CC The present invention describes a method for detecting a nucleic acid
XX CC probe, which comprises using chain extending enzymes to elongate probes.
XX CC The method comprises: (a) treating the sample with a chain terminating
XX CC reagent to prevent polynucleotide chain growth from the nucleic acid in
XX CC the sample; (b) contacting the sample with the probe containing a
XX CC terminus capable of elongation by a chain extending enzyme, where the
XX CC probe hybridises to the nucleic acid in the sample; (c) contacting the
XX CC sample with a chain extending enzyme and its substrates, which elongates
XX CC the probe; and (d) detecting the elongated hybridised probe. Also
XX CC described is a method comprising: (a) treating nucleic acid molecules or
XX CC modified nucleic acids in a sample with a reagent or reagents that render
XX CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
XX CC (b) hybridising the treated molecules with a nucleic acid probe that
XX CC includes an extendable terminus, under conditions where hybrids form;
XX CC and (c) treating any hybrids formed with a non-template dependent chain
XX CC elongating enzyme and its substrates, where any hybridised probe is
XX CC extended. The method is useful for identifying and detecting nucleic
XX CC acids, particularly DNA hybridisation probes. The present sequence
XX CC represents a tailing reaction exemplary primer, which is used in an
XX CC example from the present invention.
XX CC Sequence 19 BP; 18 A; 0 C; 0 G; 1 U; 0 other;
XX SQ Query Match 1.5%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1084 AAAAAAAAAAAAAAAAAA 1100
XX DB 1 AAAAAAAAAAAAAAAAAA 17
XX
XX RESULT 322
XX ABA91949/c
XX ID ABA91949 standard; DNA; 19 BP.
XX AC ABA91949;
XX DT 23-MAY-2002 (first entry)
XX DE Methyl thioethyl modified oligonucleotide.
XX KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;
XX KW ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 16
XX FT /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "2'-methyl thioethyl thymidine"
XX PN modified_base 17
XX XX
XX PD modified_base 17
XX XX
XX FT modified_base 18
XX FT /mod_base= "OTHER"
XX FT /note= "2'-methyl thioethyl thymidine"
XX XX
XX FT modified_base 19
XX FT /*tag= d
XX FT /mod_base= "OTHER"
XX FT /note= "2'-methyl thioethyl thymidine"
XX XX
XX US6277982-B1.
XX PN
XX 21-AUG-2001.
XX PD
XX XX
```



PF 20-AUG-1999; 99US-0378665.  
 XX 20-AUG-1999; 99US-0378665.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
 XX WPI; 2002-235143/29.  
 XX Alkylation of alcohols, amines, or thiols, useful for preparing  
 PT nucleosides that are precursors for preparation of oligomeric compounds  
 PT beneficial as therapeutics, involves use of cyclic sulfate  
 PT intermediates -  
 XX Example 15; Column 35; 45pp; English.  
 XX The present sequence is that of a chimeric oligonucleotide having  
 CC some 2'-methyl thioethyl modifications. This was compared with  
 CC oligonucleotides with methoxyethoxy (see ABA91950) and  
 CC dimethylaminopropyl (see ABA91951) modifications for resistance to  
 CC snake venom phosphodiesterase. The assay revealed the nuclease  
 CC resistance of the modified oligomers. The invention provides  
 CC methods for the alkylation of alcohols, amines, thiols and their  
 CC derivatives by cyclic sulfate intermediates. In particular, methods  
 CC for the alkylation of the 2', 3' or 5'-hydroxy position of  
 CC nucleosides and their analogues with cyclic sulfates to form the  
 CC 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.  
 CC Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile  
 CC provides 2', 3' or 5'-O-modified nucleosides and their analogues.  
 CC The methods are especially useful for the preparation of  
 CC 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that  
 CC are precursors for the preparation of oligomeric compounds useful  
 CC as therapeutics, diagnostics and research reagents.  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 19 AAAAAAAAAAAAAAAAAA 3  
 RESULT 323  
 ABA91950/C  
 ID ABA91950 standard; DNA; 19 BP.  
 XX ABA91950;  
 AC 23-MAY-2002 (first entry)  
 XX Methoxyethoxy modified oligonucleotide.  
 DE 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;  
 XX ss.  
 KW Synthetic.  
 XX Key Location/Qualifiers  
 FH modified\_base 16  
 FT /\*tag= a  
 FT /mod\_base= "OTHER"  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 17  
 FT /\*tag= b  
 FT /mod\_base= "OTHER"  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 18  
 FT /\*tag= c  
 FT /mod\_base= "OTHER"

FT modified\_base 19  
 FT /\*tag= d  
 FT /mod\_base= "OTHER"  
 FT /note= "2'-methoxyethoxy thymidine"  
 XX US6277982-B1.  
 PN 21-AUG-2001.  
 XX 20-AUG-1999; 99US-0378665.  
 XX 20-AUG-1999; 99US-0378665.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
 XX WPI; 2002-235143/29.  
 XX Alkylation of alcohols, amines, or thiols, useful for preparing  
 PT nucleosides that are precursors for preparation of oligomeric compounds  
 PT beneficial as therapeutics, involves use of cyclic sulfate  
 PT intermediates -  
 XX Example 15; Column 35; 45pp; English.  
 XX The present sequence is that of a chimeric oligonucleotide having  
 CC some 2'-methoxyethoxy modifications. This was compared with  
 CC oligonucleotides with methyl thioethyl (see ABA91949) and  
 CC dimethylaminopropyl (see ABA91951) modifications for resistance to  
 CC snake venom phosphodiesterase. The assay revealed the nuclease  
 CC resistance of the modified oligomers. The invention provides  
 CC methods for the alkylation of alcohols, amines, thiols and their  
 CC derivatives by cyclic sulfate intermediates. In particular, methods  
 CC for the alkylation of the 2', 3' or 5'-hydroxy position of  
 CC nucleosides and their analogues with cyclic sulfates to form the  
 CC 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.  
 CC Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile  
 CC provides 2', 3' or 5'-O-modified nucleosides and their analogues.  
 CC The methods are especially useful for the preparation of  
 CC 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that  
 CC are precursors for the preparation of oligomeric compounds useful  
 CC as therapeutics, diagnostics and research reagents.  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;  
 SQ Query Match 1.5%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1084 AAAAAAAAAAAAAAAAAA 1100  
 DB 19 AAAAAAAAAAAAAAAAAA 3  
 RESULT 324  
 ABA91951/C  
 ID ABA91951 standard; DNA; 19 BP.  
 XX ABA91951;  
 AC 23-MAY-2002 (first entry)  
 XX Dimethylaminopropyl modified oligonucleotide.  
 DE 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy;  
 XX ss.  
 KW Synthetic.  
 XX Key Location/Qualifiers  
 FH modified\_base 16  
 FT /\*tag= a  
 FT /mod\_base= "OTHER"  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 17  
 FT /\*tag= b  
 FT /mod\_base= "OTHER"  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 18  
 FT /\*tag= c  
 FT /mod\_base= "OTHER"

```

FT FT /*tag= a
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 17
FT FT modified_base
FT FT /*tag= b
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 18
FT FT modified_base
FT FT /*tag= c
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
FT FT 19
FT FT modified_base
FT FT /*tag= d
FT FT /mod_base= "OTHER"
FT FT /note= "2'-dimethylaminopropyl thymidine"
XX XX
XX XX US6277982-B1.
XX XX
XX XX 21-AUG-2001.
XX XX
XX XX 20-AUG-1999; 99US-0378665.
XX XX
XX XX 20-AUG-1999; 99US-0378665.
XX XX
XX XX (ISIS-) ISIS PHARM INC.
XX XX
XX XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX XX WPI; 2002-235143/29.
XX XX
XX XX Alkylation of alcohols, amines, or thiols, useful for preparing
XX XX nucleosides that are precursors for preparation of oligomeric compounds
XX XX beneficial as therapeutics, involves use of cyclic sulfate
XX XX intermediates -
XX XX
XX XX Example 15; Column 35; 45pp; English.
XX XX
XX XX The present sequence is that of a chimeric oligonucleotide having
XX XX some 2'-dimethylaminopropyl modifications. This was compared with
XX XX oligonucleotides with methyl thioethyl (see ABA91949) and
XX XX methoxyethoxy (see ABA91950) modifications for resistance to
XX XX snake venom phosphodiesterase. The assay revealed the nuclease
XX XX resistance of the modified oligomers. The invention provides
XX XX methods for the alkylation of alcohols, amines, thiols and their
XX XX derivatives by cyclic sulfate intermediates. In particular, methods
XX XX for the alkylation of the 2', 3' or 5'-hydroxy position of
XX XX nucleosides and their analogues with cyclic sulfates to form the
XX XX 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed.
XX XX Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
XX XX provides 2', 3' or 5'-O-modified nucleosides and their analogues.
XX XX The methods are especially useful for the preparation of
XX XX 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates that
XX XX are precursors for the preparation of oligomeric compounds useful
XX XX as therapeutics, diagnostics and research reagents.
XX XX
XX XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX XX
XX XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
RESULT 325
AAK98526/c
ID AAK98526 standard; DNA; 19 BP.
XX
XX AAK98526;
XX
XX 16-APR-2002 (first entry)
DT

```

```

XX DE Nucleic acid quantitative analysis related oligonucleotide #1.
XX KW Target detection; quantitative analysis; probe; medical diagnosis;
XX KW forensics; bacterial screening; tissue typing; gene expression analysis;
XX KW genotyping; ss.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "modified by thiol"
XX XX
XX PN WO200202810-A2.
XX XX
XX PD 10-JAN-2002.
XX XX
XX XX 02-JUL-2001; 2001WO-EP07575.
XX XX
XX PR 01-JUL-2000; 2000DE-1033334.
XX XX
XX PA (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX XX
XX XX Bickel R, Ehrlich R, Ellinger T, Ermantraut E, Kaiser T, Schulz T;
XX XX Wagner G;
XX XX
XX DR WPI; 2002-154760/20.
XX XX
XX XX Determining targets by interaction with probe array, useful e.g. for
XX XX diagnosis, based on detecting formation of precipitate at specific
XX XX probe sites -
XX XX
XX PS Example 5; Page 47; 92pp; German.
XX XX
XX XX The present invention relates to a method for the qualitative and
XX XX quantitative detection of targets in a sample by molecular interaction
XX XX between the target and probes in an array. The method can be used to
XX XX detect interactions between nucleic acids, antigens and antibodies or
XX XX receptor and ligands, particularly in applications such as medical
XX XX diagnosis, forensic science, bacterial screening, tissue typing for
XX XX transplantation, monitoring gene expression, and genotyping. The present
XX XX sequence is a modifying oligonucleotide used in the exemplification of
XX XX the invention.
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 other;
XX XX
XX XX Query Match 1.5%; Score 17; DB 1; Length 19;
XX XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 AAAAAAAAAAAAAAAAAA 1100
Db 19 AAAAAAAAAAAAAAAAAA 3
RESULT 326
ABZ75398/c
ID ABZ75398 standard; DNA; 19 BP.
XX
XX AC ABZ75398;
XX XX
XX DT 07-MAY-2003 (first entry)
XX XX
XX DE Synthetic nuclease-resistant oligomeric compound #54.
XX KW Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers

```

FT	modified_base	19
FT	/*tag= a	
FT	/mod_base= "OTHER"	
FT	/note= "phenoxazine"	
XX		
XX		
PN	WO2003004602-A2.	
XX		
PD	16-JAN-2003.	
XX		
PF	01-JUL-2002; 2002WO-US20934.	
PR	03-JUL-2001; 2001US-302682P.	
PR	28-NOV-2001; 2001US-0996292.	
PR	10-DEC-2001; 2001US-0013295.	
XX		
XX	(ISIS-) ISIS PHARM INC.	
PA	Manoharan M, Maier MA, Prakash TP, Rajeev KG;	
PI	WPI; 2003-247768/25.	
DR		
XX	Nuclease-resistant oligomeric compound useful as pharmaceuticals for	
PT	topical administration such as transdermal patches -	
XX		
PS	Disclosure; Page 234; 234pp; English.	
XX		
CC	The invention relates to novel nuclease-resistant oligomeric compounds.	
CC	The compounds of the invention are useful as pharmaceuticals for topical	
CC	administration such as transdermal patches. The oligomeric compound is	
CC	resistant to enzymatic degradation. The sequences shown in	
CC	ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the	
CC	invention.	
XX		
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 other;	
PT		
PT	Nuclease-resistant oligomeric compound useful as pharmaceuticals for	
PT	topical administration such as transdermal patches -	
XX		
XX		
PS	Disclosure; Page 234; 234pp; English.	
XX		
CC	The invention relates to novel nuclease-resistant oligomeric compounds.	
CC	The compounds of the invention are useful as pharmaceuticals for topical	
CC	administration such as transdermal patches. The oligomeric compound is	
CC	resistant to enzymatic degradation. The sequences shown in	
CC	ABZ75345-ABZ75399 represent the nuclease-resistant compounds of the	
CC	invention.	
XX		
Query Match	1.5%; Score 17; DB 1; Length 19;	
Best Local Similarity	100.0%; Pred. No. 2e+02;	
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1084 AAAAAAAAAAAAAA 1100	
Db	18 AAAAAAAAAAAAAA 2	
RESULT 327		
ABZ75399/c		
ID	ABZ75399 standard; DNA; 19 BP.	
AC	ABZ75399;	
DT	07-MAY-2003 (first entry)	
XX		
DE	Synthetic nuclease-resistant oligomeric compound #55.	
XX		
KW	Nuclease resistant; ds; pharmaceutical; topical administration;	
KW	transdermal patch; enzymatic degradation resistant.	
OS	Synthetic.	
Key	Location/Qualifiers	
modified_base	19	
/*tag= a		
/mod_base= "OTHER"		
/note= "G-clamp modification"		
WO2003004602-A2.		
16-JAN-2003.		
01-JUL-2002; 2002WO-US20934.		
03-JUL-2001; 2001US-302682P.		
28-NOV-2001; 2001US-0996292.		

```

PA (ISIS-) ISIS PHARM INC.
XX
XX PI Prakash TP, Manoharan M;
XX WPI; 2003-239204/23.
XX
XX PT Increasing binding of oligomeric compound to proteins useful in
XX preparation of antisense therapeutics, involves use of modified
XX oligomeric compound having oligonucleotide group -
XX
XX PS Example 27; Page 72; 122pp; English.
XX
XX CC The present sequence is an example of an oligonucleotide of the
XX invention containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine
XX (2'-O-(MTE)-5-methyluridine) modifications. In examples of the
XX invention, 2'-O-MTE was incorporated into oligonucleotides and
XX evaluated for antisense properties in comparison with the known
XX 2'-O-(2-methoxyethyl) (2'-O-MOE) modification. The 2'-O-MTE
XX modified oligonucleotides exhibited similar binding affinity to
XX target RNA as their 2'-O-MOE equivalent while binding to human
XX serum albumin was improved. The modification can be used to
XX modulate the pharmacokinetics of oligonucleotides, e.g. in
XX antisense therapy.
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 329
AAQ25565/C
ID AAQ25565 standard; DNA; 20 BP.
XX
XX AC AAQ25565;
XX
XX DT 25-MAR-2003 (updated)
XX DT 02-DEC-1992 (first entry)
XX
XX DE Dye-coupled 3'-amino modified oligonucleotide.
XX
XX KW DNA synthesis; RNA; antisense strands; detection; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 20
XX /*tag= a
XX /*note= "3-amino modified"
XX
XX PN EP490281-A1.
XX
XX PD 17-JUN-1992.
XX
XX PF 06-DEC-1991; 91EP-0120935.
XX
XX PR 11-DEC-1990; 90DE-4039488.
XX
XX PA (FARH ) HOECHST AG.
XX
XX PI Engels J, Herrlein M, Konrad R, Mag M;
XX WPI; 1992-201578/25.
XX
XX PT New dye-coupled modified nucleosides, nucleotides and
XX oligonucleotides - useful for synthesis of antisense DNA and RNA
XX strands in presence of template, also for in-vivo and in-vitro
XX detection of genetic material
XX
XX PS Example; Page 9; 17pp; German.
XX
XX CC The sequence is an example of a dye coupled 3'-amino modified oligo-
XX nucleotide, it can be used in the synthesis of DNA and RNA
XX nucleosides, nucleotides and oligonucleotides and for the synthesis
XX of opposite strands in the presence of a template strand and in
XX fluorescence microscopic and macroscopic detection in vivo and in
XX vitro of genetic material. It is labelled with a fluorescent dye.
XX See also AAQ25566 and AAQ25567.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 other;

Query Match 1.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 AAAAAAAAAAAAAAAAAA 1100
DB 20 AAAAAAAAAAAAAAAAAA 4

RESULT 330
AAQ33554/C
ID AAQ33554 standard; DNA; 20 BP.
XX
XX AC AAQ33554;
XX
XX DT 25-MAR-2003 (updated)
XX DT 02-FEB-1993 (first entry)
XX
XX DE Microsatellite sequence from clone AGLA247.
XX
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX
XX OS Bos taurus.
XX
XX PN WO9213102-A1.
XX
XX PD 06-AUG-1992.
XX
XX PF 15-JAN-1992; 92WO-US00340.
XX
XX PR 15-JAN-1991; 91US-0642342.
XX
XX PA (GENM-) GENMARK.
XX
XX PI Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX PT Polymorphic bovine DNA markers - used in genetic identification,
XX gene mapping, and selective breeding
XX
XX PS Table 7; Page 150; 517pp; English.
XX
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between
XX 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
XX One out of 50 clones cross-hybridised. Assuming independent
XX distribution of microsatellites and MboI sites, the frequency of
XX (T6)n >9 microsatellites in the bovine genome is estimated at >100,
XX 000. The sequence information for ca. 230 such bovine microsatellites
XX is summarised in the specification and indexed herein (see below).
XX The sequences upstream and downstream of the microsatellite sequence
XX were used to generate the required PCR primers for in vitro
XX amplification of the corresp. microsatellite (using the program
XX OPTIPRIM). The microsatellites may be used to identify individuals,
XX for parentage testing, and in the genetic mapping of economic trait
XX loci, or genes involved the determinism of economically important
XX traits esp. in cattle, to allow selective breeding.

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